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From: Kaushal, Sumesh
Sent: Thursday, August 19, 2004 2:14 PM
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Subject: 10787382 : Sequence search

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10/787382 : Sequence search

Title: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC ACID MOLECULES, AND USES THEREOF

Inventor: YANG, SHUMIN

Please search

DNA

- SEQ ID NO: 4 length 610
- SEQ ID NO: 7 length 402
- SEQ ID NO: 9 length 345
- SEQ ID NO: 18 length 1658
- Oligosearch for SEQ ID NO: 18 -

PRT

- SEQ ID NO: 5 length 134
- SEQ ID NO: 10 length 115

S. Kaushal

AU1636, REM2.B85

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Searcher: _____
Searcher Phone: 2- _____
Date Searcher Picked up: 8/24/04
Date Completed: 9/1/04
Searcher Prep/Rev. Time: _____
Online Time: _____

Type of Search
NA Sequence: # _____
AA Sequence: # _____
Structure: # _____
Bibliographic: _____
Litigation: _____
Patent Family: _____
Other: _____

Vendors and cost where applicable
STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: 04/02p
WWW/Internet: _____
Other(Specify): _____

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 24, 2004, 23:40:07 ; Search time 96.8675 Seconds
(without alignments)
390.857 Million cell updates/sec

Title: US-10-787-382-5
Perfect score: 696
Sequence: 1 MRMLNLSLLALGAAYVSAP.....FLDYLVFLGVINTEWTPES 134

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	696	100.0	134	3	AA58219 Canine in
2	687	98.7	134	4	AA72615 Canine in
3	610	87.6	115	3	AA58220 Canine ma
4	536	77.0	132	2	AAW08479 Ovine IL-
5	430	61.8	134	2	AA92802 Human int
6	430	61.8	134	4	AA72617 Human int
7	430	61.8	134	5	ABG94294 Human int
8	430	61.8	134	5	ABG80606 Human pre
9	430	61.8	134	5	AAU10353 Interleuk
10	430	61.8	285	6	AAO30457 hIL5-P30-
11	430	61.8	285	6	AAO30458 hIL5-P2-P
12	429	61.6	84	4	AA72616 Canine in
13	426	61.2	134	5	AAU10354 Interleuk
14	420	60.3	134	1	AP81056 Sequence
15	415.5	59.7	287	6	AAO30460 hIL5.37 v
16	413.5	59.4	287	6	AAO30459 hIL5.36 v
17	376	54.0	133	1	AA71064 Murine eo
18	376	54.0	133	2	AA96963 T cell re
19	376	54.0	133	2	AAW72949 T cell re
20	376	54.0	133	2	AAW72947 T cell re
21	376	54.0	133	2	AAW72618 Murine in
22	375	53.9	133	1	AP82969 B cell di
23	359	51.6	136	5	ABG94352 Human C-I
24	359	51.6	136	5	ABG80664 Human ILn
25	357	51.3	113	1	AA993152 Sequence

26	357	51.3	123	5	ABG94353 Human C-I
27	357	51.3	123	5	ABG80665 Human IL-
28	357	51.3	138	5	ABG94351 Human C-I
29	357	51.3	138	5	ABG80663 Human ILn
30	356	51.1	112	1	AA80279 Pleiotrop
31	356	51.1	115	1	AA81038 Sequence
32	356	51.1	115	3	AA845489 Human int
33	356	51.1	115	5	ABG94295 Human mat
34	356	51.1	115	5	ABG80607 Human mat
35	356	51.1	115	5	AAO30453 Human mat
36	355	51.0	133	1	AA80280 Murine pl
37	351	50.4	121	2	AAW43436 Human int
38	347	49.9	115	2	AAW05273 N-termina
39	347	49.9	115	2	AAW72948 Truncated
40	347	49.9	134	5	ABG94349 Mouse C-I
41	347	49.9	134	5	ABG80661 Mouse IL-
42	344	48.4	136	5	ABG94348 Mouse C-I
43	344	49.4	136	5	ABG80660 Mouse IL-
44	343	49.3	113	2	AAW05274 N-termina
45	343	49.3	113	5	ABG94296 Mouse int

ALIGNMENTS

RESULT 1
AA58219
ID AA58219 standard; protein; 134 AA.
XX
AC AA58219;
XX
DT 14-MAR-2000 (first entry)
XX
DE Canine interleukin-5 (IL-5).
XX
KW Interleukin-5; IL-5; antibody; canine; inhibitor; immune response;
KW immunoregulation; tumour; cancer; autoimmune disease; vaccine.
XX
OS Canis familiaris.
XX
PN WO9961618-A2.
XX
PD 02-DEC-1999.
XX
PF 28-MAY-1999; 99WO-US011942.
XX
PR 29-MAY-1998; 98US-0087306P.
XX
(HESK-) HESKA CORP.
XX
PI Sim G, Yang S, Dreitz MJ, Wonderling RS;
XX
DR WPI; 2000-072623/06.
DR N-PSDB; AA255546, AA255547, AA255548, AA255549.
PT Nucleic acids encoding immunoregulatory proteins from cats or dogs,
XX useful for treating or preventing e.g. tumors or autoimmune disease.
XX
PS Claim 3h; Page 224; 264pp; English.
XX
CC Sequences AA58219-Y58220 represent encoded and mature canine interleukin
CC -5 (IL-5). The invention relates to canine IL-4, canine or feline Flt-3
CC ligand, canine or feline CD40, canine or feline CD154 (CD40 ligand),
CC canine IL-5, canine IL-13, feline interferon-alpha (IFN-alpha) and feline
CC granulocyte macrophage colony-stimulating factor (GM-CSF), and nucleotides
CC which encode these immunoregulatory proteins. The proteins, their
CC associated nucleic acids, specific antibodies and inhibitors may be used
CC as vaccines for therapeutic or prophylactic regulation of an immune
CC response in animals (particularly cats, dogs, horses and humans). They
CC may be used to treat autoimmune or infectious diseases including
CC allergic tumours, inflammation and graft rejection, and to increase the
CC response from a co-administered antigen. The nucleotide sequences can
CC also be used for the recombinant production of a protein, while

CC nucleotide fragments are useful as probes, as amplification primers and
 CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).
 CC The proteins may be used to raise antibodies and to screen for modulators
 CC of activity, while the antibodies may be used in detection, and in drug
 CC targeting
 XX
 SQ Sequence 134 AA;

Query Match 100.0%; Score 696; DB 3; Length 134;
 Best Local Similarity 100.0%; Pred. No. 6.8e-75;
 Matches 134; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRMLNLSLLALGAAYVSAPAVENPMNLVAETLLTLLSTHRTWLIGDGNLMPTPENKXH 60
 DB 1 MRMLNLSLLALGAAYVSAPAVENPMNLVAETLLTLLSTHRTWLIGDGNLMPTPENKXH 60
 QY 61 QLCIKEVFGQIDTLKQNTAHEAVDKLFQNLSLIKEHIEROKKRCAGRWRTKFLDYLO 120
 DB 61 QLCIKEVFGQIDTLKQNTAHEAVDKLFQNLSLIKEHIEROKKRCAGRWRTKFLDYLO 120
 QY 121 VFLGVINTEWTPES 134
 DB 121 VFLGVINTEWTPES 134

RESULT 2
 AAB72615
 ID AAB72615 standard; protein; 134 AA.

XX AAB72615;

DT 04-MAY-2001 (first entry)

DE Canine interleukin-5 protein #1.

KW Dog; interleukin-5; IL-5; allergy; cancer; gene therapy;
 KW inflammatory reaction.

XX Canis sp.

OS WO200111049-A2.

FN 15-FEB-2001.

PF 09-AUG-2000; 2000WO-US021651.

PR 10-AUG-1999; 99US-00371615.

XX (IDEX-) IDEXX LAB INC.

PI Guo H, Lawton R, Mermer B, Aiyappa AP;

XX WPI; 2001-191542/19.

DR N-PSDB; AAF74300.

XX Novel canine interleukin 5 polynucleotide and polypeptides are used for
 XX generating antibodies which are useful in treating allergies in dogs.

PT Claim 29; Page 46-47; 48pp; English.

XX The present invention provides the protein and coding sequences of the
 CC canine interleukin-5 (IL-5) protein. This can be used to treat allergies,
 CC cancer and inflammatory reactions in dogs. The present sequence is one
 CC version of the IL-5 protein shown in the specification
 XX

SQ Sequence 134 AA;

Query Match 98.7%; Score 687; DB 4; Length 134;
 Best Local Similarity 99.3%; Pred. No. 8.2e-74;
 Matches 133; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MRMLNLSLLALGAAYVSAPAVENPMNLVAETLLTLLSTHRTWLIGDGNLMPTPENKXH 60

DB 1 MRMLNLSLLALGAAYVSAPAVENPMNLVAETLLTLLSTHRTWLIGDGNLMPTPENKXH 60
 QY 61 QLCIKEVFGQIDTLKQNTAHEAVDKLFQNLSLIKEHIEROKKRCAGRWRTKFLDYLO 120
 DB 61 QLCIKEVFGQIDTLKQNTAHEAVDKLFQNLSLIKEHIEROKKRCAGRWRTKFLDYLO 120
 QY 121 VFLGVINTEWTPES 134
 DB 121 VFLGVINTEWTPES 134

RESULT 3

AA58220

ID AA58220 standard; protein; 115 AA.

XX AA58220;

AC AA58220;

XX 14-MAR-2000 (first entry)

DE Canine mature interleukin-5 (IL-5).

XX Interleukin-5; IL-5; antibody; canine; inhibitor; immune response;

KW immunoregulation; tumour; cancer; autoimmune disease; vaccine.

XX Canis familiaris.

OS WO9961618-A2.

PN 02-DEC-1999.

XX 28-MAY-1999; 99WO-US011942.

XX 29-MAY-1998; 98US-0087306P.

PA (HESK-) HESKA CORP.

XX Sim G, Yang S, Dreitz MJ, Wonderling RS;

XX WPI; 2000-072623/06.

DR N-PSDB; AA555550, AA555551.

XX Nucleic acids encoding immunoregulatory proteins from cats or dogs,
 XX useful for treating or preventing e.g. tumors or autoimmune disease.

PT Claim 3h; Page 227; 264pp; English.

XX Sequences AA58219-Y58220 represent encoded and mature canine interleukin
 CC -5 (IL-5). The invention relates to canine IL-4, canine or feline Flt-3
 CC ligand, canine or feline CD40, canine or feline CD154 (CD40 ligand),
 CC canine IL-5, canine IL-13, feline interferon-alpha (IFN-alpha) and feline
 CC granulocyte macrophage colony-stimulating factor (GM-CSF), and nucleotides
 CC which encode these immunoregulatory proteins. The proteins, their
 CC as vaccines for therapeutic or prophylactic regulation of an immune
 CC response in animals (particularly cats, dogs, horses and humans). They
 CC may be used to treat autoimmune or infectious diseases including
 CC allergies, tumours, inflammation and graft rejection, and to increase the
 CC response from a co-administered antigen. The nucleotide sequences can
 CC also be used for the recombinant production of a protein, while
 CC nucleotide fragments are useful as probes, as amplification primers and
 CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).
 CC The proteins may be used to raise antibodies and to screen for modulators
 CC of activity, while the antibodies may be used in detection, and in drug
 CC targeting
 XX

SQ Sequence 115 AA;

Query Match 87.6%; Score 610; DB 3; Length 115;
 Best Local Similarity 100.0%; Pred. No. 1.1e-64;
 Matches 115; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 PAVENPMNLVAETLLTLLSTHRTWLIGDGNLMPTPENKXHOLCIKEVFGQIDTLKNOTA 79

Db 1 FAVENPMRLVAETLLTLLSTHRTWLIGDGNLMIPTPENKNHQLCIKEVFOGIDTLKNQTA 60
 Qy 80 HGEAVDKLFQNLSLIKHEHIERQKRCAGRWRTKFLDYLOVFLGVINTEWTPES 134
 Db 61 HGEAVDKLFQNLSLIKHEHIERQKRCAGRWRTKFLDYLOVFLGVINTEWTPES 115

RESULT 4
 ID AAW08479 standard; protein; 132 AA.
 XX AAW08479;
 AC AAW08479;
 XX AAW08479;
 DT 17-OCT-2003 (revised)
 DT 24-SEP-1997 (first entry)
 XX XX
 DE Ovine IL-5.
 XX Cytokine; ovine; sheep; interleukin-5; interleukin-12; IL-5; IL-12;
 KW livestock; cow; stress; transport; vaccine adjuvant; veterinary; cancer;
 KW immunosuppression; allergy; reproductive system; growth; early maturity;
 KW antibody; diagnosis; immunopotentiator;
 KW early haematopoietic progenitor cell; cytotoxic cell; thymocyte;
 KW secretion; IgM; IgA; bacterial endotoxin; gamma-interferon.
 XX OS Ovis aries.
 XX WO9700321-A1.
 XX XX
 XX 03-JAN-1997.
 XX XX
 XX 14-JUN-1996; 96WO-AU000360.
 XX XX
 XX 14-JUN-1995; 95AU-00003502.
 PR 27-OCT-1995; 95AU-00006244.
 XX XX
 XX (CSIR) COMMONWEALTH SCI & IND RES ORG.
 XX XX
 XX Seow H, Wood P;
 PI WPI; 1997-077528/07.
 DR N-PSDB; AAT50755; AAT50756.
 XX XX
 XX Nucleic acid encoding ovine interleukin-5 or -12 - used as vaccine
 PT adjuvants and to treat or prevent microbial infections in livestock.
 PT XX
 FS Claim 31; Page 39-40; 78pp; English.

CC This protein sequence represents ovine interleukin-5 (IL-5). Ovine IL-5
 CC or IL-12 are used to treat and/or prevent infections in livestock (esp.
 CC cows and sheep). Particularly where the animals are stressed, e.g. during
 CC transport, IL-5 and IL-12 can also be used as adjuvants in vaccines for
 CC veterinary use (partic. weakly immunogenic subunit or synthetic peptide
 CC vaccines). They may also be used to treat cancer, immunosuppression and
 CC allergy, to enhance/suppress the reproductive system and to promote
 CC growth or early maturity. Optionally interleukin can be delivered from
 CC constructs or delivery cells and antibodies are useful in enzyme
 CC immunoassays for rapid diagnosis of infection. The interleukins are
 CC immunopotentiators, especially IL-5 promotes growth of early
 CC haematopoietic progenitor cells and generation of cytotoxic cells from
 CC thymocytes, also it stimulates production and secretion of IgM and IgA
 CC (in synergism with bacterial endotoxin). IL-12 induces production of
 CC gamma-interferon by, and proliferation of, T and NK cells and increases
 CC the (non-)specific cytolytic lymphocyte response. The genetic constructs
 CC can also be used for in vitro production of IL-5 or -12. (Updated on 17-
 CC OCT-2003 to standardise OS field)
 XX XX
 SQ Sequence 132 AA;

Query Match 77.0%; Score 536; DB 2; Length 132;
 Best Local Similarity 78.8%; Pred. No. 9.6e-56;
 Matches 104; Conservative 15; Mismatches 13; Indels 0; Gaps 0;

Qy 3 MLNLNLSLLAAGAAVVSFAVENPMRLVAETLLTLLSTHRTWLIGDGNLMIPTPENKNHOL 62
 Db 1 MHLRLTLVALGAAYVCANAVESTMRLVAETLLTLLSTHRTWLIGDGNLMIPTPQHTNHL 60
 Qy 63 CIKEVFOGIDTLKNQTAHGEAVDKLFQNLSLIKHEHIERQKRCAGRWRTKFLDYLOVFL 122
 Db 61 CIEEVFOGIDTLKNQTAOGDAVKKIFRNLSLIKEDYDQKRCGGERWRVQFLDYLOVFL 120

Qy 123 LGVINTEWTPES 134
 Db 121 LGVINTEWTPES 132

RESULT 5
 ID AAR92802 standard; protein; 134 AA.
 XX AAR92802;
 AC AAR92802;
 XX AAR92802;
 DT 24-MAY-1996 (first entry)
 XX XX
 DE Human interleukin-5.
 XX Cytokine; mutein; interleukin-5; agonist; antagonist; diagnosis; therapy;
 KW cancer; inflammation; degenerative disease.
 XX OS Homo sapiens.
 XX WO9604306-A2.
 XX 15-FEB-1996.
 XX 31-JUL-1995; 95WO-US008950.
 PR 01-AUG-1994; 94US-00284393.
 XX XX
 XX (SCHE) SCHERING CORP.
 XX Zurawski SM, Zurawski G;
 PI WPI; 1996-129335/13.
 DR Mutein(s) of human and murine cytokine(s), esp. interleukin(s) and murine
 PT P600 contg. amino acid substitutions. - useful for the diagnosis and
 PT treatment of cancer, inflammation, etc.
 XX XX
 PS Disclosure; Page 43; 52pp; English.

CC Muteins of human interleukin-5 (AAR92802) and other cytokines (see also
 CC AAR92790-801) are obtd. by site-directed mutagenesis of natural cytokine
 CC sequences at positions identified as critical for activity. The muteins
 CC are useful in the screening of cytokine and cytokine receptor levels, and
 CC in the diagnosis or treatment of e.g. inflammation, cancer, and
 CC degenerative disorders
 XX XX
 SQ Sequence 134 AA;

Query Match 61.8%; Score 430; DB 2; Length 134;
 Best Local Similarity 64.9%; Pred. No. 4.8e-43;
 Matches 87; Conservative 17; Mismatches 30; Indels 0; Gaps 0;

Qy 1 MRMLNLSLLAAGAAVVSFAVENPMRLVAETLLTLLSTHRTWLIGDGNLMIPTPENKNH 60
 Db 1 MRMLNLSLLAAGAAVVSFAVENPMRLVAETLLTLLSTHRTWLIGDGNLMIPTPENKNH 60

Qy 61 QICKEVFOGIDTLKNQTAHGEAVDKLFQNLSLIKHEHIERQKRCAGRWRTKFLDYLOV 120
 Db 61 QJCTEEIFOGITLESQTVGGTVERLFLNLSLNKYIDGQKKCGEERRVNFQFLDYLO 120

Qy 121 VFGLVINTEWTPES 134
 Db 121 EFLGVNTEWTPES 134

```

RESULT 6
AAB72617
ID AAB72617 standard; protein; 134 AA.
AC
XX AAB72617;
XX
DT 04-MAY-2001 (first entry)
XX
DE Human interleukin-5.
XX
XX Dog; interleukin-5; IL-5; allergy; cancer; gene therapy;
KW inflammatory reaction; human.
XX
OS Homo sapiens.
XX
PI WO200111049-A2.
XX
PD 15-FEB-2001.
XX
PF 09-AUG-2000; 2000WO-US021651.
XX
PR 10-AUG-1999; 99US-00371615.
XX
PA (INDEX-) IDEXX LAB INC.
XX
PI Guo H, Lawton R, Mermer B, Aiyappa AP;
XX
DR WPI; 2001-191542/19.
XX
XX Novel canine interleukin 5 polynucleotide and polypeptides are used for
PT generating antibodies which are useful in treating allergies in dogs.
XX
XX Disclosure; Fig 2; 48pp; English.
XX
CC The present invention provides the protein and coding sequences of the
CC canine interleukin-5 (IL-5) protein. This can be used to treat allergies,
CC cancer and inflammatory reactions in dogs. The present sequence is human
CC IL-5
XX
XX Sequence 134 AA;
XX
Query Match 61.8%; Score 430; DB 4; Length 134;
Best Local Similarity 64.9%; Pred. No. 4.8e-43;
Matches 87; Conservative 17; Mismatches 30; Indels 0; Gaps 0;
Qy 1 MRMLNLISLLALGAAYVSFAVENPMNRLVAETLTLLSTHRTWLIGDGNLMIPTPENKXH 60
Db 1 MRMLHLISLLALGAAYVTAIPTPTISALVKETLALLSTHRTLLIANETLRIPVPVHKH 60
Qy 61 QLCIKVEFGQIDTLKNOTAHGEAVDKLFQNLISLKEHIERQKRCACGERWRVTKFLDYLQ 120
Db 61 QLCTEEIFQGGIGTLESQTVGGTVERLFKNLSLIKVIYDQKKKGERRRVNQFLDYLQ 120
Qy 121 VFLGVINTEWTPES 134
Db 121 EFLGVMNTEWIIES 134
RESULT 7
ABG94294
ID ABG94294 standard; protein; 134 AA.
XX
AC ABG94294;
XX
XX 10-DEC-2002 (first entry)
XX
DE Human interleukin 5 precursor protein.
XX
XX Human; mouse; rat; antimicrobial; antiallergic; immunomodulatory;
KW cytosolic; antiviral; antidiabetic; hypoglycaemic; antigen array;
KW vaccine; infectious disease.
XX
XX
OS Homo sapiens.
XX
PI WO200256905-A2.
XX
PD 25-JUL-2002.
XX
PF 21-JAN-2002; 2002WO-IB000166.
XX
PR 19-JAN-2001; 2001US-0262379P.
XX
PR 04-MAY-2001; 2001US-0288549P.
XX
PR 05-OCT-2001; 2001US-0326998P.
XX
PR 07-NOV-2001; 2001US-0331045P.
XX
PA (CYTO-) CYTOS BIOTECHNOLOGY AG.
XX
XX Renner WA, Bachmann M, Tissot A, Maurer P, Lechner F, Sebbel P;
PI Piossek C;
XX
XX WPI; 2002-627351/67.
XX
XX Molecular antigen array used in the production of vaccines for infectious
PT diseases.
XX
PS Disclosure; Page 422; 441pp; English.
XX
CC This invention relates to a novel ordered and repetitive antigen array
CC used in the production of vaccines for infectious diseases. The invention
CC also discloses a composition comprising a non-natural molecular scaffold
CC comprising a core particle selected from a core particle of a non-natural
CC origin and a core particle of natural origin and an organiser comprising
CC at least one first attachment site, where the organiser is connected to
CC the core particle by at least one covalent bond. Also disclosed is an
CC antigen or antigenic determinant with at least one second attachment
CC site, where the antigen or antigenic determinant is amyloid beta peptide
CC (Abeta1-42) or its fragment and where the second attachment site is a
CC selected from an attachment site not naturally occurring with the antigen
CC or antigenic determinant and an attachment site naturally occurring with
CC the antigen or antigenic determinant, where the second attachment site is
CC capable of association through at least one non-peptide bond to the first
CC attachment site and where the antigen or antigenic determinant and the
CC scaffold interact through the association to form an ordered and
CC repetitive antigen array. The invention also comprises a coat protein
CC capable of forming a capsid which comprises mutant beta coat proteins
CC having an amino acid sequence selected from five amino acid sequences
CC fully defined in the specification. The compounds of the invention may
CC have antimicrobial, antiallergic, immunomodulatory, cytostatic,
CC antiviral, antidiabetic, or hypoglycaemic activities and may be used in
CC immunisation and as a vaccine. The present sequence represents a protein
CC sequence used to create the compositions of the invention
XX
XX Sequence 134 AA;
XX
Query Match 61.8%; Score 430; DB 5; Length 134;
Best Local Similarity 64.9%; Pred. No. 4.8e-43;
Matches 87; Conservative 17; Mismatches 30; Indels 0; Gaps 0;
Qy 1 MRMLNLISLLALGAAYVSFAVENPMNRLVAETLTLLSTHRTWLIGDGNLMIPTPENKXH 60
Db 1 MRMLHLISLLALGAAYVTAIPTPTISALVKETLALLSTHRTLLIANETLRIPVPVHKH 60
Qy 61 QLCIKVEFGQIDTLKNOTAHGEAVDKLFQNLISLKEHIERQKRCACGERWRVTKFLDYLQ 120
Db 61 QLCTEEIFQGGIGTLESQTVGGTVERLFKNLSLIKVIYDQKKKGERRRVNQFLDYLQ 120
Qy 121 VFLGVINTEWTPES 134
Db 121 EFLGVMNTEWIIES 134
RESULT 8
ABG80606
ID ABG80606 standard; protein; 134 AA.
XX
XX

```

AC ABG80606;
 XX
 DT 29-NOV-2002 (first entry)
 XX
 DE Human precursor Interleukin 5.
 XX
 KW Molecular antigen array; vaccine; antigen; antimicrobial;
 KW molecular scaffold; amyloid beta; Abeta 1-42; influenza;
 KW graft versus host disease; IGE-mediated allergic reaction; anaphylaxis;
 KW adult respiratory distress syndrome; ARDS; Crohn's disease;
 KW allergic asthma; acute lymphoblastic leukaemia; non-Hodgkin's lymphoma;
 KW Grave's disease; systemic lupus erythematosus; osteoporosis;
 KW inflammatory immune disease; myasthenia gravis; multiple sclerosis;
 KW immunoproliferative disease lymphadenopathy; Alzheimer's disease;
 KW angioimmunoproliferative lymphadenopathy; immunoblastic lymphadenopathy;
 KW rheumatoid arthritis; diabetes; infectious disease; factor Xa;
 KW enterokinase; cysteine-containing linker.
 XX
 OS Homo sapiens.
 XX
 XX WO200256907-A2.
 XX
 PD 25-JUL-2002.
 XX
 PP 21-JAN-2002; 2002WO-IB000168.
 XX
 PR 19-JAN-2001; 2001US-0262379P.
 PR 04-MAY-2001; 2001US-0288549P.
 PR 05-OCT-2001; 2001US-0326998P.
 PR 07-NOV-2001; 2001US-0331045P.
 XX
 XX (CYTO-) CYTOS BIOTECHNOLOGY AG.
 PA (NOVS) NOVARTIS PHARMA AG.
 PA (MAUR) MAURER P.
 PA (LECH) LECHNER F.
 PA (ORTM) ORTMANN R.
 PA (LUEO) LUEOEND R.
 PA (STAU) STAUFENBIEL M.
 PA (FREY) FREY P.
 XX
 PI Maurer P, Lechner F, Ortmann R, Lueoend R, Staufenbiel M, Frey P;
 PI Renner WA, Bachmann M, Tissot A, Sebbel P, Piossek C;
 XX
 XX WPI; 2002-636514/68.
 DR
 XX
 PT Molecular antigen array used in the production of vaccines for infectious
 PT diseases.
 XX
 PS Disclosure; Page 399; 418pp; English.
 XX
 CC The invention relates to a composition comprising: (a) a non-natural
 CC molecular scaffold comprising: (i) a core particle selected from: (1) a
 CC core particle of a non-natural origin; and (2) a core particle of natural
 CC origin; and (ii) an organiser comprising at least one first attachment
 CC site, where the organiser is connected to the core particle by at least
 CC one covalent bond; (b) an antigen or antigenic determinant with at least
 CC one second attachment site, where the antigen or antigenic determinant is
 CC amyloid beta peptide (Abeta 1-42) or its fragment, and where the second
 CC attachment site is selected from: (i) an attachment site not naturally
 CC occurring with the antigen or antigenic determinant; and (ii) an
 CC attachment site naturally occurring with the antigen or antigenic
 CC determinant, where the second attachment site is capable of association
 CC through at least one non-peptide bond to the first attachment site; and
 CC where the antigen or antigenic determinant and the scaffold interact
 CC through the association to form an ordered and repetitive antigen array.
 CC Also included is a process for producing a non-naturally occurring
 CC ordered and repetitive antigen array. The composition is used in
 CC immunisation and as a vaccine for diseases such as influenza, graft
 CC versus host disease, IGE-mediated allergic reactions, anaphylaxis, adult
 CC respiratory distress syndrome (ARDS), Crohn's disease, allergic asthma,
 CC acute lymphoblastic leukaemia, non-Hodgkin's lymphoma, Grave's disease,
 CC systemic lupus erythematosus, inflammatory immune diseases, myasthenia
 CC gravis, immunoproliferative disease lymphadenopathy.

CC angioimmunoproliferative lymphadenopathy, immunoblastic lymphadenopathy,
 CC rheumatoid arthritis, diabetes, multiple sclerosis, Alzheimer's disease,
 CC osteoporosis and infectious diseases. The present sequence is an antigen
 CC for use in the array of the invention. The antigen is modified to possess
 CC a cleavage site (enterokinase or factor Xa) and a cysteine- containing N-
 CC or C-terminal linker peptide which serves as the attachment point to a
 CC virus like particle or bacterial protein (the scaffold protein)
 XX
 SQ Sequence 134 AA;
 Query Match 61.8%; Score 430; DB 5; Length 134;
 Best Local Similarity 64.9%; Pred. No. 4.8e-43;
 Matches 87; Conservative 17; Mismatches 30; Indels 0; Gaps 0;
 QY 1 MEMLNLSLLALGAAYVSFAFVPMNRLVAETLLSTHRTWLTGDNLMIPDENKH 60
 DB 1 MEMLNLSLLALGAAYVSFAFVPMNRLVAETLLSTHRTWLTGDNLMIPDENKH 60
 QY 61 QLCIXEVFGIDTTLKNQTAHGEAVDKLPQNLSLKEHIEROKRCAGRWYTKFDLYLQ 120
 DB 61 QLCITEIFQIGTLESQTVGGTVLRFNLSLIKYYIDGKKKGGEERRVNOFLDYLQ 120
 QY 121 VFLGVINTEWTPES 134
 DB 121 EFLGVNTEWIES 134
 RESULT 9
 AAU10353
 ID AAU10353 standard; protein; 134 AA.
 XX AC AAU10353;
 XX DT 14-FEB-2002 (first entry)
 XX DE Interleukin 5 (IL5).
 XX KW Human; interleukin 5; IL5; antiinflammatory; antiasthmatic; asthma;
 XX KW haplotyping; inflammatory disorder.
 XX OS Homo sapiens.
 XX PN WO200177132-A2.
 XX PD 18-OCT-2001.
 XX PF 11-APR-2001; 2001WO-US012011.
 XX PR 11-APR-2000; 2000US-0196250P.
 XX (GENA-) GENAISSANCE PHARM INC.
 XX Bentivegna SC, Chew A, Choi JY, Denton RR, Kazemi A;
 XX Nandabalan K, Parks KE;
 XX WPI; 2002-041289/05.
 XX DR N-PSDB; AAS15002.
 XX PT New haplotypes of the human interleukin 5 gene, useful to diagnose and
 XX treat diseases associated with the gene including inflammatory disorders
 XX such as asthma.
 XX Claim 27; Fig 3; 65pp; English.
 CC The invention relates to haplotyping the human interleukin 5 (IL5) gene
 CC of an individual, comprising determining if the individual has one of the
 CC IL5 haplotypes or haplotype pairs fully defined in the specification.
 CC Haplotyping the IL5 gene of an individual, comprises determining the
 CC identity of the nucleotide at two or more polymorphic sites in one copy
 CC of the gene. The method also involves identifying an association between
 CC a trait and a haplotype or haplotype pair of the IL5 gene, comprising
 CC comparing the frequency of the haplotype/pair in a population exhibiting
 CC the trait with that of a reference population. A higher frequency in the

CC trait population indicates the trait is associated with the haplotype.
 CC The polynucleotides and screened compounds are useful to develop
 CC treatment for diseases associated with IL-5 activity including
 CC inflammatory disorders such as asthma. The present sequence represents
 CC the amino acid sequence of interleukin 5 (IL5) as described in the method
 CC of the invention
 CC
 XX Sequence 134 AA;

Query Match 61.8%; Score 430; DB 5; Length 134;
 Best Local Similarity 64.9%; Pred. No. 4.8e-43;
 Matches 87; Conservative 17; Mismatches 30; Indels 0; Gaps 0;
 QY 1 MRMLNLISLLALGAAYVSFAFVAVENPMRLVAETLLTSLTHRTWLGDNLMIPTEPKNH 60
 Db 1 MRMLHLISLLALGAAYVVAIPTPTSAVKETLALLSTHRTLLIANETLRIPVVKNH 60
 QY 61 QLCIKVFGQIDTLKNTAHGEAVDKLPQNLISLKEHIERQKRCAGERRVTKFLDYQLQ 120
 Db 61 QLCTEEIPIQIGTLESQTVQGGTVERLFKNLSLTKKYIDGQKKCGERRRVNQFLDYQLQ 120
 QY 121 VFLGVINTEWTPES 134
 Db 121 EFLGVMNTEWIES 134

RESULT 10
 AAO30457
 ID AAO30457 standard; protein; 285 AA.

XX AC AAO30457;
 XX DT 22-SEP-2003 (first entry)
 XX DE hIL5-P30-P2-hIL5 (hIL5.34) fusion construct protein.
 XX KW Multimeric protein; interleukin 5; IL5; TNFalpha; inflammatory disease;
 KW tumour necrosis factor alpha; gene therapy; arthritis; interleukin 5;
 KW IL5; epitope; human; tetanus toxoid; chimeric.

OS Homo sapiens.
 OS Unidentified.
 OS Chimeric.
 XX FH Key Location/Qualifiers
 FT Peptide 1..19
 FT Protein /note= "Human IL5 leader peptide"
 FT /note= "Mature hIL5.34 protein"

XX WO2003042244-A2.
 XX PD 22-MAY-2003.
 XX PF 15-NOV-2002; 2002WO-DK000764.
 XX PR 16-NOV-2001; 2001DK-00001702.
 XX PR 16-NOV-2001; 2001US-0331575P.

XX (PHAR-) PHARMEXA AS.
 XX PA (KLYS/) KLYSNER S.
 XX PA (NIEL/) NIELSEN F S.
 XX PA (BRAT/) BRATT T.
 XX PA (VOLD/) VOLDBORG B.
 XX PA (MOUR/) MOURITSEN S.
 XX Klysner S, Nielsen FS, Bratt T, Voldborg B, Mouritsen S;
 XX WPI; 2003-449558/42.
 XX DR N-PSDB; AAL61293.

XX New immunogenic analogue of a polymeric protein, useful for preparing a
 PT composition for treating inflammatory diseases e.g. arthritis.

XX Claim 20; Page 109-110; 196pp; English.
 XX The invention relates to immunogenic analogues of multimeric proteins
 CC such as immunogenic variants of interleukin 5 (IL5) and tumour necrosis
 CC factor alpha (TNF, TNFalpha) and methods for production of immunogenic
 CC analogues. The immunogenic analogue is useful for preparing a composition
 CC for treating inflammatory diseases, e.g., arthritis. It is also used in
 CC gene therapy. The present sequence is a fusion construct which comprises
 CC 2 human interleukin 5 (IL5) monomers joined by tetanus toxoid epitopes
 CC P30 and P2. This sequence is used to illustrate the method of the
 CC invention

XX Sequence 285 AA;

Query Match 61.8%; Score 430; DB 6; Length 285;
 Best Local Similarity 64.9%; Pred. No. 1.5e-42;
 Matches 87; Conservative 17; Mismatches 30; Indels 0; Gaps 0;
 QY 1 MRMLNLISLLALGAAYVSFAFVAVENPMRLVAETLLTSLTHRTWLGDNLMIPTEPKNH 60
 Db 1 MRMLHLISLLALGAAYVVAIPTPTSAVKETLALLSTHRTLLIANETLRIPVVKNH 60
 QY 61 QLCIKVFGQIDTLKNTAHGEAVDKLPQNLISLKEHIERQKRCAGERRVTKFLDYQLQ 120
 Db 61 QLCTEEIPIQIGTLESQTVQGGTVERLFKNLSLTKKYIDGQKKCGERRRVNQFLDYQLQ 120
 QY 121 VFLGVINTEWTPES 134
 Db 121 EFLGVMNTEWIES 134

RESULT 11
 AAO30458

ID AAO30458 standard; protein; 285 AA.

XX AC AAO30458;
 XX DT 22-SEP-2003 (first entry)
 XX DE hIL5-P2-P30-hIL5 (hIL5.35) fusion construct protein.
 XX KW Multimeric protein; interleukin 5; IL5; TNFalpha; inflammatory disease;
 KW tumour necrosis factor alpha; gene therapy; arthritis; interleukin 5;
 KW IL5; epitope; human; tetanus toxoid; chimeric.

OS Homo sapiens.
 OS Unidentified.
 OS Chimeric.

XX FH Key Location/Qualifiers
 FT Peptide 1..19
 FT Protein /note= "Human IL5 leader peptide"
 FT /note= "Mature hIL5.35 protein"

XX WO2003042244-A2.
 XX PD 22-MAY-2003.
 XX PF 15-NOV-2002; 2002WO-DK000764.
 XX PR 16-NOV-2001; 2001DK-00001702.
 XX PR 16-NOV-2001; 2001US-0331575P.

XX (PHAR-) PHARMEXA AS.
 XX PA (KLYS/) KLYSNER S.
 XX PA (NIEL/) NIELSEN F S.
 XX PA (BRAT/) BRATT T.
 XX PA (VOLD/) VOLDBORG B.
 XX PA (MOUR/) MOURITSEN S.

XX Klysner S, Nielsen FS, Bratt T, Voldborg B, Mouritsen S;
 PI composition for treating inflammatory diseases e.g. arthritis.

```

XX DR WPI; 2003-449558/42.
XX DR N-PSDB; AAL61294.
XX PT New immunogenic analogue of a polymeric protein, useful for preparing a
XX PT composition for treating inflammatory diseases e.g. arthritis.
XX FS Claim 20; Page 112-113; 196pp; English.
XX CC The invention relates to immunogenic analogues of multimeric proteins
XX CC such as immunogenic variants of interleukin 5 (IL5) and tumour necrosis
XX CC factor alpha (TNF, TNFalpha) and methods for production of immunogenic
XX CC analogues. The immunogenic analogue is useful for preparing a composition
XX CC for treating inflammatory diseases, e.g., arthritis. It is also used in
XX CC gene therapy. The present sequence is a fusion construct which comprises
XX CC 2 human interleukin 5 (IL5) monomers joined by tetanus toxoid epitopes
XX CC P30 and P2. This sequence is used to illustrate the method of the
XX CC invention
XX SQ Sequence 285 AA;

Query Match 61.8%; Score 430; DB 6; Length 285;
Best Local Similarity 64.9%; Pred. No. 1.5e-42;
Matches 87; Conservative 17; Mismatches 30; Indels 0; Gaps 0;

QY 1 MRMLNLSLLALGAAVVSAPAVENPMNRLVAETLLSTHRTWLIGDGNLMPTPENKNH 60
DB 1 MRMLNLSLLALGAAVVSAPAVENPMNRLVAETLLSTHRTWLIGDGNLMPTPENKNH 60

QY 61 QLCIKVFQGITLKNQTAHGEAVDKLQNLSTLKEHIERQKRCAGERNVTKFLDYLQ 120
DB 61 QLCTEEIFQGITLESQTQGGTVRFLKNSLTKYIDGQKKCGEERRRVNQFLDYLQ 120

QY 121 VFLGVINTEWTPES 134
DB 121 EFLGVNTEWIIIES 134

RESULT 12
AAB72616
ID AAB72616 standard; protein; 84 AA.
XX AC AAB72616;
XX DT 04-MAY-2001 (first entry)
XX DE Canine interleukin-5 protein #2.
XX KW Dog; interleukin-5; IL-5; allergy; cancer; gene therapy;
XX KW inflammatory reaction.
XX OS Canis sp.
XX PN WO200111049-A2.
XX FD 15-FEB-2001.
XX PF 09-AUG-2000; 2000WO-US021651.
XX PR 10-AUG-1999; 99US-00371615.
XX PA (INDEX-) IDEXX LAB INC.
XX PI Guo H, Lawton R, Mermer B, Aiyappa AP;
XX DR WPI; 2001-191542/19.
XX DR N-PSDB; AAF74305.
XX PT Novel canine interleukin 5 polynucleotide and polypeptides are used for
XX PT generating antibodies which are useful in treating allergies in dogs.
XX PS Example 1; Fig 1; 48pp; English.
XX

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The present invention provides the protein and coding sequences of the canine interleukin-5 (IL-5) protein. This can be used to treat allergies, cancer and inflammatory reactions in dogs. The present sequence is one version of the IL-5 protein shown in the specification

Sequence 84 AA;

Query Match 61.6%; Score 429; DB 4; Length 84; Best Local Similarity 100.0%; Pred. No. 3.2e-43; Matches 84; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRMLNLSLLALGAAVVSAPAVENPMNRLVAETLLSTHRTWLIGDGNLMPTPENKNH 60

DB 1 MRMLNLSLLALGAAVVSAPAVENPMNRLVAETLLSTHRTWLIGDGNLMPTPENKNH 60

QY 61 QLCIKVFQGITLKNQTAHGEAV 84

DB 61 QLCIKVFQGITLKNQTAHGEAV 84

RESULT 13

AAU10354

ID AAU10354 standard; protein; 134 AA.

XX AC AAU10354;

XX DT 14-FEB-2002 (first entry)

XX DE Interleukin 5 (IL5) isoform.

XX KW Human; interleukin 5; IL5; antiinflammatory; antiasthmatic; asthma;

XX KW haplotyping; inflammatory disorder.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

FT Misc-difference 93 /note= "Wild type Leu substituted by Phe"

XX PN WO200177132-A2.

XX PD 18-OCT-2001.

XX PF 11-APR-2001; 2001WO-US012011.

XX PR 11-APR-2000; 2000US-0196250P.

XX PA (GENA-) GENAISSANCE PHARM INC.

XX PI Bentivegna SC, Chew A, Choi JY, Denton RR, Kazemi A;

XX PI Nandabalan K, Parks KE;

XX DR WPI; 2002-041289/05.

XX PT New haplotypes of the human interleukin 5 gene, useful to diagnose and

XX PT treat diseases associated with the gene including inflammatory disorders

XX PT such as asthma.

XX PS Disclosure; Page; 65pp; English.

XX CC The invention relates to haplotyping the human interleukin 5 (IL5) gene

XX CC of an individual, comprising determining if the individual has one of the

XX CC IL5 haplotypes or haplotype pairs fully defined in the specification.

XX CC Haplotyping the IL5 gene of an individual, comprises determining the

XX CC identity of the nucleotide at two or more polymorphic sites in one copy

XX CC of the gene. The method also involves identifying an association between

XX CC a trait and a haplotype or haplotype pair of the IL5 gene, comprising

XX CC comparing the frequency of the haplotype/pair in a population exhibiting

XX CC the trait with that of a reference population. A higher frequency in the

XX CC trait population indicates the trait is associated with the haplotype.

XX CC The polynucleotides and screened compounds are useful to develop

XX CC treatment for diseases associated with IL-5 activity including

XX CC inflammatory disorders such as asthma. The present sequence represents

CC the amino acid sequence of interleukin 5 (IL5) isoform as described in
CC the method of the invention. Note: The present sequence is not shown in
CC the specification, but is derived from the human IL5 sequence given in
CC figure 3 (see AAU10353)
XX
SQ Sequence 134 AA;
Query Match 61.2%; Score 426; DB 5; Length 134;
Best Local Similarity 64.2%; Pred. No. 1.5e-42;
Matches 86; Conservative 17; Mismatches 31; Indels 0; Gaps 0;
QY 1 MRMLNLSSLLALGAAYVSAPAVENPMRLVAETLTLLSTHRTWLGDNLMIPENKNH 60
DB 1 MRMLNLSSLLALGAAYVVAIPTETPSALVKETLALLSTHRTLLIANETRLILVPVHKH 60
QY 61 QLCIKEVFQGITLTKNOTAHGEAVDKLFQNLSLIKEHIERQKRCACGERWRVTKFLDYLQ 120
DB 61 QLCTEEIFQGITLESQTVOGTVVERLFPKLSIKKYIDQKKKCGEERRVNOFLDYLQ 120
QY 121 VFLGVINTEWTPES 134
DB 121 EFLGVNTEWIIIES 134

RESULT 14
AAP81056
ID AAP81056 standard; protein; 134 AA.
XX
AC AAP81056;
XX
DT 25-MAR-2003 (revised)
DT 04-DEC-1990 (first entry)
XX
XX Sequence of human B-cell differentiation factor.
DE Immunodeficiency disease; cancer therapy; interleukin; lymphocyte.
XX
XX Homo sapiens.
XX
FH Key Location/Qualifiers
FT Region 1..48
FT /note= "Encoded by exon 1"
FT Region 49..59
FT /note= "Encoded by exon 2"
FT Region 60..102
FT /note= "Encoded by exon 3"
FT Region 103..134
FT /note= "Encoded by exon 4"
XX
PN EP261625-A.
XX
XX 30-MAR-1988.
PD
XX
XX 21-SEP-1987; 87EP-00113774.
PF
XX
XX 20-SEP-1986; 86JP-00223284.
PR
XX 21-SEP-1987; 87JP-00236842.
XX
XX (HONJ/) HONJO T.
XX
XX Honjo T, Takatu K, Severinson E;
XX
XX WPI; 1988-085927/13.
DR
XX N-PSDB; AAN81380, AAN81381.
XX
XX Recombinant human B-cell differentiation factor - used for diagnosis or
XX treatment of immunodeficiency diseases, various infections and cancers.
XX
XX Disclosure; Page ?; 5pp; English.
XX
XX Encoded by the human BCDF cDNA sequence which is claimed and by human
XX BCDF chromosomal gene (see FT). The BCDF is useful in the diagnosis or
XX treatment of e.g. immunodeficiency diseases which occur due to the

CC deficiency of this factor in a living body and also in the treatment of
CC various infections and cancers. (Updated on 25-MAR-2003 to correct PR
CC field.)
XX
SQ Sequence 134 AA;
Query Match 60.3%; Score 420; DB 1; Length 134;
Best Local Similarity 64.2%; Pred. No. 7.6e-42;
Matches 86; Conservative 17; Mismatches 31; Indels 0; Gaps 0;
QY 1 MRMLNLSSLLALGAAYVSAPAVENPMRLVAETLTLLSTHRTWLGDNLMIPENKNH 60
DB 1 MRMLNLSSLLALGAAYVVAIPTETPSALVKETLALLSTHRTLLIANETRLILVPVHKH 60
QY 61 QLCIKEVFQGITLTKNOTAHGEAVDKLFQNLSLIKEHIERQKRCACGERWRVTKFLDYLQ 120
DB 61 QLCTEEIFQGITLESQTVOGTVVERLFPKLSIKKYIDQKKKCGEERRVNOFLDYLQ 120
QY 121 VFLGVINTEWTPES 134
DB 121 EFLGVNTEWIIIES 134

RESULT 15
AAO30460
ID AAO30460 standard; protein; 287 AA.
XX
AC AAO30460;
XX
DT 22-SEP-2003 (first entry)
DT
DE hIL5.37 variant protein.
XX
XX Multimeric protein; interleukin 5; IL5; TNFalpha; inflammatory disease;
XX tumour necrosis factor alpha; gene therapy; arthritis; interleukin 5;
XX IL5; epitope; human; tetanus toxoid; chimeric; variant; mutant; mutein.
XX
XX Homo sapiens.
XX Unidentified.
XX Chimeric.
XX
FH Key Location/Qualifiers
FT Peptide 1..19
FT /note= "Human IL5 leader peptide"
FT Protein 20..287
FT /note= "Mature hIL5.37 protein"
FT Region 24..38
FT /note= "Tetanus toxoid P2 epitope"
FT Region 273..287
FT /note= "Tetanus toxoid P30 epitope"
XX
XX WO2003042244-A2.
PN
XX
XX 22-MAY-2003.
PD
XX
XX 15-NOV-2002; 2002WO-DK000764.
PF
XX
XX 16-NOV-2001; 2001DK-00001702.
PR
XX 16-NOV-2001; 2001US-0331575P.
XX
XX (PHAR-) PHARMEXA AS.
XX (KLYS/) KLYSNER S.
XX (NIEL/) NIELSEN P S.
XX (BRAT/) BRATT T.
XX (VOLD/) VOLDORF B.
XX (MOUR/) MOURITSEN S.
XX
XX Klyener S, Nielsen FS, Bratt T, Voldborg B, Mouritsen S;
XX
XX WPI; 2003-449558/42.
DR
XX N-PSDB; AAL61296.
XX
XX New immunogenic analogue of a polymeric protein, useful for preparing a

PT composition for treating inflammatory diseases e.g. arthritis.
XX
PS
XX Claim 20; Page 117-120; 196pp; English.

CC The invention relates to immunogenic analogues of multimeric proteins
CC such as immunogenic variants of interleukin 5 (IL5) and tumour necrosis
CC factor alpha (TNF, TNFalpha) and methods for production of immunogenic
CC analogues. The immunogenic analogue is useful for preparing a composition
CC for treating inflammatory diseases, e.g., arthritis. It is also used in
CC gene therapy. The present sequence is a fusion construct variant which
CC comprises 2 human interleukin 5 (IL5) monomers joined by diglycine linker
CC and including terminally positioned tetanus toxoid epitopes P30 and P2.
CC This sequence is used to illustrate the method of the invention

XX SQ Sequence 287 AA;

Query Match	59.7%;	Score 415.5;	DB 6;	Length 287;
Best Local Similarity	58.4%;	Pred. No. 8e-41;		
Matches	87;	Conservative	17;	Mismatches 30; Indels 15; Gaps 1;
Qy	1	MRMLNLSLLALGAAYVSAFVEN-----PMNRLVAETTLTLLSTHRTWLI	45	
Db	1	MRMLNLSLLALGAAYVYAIPTQYIKANSKFGITELIPTSAIVKETLALLSTHRTLLI	60	
Qy	46	GDGNLMIPTEPNKNHOLCIKEVFQIDTLKNQTAHGEAVDKLPONLSLIKEHIEROKKRC	105	
Db	61	ANETLRIPVPVHNKHQLCTEEIFQGIQTLESQTVQSGTVERLPKNLSLIKXIDGOKKXC	120	
Qy	106	AGERVRVKFDYLDYQVFLGVINTEWTPES	134	
Db	121	GEERRRVNQFLDYLDYQVFLGVINTEWTPES	149	

Search completed: August 25, 2004, 00:02:24
Job time : 99.8675 secs

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OM protein - protein search, using sw model

Run on: August 24, 2004, 23:59:38 ; Search time 24.2169 Seconds
(without alignments)
285.664 Million cell updates/sec

Title: US-10-787-382-5
Perfect score: 596
Sequence: 1 MRMLNLSLLALGAAYVSFAF.....FLDYQVFLGVINTEWTPES 134

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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3: /cgn2_6/ptodata/2/iaa/6A COMB.pep.*
4: /cgn2_6/ptodata/2/iaa/6B COMB.pep.*
5: /cgn2_6/ptodata/2/iaa/6C COMB.pep.*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	696	100.0	134	4	US-09-322-409-81
2	696	100.0	134	4	US-09-451-527-81
3	687	98.7	134	4	US-09-371-615A-2
4	610	87.6	115	4	US-09-322-409-86
5	610	87.6	115	4	US-09-451-527-86
6	430	61.8	134	1	US-08-284-393B-13
7	430	61.8	134	3	US-08-759-828-9
8	430	61.8	134	4	US-09-371-615A-7
9	430	61.8	134	4	US-09-462-941-12
10	430	61.8	134	5	PCT-US95-08950-13
11	430	61.8	134	6	5324640-2
12	376	54.0	133	4	US-09-371-615A-8
13	351	50.4	121	4	US-09-180-864-2
14	74.5	10.7	407	4	US-09-489-847-280
15	74	10.6	323	4	US-09-134-000C-5535
16	72.5	10.4	686	4	US-09-914-259-33
17	72	10.3	15	5	PCT-US94-06555-4
18	71.5	10.3	521	4	US-09-543-681A-6857
19	71.5	10.3	599	4	US-09-252-991A-20368
20	71.5	10.3	673	4	US-09-328-352-5834
21	70.5	10.1	429	4	US-09-328-352-7087
22	69.5	10.0	312	4	US-09-107-532A-6369
23	69.5	10.0	976	3	US-09-560-005-2
24	69.5	10.0	976	3	US-09-195-868-14
25	69.5	10.0	976	3	US-09-418-540-2
26	69.5	10.0	976	4	US-09-969-528-2
27	69.5	10.0	1187	3	US-08-684-362B-8

28	69.5	10.0	1187	3	US-09-311-743-8	Sequence 8, Appli
29	69.5	10.0	1189	3	US-09-195-868-15	Sequence 15, Appl
30	69.5	10.0	1229	3	US-09-195-868-28	Sequence 28, Appl
31	67.5	9.7	364	4	US-09-252-991A-18473	Sequence 18473, A
32	67.5	9.7	968	1	US-08-434-730-14	Sequence 14, Appl
33	67.5	9.7	1185	3	US-08-664-962B-2	Sequence 2, Appli
34	67.5	9.7	1185	3	US-09-311-743-2	Sequence 2, Appli
35	66.5	9.6	2311	4	US-08-934-386-9	Sequence 9, Appli
36	66.5	9.6	485	4	US-09-134-001C-4294	Sequence 4294, Ap
37	66.5	9.6	589	4	US-09-543-681A-4194	Sequence 4194, Ap
38	66	9.5	465	4	US-09-240-639-8	Sequence 8, Appli
39	66	9.5	465	4	US-09-557-800C-56	Sequence 56, Appl
40	66	9.5	465	4	US-09-370-625A-39	Sequence 39, Appl
41	66	9.5	984	4	US-09-328-352-6926	Sequence 6926, Ap
42	66	9.5	2325	3	US-08-417-089-6	Sequence 6, Appli
43	66	9.5	2325	3	US-08-695-651-6	Sequence 6, Appli
44	66	9.5	2325	3	US-08-930-285-6	Sequence 6, Appli
45	66	9.5	2325	3	US-08-695-421-6	Sequence 6, Appli

ALIGNMENTS

RESULT 1
US-09-322-409-81
; Sequence 81, Application US/09322409
; Patent No. 6471957
; GENERAL INFORMATION:
; APPLICANT: Yang, Shumin
; APPLICANT: Sim, Gek-Ke
; APPLICANT: Dreitz, Matthew J.
; APPLICANT: Wonderling, Ramani S.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; FILE REFERENCE: IM-2-CI
; CURRENT APPLICATION NUMBER: US/09/322,409
; EARLIER APPLICATION NUMBER: 60/087,306
; EARLIER FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 154
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 81
; LENGTH: 134
; TYPE: PRT
; ORGANISM: Canis familiaris
US-09-322-409-81

Query Match 100.0%; Score 696; DB 4; Length 134;
Best Local Similarity 100.0%; Pred. No. 3.7e-81;
Matches 134; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MRMLNLSLLALGAAYVSFAFVPMNLVAETLLSTHRTWLIGDGNLMIPTENKNH 60
Db 1 MRMLNLSLLALGAAYVSFAFVPMNLVAETLLSTHRTWLIGDGNLMIPTENKNH 60
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QY 121 VFLGVINTEWTPES 134
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RESULT 2
US-09-451-527-81
; Sequence 81, Application US/09451527
; Patent No. 6482403
; GENERAL INFORMATION:
; APPLICANT: Sim, Gek-Ke
; APPLICANT: Yang, Shumin
; APPLICANT: Dreitz, Matthew J.
; APPLICANT: Wonderling, Ramani S.

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; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; FILE OF INVENTION: ACID MOLECULES, AND USES THEREOF
; FILE REFERENCE: IM-2-C2
; CURRENT APPLICATION NUMBER: US/09/451,527
; CURRENT FILING DATE: 1999-12-01
; EARLIER APPLICATION NUMBER: 09/322,409
; EARLIER FILING DATE: 1998-05-28
; EARLIER APPLICATION NUMBER: 60/087,306
; EARLIER FILING DATE: 1998-05-29
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 81
; LENGTH: 134
; TYPE: PRT
; ORGANISM: Canis familiaris
; US-09-451-527-81

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Matches 133; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy 61 QLCIKVEFGIDTLKNOTAHGEAVDKLFQNLSLIKEHIERQKRCAGRWRTKFLDYDLYQ 120
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Qy 121 VFLGVINTEWTPES 134
Db 121 VFLGVINTEWTPES 134

RESULT 3
US-09-371-615A-2
; Sequence 2, Application US/09371615A
; Patent No. 6537781
; GENERAL INFORMATION:
; APPLICANT: IDEXX LABORATORIES
; TITLE OF INVENTION: METHODS AND COMPOSITIONS CONCERNING
; FILE REFERENCE: 036040017000US00
; CURRENT APPLICATION NUMBER: US/09/371,615A
; CURRENT FILING DATE: 1999-08-10
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 134
; TYPE: PRT
; ORGANISM: Canis familiaris
; US-09-371-615A-2

Query Match      98.7%; Score 687; DB 4; Length 134;
Best Local Similarity 99.3%; Pred. No. 5.2e-80;
Matches 133; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MRMLNLSSLLALGAAYSAFAVENPMNRLVAETLTLLSTHRTWLIGDGNLMIPTPENKQH 60
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Qy 61 QLCIKVEFGIDTLKNOTAHGEAVDKLFQNLSLIKEHIERQKRCAGRWRTKFLDYDLYQ 120
Db 61 QLCIKVEFGIDTLKNOTAHGEAVDKLFQNLSLIKEHIERQKRCAGRWRTKFLDYDLYQ 120

Qy 121 VFLGVINTEWTPES 134
Db 121 VFLGVINTEWTPES 134

RESULT 4
US-09-322-409-86
; Sequence 86, Application US/09322409
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; Patent No. 6471957
; GENERAL INFORMATION:
; APPLICANT: Sim, Gek-kee
; APPLICANT: Yang, Shumin
; APPLICANT: Dreitz, Matthew J.
; APPLICANT: Wonderling, Ramani S.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; FILE OF INVENTION: ACID MOLECULES, AND USES THEREOF
; FILE REFERENCE: IM-2-C1
; CURRENT APPLICATION NUMBER: US/09/322,409
; CURRENT FILING DATE: 1999-05-28
; EARLIER APPLICATION NUMBER: 60/087,306
; EARLIER FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 154
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 86
; LENGTH: 115
; TYPE: PRT
; ORGANISM: Canis familiaris
; US-09-322-409-86

Query Match      87.6%; Score 610; DB 4; Length 115;
Best Local Similarity 100.0%; Pred. No. 3e-70;
Matches 115; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 80 HGEAVDKLFQNLSLIKEHIERQKRCAGRWRTKFLDYDLYQVFLGVINTEWTPES 134
Db 61 HGEAVDKLFQNLSLIKEHIERQKRCAGRWRTKFLDYDLYQVFLGVINTEWTPES 115

RESULT 5
US-09-451-527-86
; Sequence 86, Application US/09451527
; Patent No. 6482403
; GENERAL INFORMATION:
; APPLICANT: Sim, Gek-kee
; APPLICANT: Yang, Shumin
; APPLICANT: Dreitz, Matthew J.
; APPLICANT: Wonderling, Ramani S.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; FILE OF INVENTION: ACID MOLECULES, AND USES THEREOF
; FILE REFERENCE: IM-2-C2
; CURRENT APPLICATION NUMBER: US/09/451,527
; CURRENT FILING DATE: 1999-12-01
; EARLIER APPLICATION NUMBER: 09/322,409
; EARLIER FILING DATE: 1999-05-28
; EARLIER APPLICATION NUMBER: 60/087,306
; EARLIER FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 86
; LENGTH: 115
; TYPE: PRT
; ORGANISM: Canis familiaris
; US-09-451-527-86

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Qy 80 HGEAVDKLFQNLSLIKEHIERQKRCAGRWRTKFLDYDLYQVFLGVINTEWTPES 134
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; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/759,628
; FILING DATE: 05-DEC-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/008,574
; FILING DATE: 06-DEC-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: DX0552Q
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-852-9196
; TELEFAX: 415-496-1200
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 134 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 20..134
; OTHER INFORMATION: /note= "Peptide of Figure 1"
; US-08-759-628-9

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Matches 87; Conservative 17; Mismatches 30; Indels 0; Gaps 0;

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DB 61 QLCTEIFQIGITLSEQTVOGTVERLFKNLSLIKXYIDGKKCKGEERRVYNQFLDYLQ 120
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DB 121 EFLGVNTEWIIES 134

RESULT 8
US-09-371-615A-7
; Sequence 7, Application US/09371615A
; Patent No. 6537781
; GENERAL INFORMATION:
; APPLICANT: IDEXX LABORATORIES
; TITLE OF INVENTION: METHODS AND COMPOSITIONS CONCERNING
; TITLE OF INVENTION: CANINE INTERLEUKIN 5
; FILE REFERENCE: 036040017000S00
; CURRENT APPLICATION NUMBER: US/09/371,615A
; CURRENT FILING DATE: 1999-08-10
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 134
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Interleukin 5
; US-09-371-615A-7

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RESULT 6
US-08-284-393B-13
; Sequence 13, Application US/08284393B
; Patent No. 5696234
; GENERAL INFORMATION:
; APPLICANT: Zurawski, Sandra M.
; APPLICANT: Zurawski, Gerard
; TITLE OF INVENTION: MUTINS OF MAMMALIAN CYTOKINES
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/284,393B
; FILING DATE: 01-AUG-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: DX0389
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-852-9196
; TELEFAX: 415-496-1200
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 134 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-284-393B-13

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Best Local Similarity 64.9%; Pred. No. 4.2e-47;
Matches 87; Conservative 17; Mismatches 30; Indels 0; Gaps 0;

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QY 61 QLCIKVEFQGITLKNQTAHGEAVDKLFQNLISLIEKHIERQKRCAGRWVTFDYLQ 120
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QY 121 VFLGVINTEWTPES 134
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RESULT 7
US-08-759-628-9
; Sequence 9, Application US/08759628
; Patent No. 6225446
; GENERAL INFORMATION:
; APPLICANT: Altmann, Scott W.
; APPLICANT: Rock, Fernando L.
; APPLICANT: Bazan, J. Fernando
; APPLICANT: Kastelein, Robert A.
; TITLE OF INVENTION: MUTATIONAL VARIANTS OF MAMMLIAN PROTEINS
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; STREET: 901 California Avenue
; CITY: Palo Alto

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OM protein - protein search, using sw model

Run on: August 25, 2004, 00:05:39 ; Search time 90.9478 Seconds
(without alignments)
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Perfect score: 696
Sequence: 1 MRMLNLSLALGAAYVSFA.....FLDYLOVFLGVINTEWTPES 134

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Total number of hits satisfying chosen parameters: 1295152

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Listing first 45 summaries

Database : Published Applications AA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	696	100.0	134	9	US-09-755-633-5
2	696	100.0	134	14	Sequence 5, Appli
3	696	100.0	134	14	Sequence 81, Appl
4	610	87.6	115	9	US-09-755-633-10
5	610	87.6	115	14	Sequence 10, Appl
6	610	87.6	115	14	Sequence 86, Appl
7	430	61.8	134	14	US-10-218-654-86
8	430	61.8	134	14	US-10-262-439-86
9	430	61.8	134	14	US-10-289-454-233
10	430	61.8	134	14	US-10-400-377-12
11	430	61.8	134	14	US-10-400-708-12
12	430	61.8	134	14	US-10-298-148-12
13	430	61.8	134	14	US-10-050-902-233
14	430	61.8	134	14	US-10-050-898-233
15	430	61.8	285	14	US-10-295-074-9
16	430	61.8	285	14	US-10-295-074-11
17	415.5	59.7	287	14	US-10-295-074-15

16	413.5	59.4	287	14	US-10-295-074-13	Sequence 13, Appl
17	359	51.6	136	14	US-10-289-454-336	Sequence 336, App
18	359	51.6	136	14	US-10-050-902-336	Sequence 336, App
19	359	51.6	136	14	US-10-050-898-336	Sequence 336, App
20	358	51.4	115	16	US-10-658-834A-588	Sequence 588, App
21	357	51.3	115	16	US-10-658-834A-569	Sequence 569, App
22	357	51.3	123	14	US-10-289-454-337	Sequence 337, App
23	357	51.3	123	14	US-10-050-902-337	Sequence 337, App
24	357	51.3	123	14	US-10-050-898-337	Sequence 337, App
25	357	51.3	138	14	US-10-289-454-335	Sequence 335, App
26	357	51.3	138	14	US-10-050-902-335	Sequence 335, App
27	357	51.3	138	14	US-10-050-898-335	Sequence 335, App
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32	356	51.1	115	16	US-10-658-834A-208	Sequence 208, App
33	356	51.1	115	16	US-10-658-834A-574	Sequence 574, App
34	356	51.1	115	16	US-10-658-834A-580	Sequence 580, App
35	356	51.1	115	16	US-10-658-834A-587	Sequence 587, App
36	356	51.1	115	16	US-10-658-834A-589	Sequence 589, App
37	356	51.1	115	16	US-10-658-834A-595	Sequence 595, App
38	355	51.0	115	16	US-10-658-834A-568	Sequence 568, App
39	355	51.0	115	16	US-10-658-834A-575	Sequence 575, App
40	355	51.0	115	16	US-10-658-834A-581	Sequence 581, App
41	355	51.0	115	16	US-10-658-834A-585	Sequence 585, App
42	355	51.0	115	16	US-10-658-834A-596	Sequence 596, App
43	355	51.0	115	16	US-10-658-834A-597	Sequence 597, App
44	354	50.9	115	16	US-10-658-834A-576	Sequence 576, App
45	354	50.9	115	16	US-10-658-834A-582	Sequence 582, App

ALIGNMENTS

RESULT 1
US-09-755-633-5
; Sequence 5, Application US/09755633
; Patent No. US20020127200A1
; GENERAL INFORMATION:
; APPLICANT: Yang, Shumin
; APPLICANT: McCall, Catherine A.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF
; FILE REFERENCE: IN-2-C1-C1
; CURRENT APPLICATION NUMBER: US/09/755,633
; CURRENT FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: 05/322,409
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/087,306
; PRIOR FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 21
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; SEQ ID NO 5
; LENGTH: 134
; TYPE: PRT
; ORGANISM: Canis familiaris
; US-09-755-633-5

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Best Local Similarity 100.0%; Pred. No. 4.1e-73;
Matches 134; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 121 VFLGVINTEWTPES 134

Db 121 VFLGVINTEWTPES 134
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US-10-218-654-81
; Sequence 81, Application US/10218654
; Publication No. US20030099609A1
; GENERAL INFORMATION:
; APPLICANT: Sim, Gek-kee
; APPLICANT: Yang, Shumin
; APPLICANT: Dreitz, Matthew J.
; APPLICANT: Wonderling, Ramani S.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF
; FILE REFERENCE: IM-2-C1
; CURRENT APPLICATION NUMBER: US/10/218,654
; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: US/09/322,409
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/087,306
; PRIOR FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 154
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 81
; LENGTH: 134
; TYPE: PRT
; ORGANISM: Canis familiaris
US-10-218-654-81
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US-10-262-439-81
RESULT 3
US-10-262-439-81
; Sequence 81, Application US/10262439
; Publication No. US20030143196A1
; GENERAL INFORMATION:
; APPLICANT: Sim, Gek-kee
; APPLICANT: Yang, Shumin
; APPLICANT: Dreitz, Matthew J.
; APPLICANT: Wonderling, Ramani S.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF
; FILE REFERENCE: IM-2-C2
; CURRENT APPLICATION NUMBER: US/10/262,439
; CURRENT FILING DATE: 2002-09-30
; PRIOR APPLICATION NUMBER: US/09/451,527
; PRIOR FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: 09/322,409
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/087,306
; PRIOR FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 81
; LENGTH: 134
; TYPE: PRT
; ORGANISM: Canis familiaris

US-10-262-439-81
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Best Local Similarity 100.0%; Pred. No. 4.le-73;
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Qy 61 QLCIKVEFGQIDTLKNOTAHGEAVDKLFQNLISLKEHIERQKRCAGRWRTKFDLYLQ 120
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RESULT 4
US-09-755-633-10
; Sequence 10, Application US/09755633
; Patent No. US20020127200A1
; GENERAL INFORMATION:
; APPLICANT: Yang, Shumin
; APPLICANT: McCall, Catherine A.
; APPLICANT: Weber, Eric R.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF
; FILE REFERENCE: IM-2-C1-C1
; CURRENT APPLICATION NUMBER: US/09/755,633
; CURRENT FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: 09/322,409
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/087,306
; PRIOR FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 115
; TYPE: PRT
; ORGANISM: Canis familiaris
US-09-755-633-10
Query Match 87.6%; Score 610; DB 9; Length 115;
Best Local Similarity 100.0%; Pred. No. 3.8e-63;
Matches 115; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 20 FAVENPMNRLVAETLLTSLTHTWLTGDNLMIPPTENKNHQLCKIKVEFGQIDTLKNQTA 79
Db 1 FAVENPMNRLVAETLLTSLTHTWLTGDNLMIPPTENKNHQLCKIKVEFGQIDTLKNQTA 60
Qy 80 HGEAVDKLFQNLISLKEHIERQKRCAGRWRTKFDLYLQVFLGVINTEWTPES 134
Db 61 HGEAVDKLFQNLISLKEHIERQKRCAGRWRTKFDLYLQVFLGVINTEWTPES 115
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RESULT 5
US-10-218-654-86
; Sequence 86, Application US/10218654
; Publication No. US20030099609A1
; GENERAL INFORMATION:
; APPLICANT: Sim, Gek-kee
; APPLICANT: Yang, Shumin
; APPLICANT: Dreitz, Matthew J.
; APPLICANT: Wonderling, Ramani S.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF
; FILE REFERENCE: IM-2-C1
; CURRENT APPLICATION NUMBER: US/10/218,654
; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: US/09/322,409
; PRIOR FILING DATE: 1999-05-28

FILE REFERENCE: 1700.0360001	FILE REFERENCE: 1700.0360001
CURRENT APPLICATION NUMBER: US/10/289,454	CURRENT APPLICATION NUMBER: US/10/289,454
CURRENT FILING DATE: 2003-02-10	CURRENT FILING DATE: 2003-02-10
PRIOR APPLICATION NUMBER: US 60/396,636	PRIOR APPLICATION NUMBER: US 60/396,636
PRIOR FILING DATE: 2002-07-19	PRIOR FILING DATE: 2002-07-19
PRIOR APPLICATION NUMBER: PCT/IB02/00166	PRIOR APPLICATION NUMBER: PCT/IB02/00166
PRIOR FILING DATE: 2002-01-21	PRIOR FILING DATE: 2002-01-21
PRIOR APPLICATION NUMBER: US 10/050,902	PRIOR APPLICATION NUMBER: US 10/050,902
PRIOR FILING DATE: 2002-01-18	PRIOR FILING DATE: 2002-01-18
PRIOR APPLICATION NUMBER: US 60/331,045	PRIOR APPLICATION NUMBER: US 60/331,045
PRIOR FILING DATE: 2001-11-07	PRIOR FILING DATE: 2001-11-07
NUMBER OF SEQ ID NOS: 386	NUMBER OF SEQ ID NOS: 386
SOFTWARE: PatentIn version 3.2	SOFTWARE: PatentIn version 3.2
SEQ ID NO 233	SEQ ID NO 233
LENGTH: 134	LENGTH: 134
TYPE: PRT	TYPE: PRT
ORGANISM: precursor human IL-5	ORGANISM: precursor human IL-5
US-10-289-454-233	US-10-289-454-233
Query Match 61.8%; Score 430; DB 14; Length 134;	Query Match 61.8%; Score 430; DB 14; Length 134;
Best Local Similarity 64.9%; Pred. No. 5.3e-42;	Best Local Similarity 64.9%; Pred. No. 5.3e-42;
Matches 87; Conservative 17; Mismatches 30; Indels 0; Gaps 0;	Matches 87; Conservative 17; Mismatches 30; Indels 0; Gaps 0;
QY 1 MEMLNLSLLALGAAYVSAPAVENPMNRLVAETLLSTHRTWLGDNLMIPENKHN 60	QY 1 MEMLNLSLLALGAAYVSAPAVENPMNRLVAETLLSTHRTWLGDNLMIPENKHN 60
DB 1 MEMLLHLSLLALGAAYVVAIPTETPTTSALVKETLALLSTHRTLLIANETLRIIPVPHKN 60	DB 1 MEMLLHLSLLALGAAYVVAIPTETPTTSALVKETLALLSTHRTLLIANETLRIIPVPHKN 60
QY 61 QLCIKEVFQGITLKNQTAHGEAVDKLFQNLSLIKEHIEROKKRCACGERWRVTKFLDYLO 120	QY 61 QLCIKEVFQGITLKNQTAHGEAVDKLFQNLSLIKEHIEROKKRCACGERWRVTKFLDYLO 120
DB 61 QLCTEEIQQIGTLESQIVQGVTVRFLFKNLSLIKKYIDGQKKCGERRRVNQFLDYLO 120	DB 61 QLCTEEIQQIGTLESQIVQGVTVRFLFKNLSLIKKYIDGQKKCGERRRVNQFLDYLO 120
QY 121 VELGVINTEWTPES 134	QY 121 VELGVINTEWTPES 134
DB 121 EFLGVNTEWTPES 134	DB 121 EFLGVNTEWTPES 134
RESULT 8	RESULT 8
US-10-400-377-12	US-10-400-377-12
Sequence 12, Application US/10400377	Sequence 12, Application US/10400377
Publication No. US20030162949A1	Publication No. US20030162949A1
GENERAL INFORMATION:	GENERAL INFORMATION:
APPLICANT: Cox III, George N	APPLICANT: Cox III, George N
APPLICANT: Boldor Biotechnology, Inc.	APPLICANT: Boldor Biotechnology, Inc.
TITLE OF INVENTION: Derivatives of Growth Hormone and Related Proteins	TITLE OF INVENTION: Derivatives of Growth Hormone and Related Proteins
FILE REFERENCE: 4152-1-PUS	FILE REFERENCE: 4152-1-PUS
CURRENT APPLICATION NUMBER: US/10/400,377	CURRENT APPLICATION NUMBER: US/10/400,377
CURRENT FILING DATE: 2003-03-26	CURRENT FILING DATE: 2003-03-26
PRIOR APPLICATION NUMBER: US/09/462,941	PRIOR APPLICATION NUMBER: US/09/462,941
PRIOR FILING DATE: 2000-01-14	PRIOR FILING DATE: 2000-01-14
PRIOR APPLICATION NUMBER: 60/052,516	PRIOR APPLICATION NUMBER: 60/052,516
PRIOR FILING DATE: 1997-07-14	PRIOR FILING DATE: 1997-07-14
NUMBER OF SEQ ID NOS: 41	NUMBER OF SEQ ID NOS: 41
SOFTWARE: PatentIn Ver. 2.0	SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 12	SEQ ID NO 12
LENGTH: 134	LENGTH: 134
TYPE: PRT	TYPE: PRT
ORGANISM: Homo sapiens	ORGANISM: Homo sapiens
US-10-400-377-12	US-10-400-377-12
Query Match 61.8%; Score 430; DB 14; Length 134;	Query Match 61.8%; Score 430; DB 14; Length 134;
Best Local Similarity 64.9%; Pred. No. 5.3e-42;	Best Local Similarity 64.9%; Pred. No. 5.3e-42;
Matches 87; Conservative 17; Mismatches 30; Indels 0; Gaps 0;	Matches 87; Conservative 17; Mismatches 30; Indels 0; Gaps 0;
QY 1 MEMLNLSLLALGAAYVSAPAVENPMNRLVAETLLSTHRTWLGDNLMIPENKHN 60	QY 1 MEMLNLSLLALGAAYVSAPAVENPMNRLVAETLLSTHRTWLGDNLMIPENKHN 60
DB 1 MEMLLHLSLLALGAAYVVAIPTETPTTSALVKETLALLSTHRTLLIANETLRIIPVPHKN 60	DB 1 MEMLLHLSLLALGAAYVVAIPTETPTTSALVKETLALLSTHRTLLIANETLRIIPVPHKN 60
QY 61 QLCIKEVFQGITLKNQTAHGEAVDKLFQNLSLIKEHIEROKKRCACGERWRVTKFLDYLO 120	QY 61 QLCIKEVFQGITLKNQTAHGEAVDKLFQNLSLIKEHIEROKKRCACGERWRVTKFLDYLO 120
DB 61 QLCTEEIQQIGTLESQIVQGVTVRFLFKNLSLIKKYIDGQKKCGERRRVNQFLDYLO 120	DB 61 QLCTEEIQQIGTLESQIVQGVTVRFLFKNLSLIKKYIDGQKKCGERRRVNQFLDYLO 120
QY 121 VELGVINTEWTPES 134	QY 121 VELGVINTEWTPES 134
DB 121 EFLGVNTEWTPES 134	DB 121 EFLGVNTEWTPES 134

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Db 121 EFLGVMNTEWIIIES 134
RESULT 9
US-10-400-708-12
; Sequence 12, Application US/10400708
; Publication No. US2003016685A1
; GENERAL INFORMATION:
; APPLICANT: Cox III, George N
; TITLE OF INVENTION: Derivatives of Growth Hormone and Related Proteins
; CURRENT APPLICATION NUMBER: US/10/400,708
; CURRENT FILING DATE: 2003-03-26
; PRIOR APPLICATION NUMBER: US/09/462,941
; PRIOR FILING DATE: 2000-01-14
; PRIOR APPLICATION NUMBER: 60/052,516
; PRIOR FILING DATE: 1997-07-14
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 12
; LENGTH: 134
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-400-708-12
Query Match 61.8%; Score 430; DB 14; Length 134;
Best Local Similarity 64.9%; Pred. No. 5.3e-42;
Matches 87; Conservative 17; Mismatches 30; Indels 0; Gaps 0;
QY 1 MRMLNLSSLALGAAYSAFAVENPMRLVAETLLTSLTHTWLIGDGNLMIPTPKNKH 60
Db 1 MRMLHLSSLALGAAYVAIPTPTSAVKETLALLSTHRTLLIANETLRIPVPVKNH 60
QY 61 QLCIKVEFGIDTLKNQTAHGEAVDKLFQNLISLKEHIERQKKECAGERWRVTKFLDYIQ 120
Db 61 QLCTEEIFQGITLESQTVQGGTVVERLFFKNLSLIKKYIDGKKKCGERRRVNQFLDYIQ 120
QY 121 VFLGVINTEWTPES 134
Db 121 EFLGVMNTEWIIIES 134
RESULT 11
US-10-050-902-233
; Sequence 233, Application US/10050902
; Publication No. US20030175290A1
; GENERAL INFORMATION:
; APPLICANT: Renner, Wolfgang A.
; APPLICANT: Bachmann, Martin
; APPLICANT: Tissot, Alain
; APPLICANT: Maurer, Patrick
; APPLICANT: Lechner, Franziska
; APPLICANT: Sebbel, Peter
; APPLICANT: Piossek, Christine
; TITLE OF INVENTION: Molecular Antigen Array
; FILE REFERENCE: 1700.0190004
; CURRENT APPLICATION NUMBER: US/10/050,902
; CURRENT FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: US 60/262,379
; PRIOR FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: US 60/288,549
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: US 60/326,998
; PRIOR FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: US 60/331,045
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 350
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 233
; LENGTH: 134
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-050-902-233
Query Match 61.8%; Score 430; DB 14; Length 134;
Best Local Similarity 64.9%; Pred. No. 5.3e-42;
Matches 87; Conservative 17; Mismatches 30; Indels 0; Gaps 0;
QY 1 MRMLNLSSLALGAAYSAFAVENPMRLVAETLLTSLTHTWLIGDGNLMIPTPKNKH 60
Db 1 MRMLHLSSLALGAAYVAIPTPTSAVKETLALLSTHRTLLIANETLRIPVPVKNH 60
QY 61 QLCIKVEFGIDTLKNQTAHGEAVDKLFQNLISLKEHIERQKKECAGERWRVTKFLDYIQ 120
Db 61 QLCTEEIFQGITLESQTVQGGTVVERLFFKNLSLIKKYIDGKKKCGERRRVNQFLDYIQ 120
QY 121 VFLGVINTEWTPES 134
Db 121 EFLGVMNTEWIIIES 134
RESULT 12
US-10-050-898-233
; Sequence 233, Application US/10050898
; Publication No. US2003017571A1
; GENERAL INFORMATION:
; APPLICANT: Renner, Wolfgang A.
; APPLICANT: Tissot, Alain
; APPLICANT: Maurer, Patrick
; APPLICANT: Lechner, Franziska
; APPLICANT: Sebbel, Peter
; APPLICANT: Piossek, Christine
; APPLICANT: Ortmann, Rainer
; APPLICANT: Luond, Rainer
US-10-050-898-233
Query Match 61.8%; Score 430; DB 14; Length 134;
Best Local Similarity 64.9%; Pred. No. 5.3e-42;
Matches 87; Conservative 17; Mismatches 30; Indels 0; Gaps 0;
QY 1 MRMLNLSSLALGAAYSAFAVENPMRLVAETLLTSLTHTWLIGDGNLMIPTPKNKH 60
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QY 61 QLCIKVEFGIDTLKNQTAHGEAVDKLFQNLISLKEHIERQKKECAGERWRVTKFLDYIQ 120
Db 61 QLCTEEIFQGITLESQTVQGGTVVERLFFKNLSLIKKYIDGKKKCGERRRVNQFLDYIQ 120
QY 121 VFLGVINTEWTPES 134
Db 121 EFLGVMNTEWIIIES 134
RESULT 12
US-10-298-148-12
; Sequence 12, Application US/10298148
; Publication No. US2003017284A1
; GENERAL INFORMATION:
; APPLICANT: Cox III, George N
; TITLE OF INVENTION: Derivatives of Growth Hormone and Related Proteins
; FILE REFERENCE: 4152-1-PUS
; CURRENT APPLICATION NUMBER: US/10/298,148
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: US/09/462,941
; PRIOR FILING DATE: 2000-01-14
; PRIOR APPLICATION NUMBER: 60/052,516
; PRIOR FILING DATE: 1997-07-14
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 12
; LENGTH: 134
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-298-148-12
Query Match 61.8%; Score 430; DB 14; Length 134;
Best Local Similarity 64.9%; Pred. No. 5.3e-42;
Matches 87; Conservative 17; Mismatches 30; Indels 0; Gaps 0;
QY 1 MRMLNLSSLALGAAYSAFAVENPMRLVAETLLTSLTHTWLIGDGNLMIPTPKNKH 60
Db 1 MRMLHLSSLALGAAYVAIPTPTSAVKETLALLSTHRTLLIANETLRIPVPVKNH 60
QY 61 QLCIKVEFGIDTLKNQTAHGEAVDKLFQNLISLKEHIERQKKECAGERWRVTKFLDYIQ 120
Db 61 QLCTEEIFQGITLESQTVQGGTVVERLFFKNLSLIKKYIDGKKKCGERRRVNQFLDYIQ 120
QY 121 VFLGVINTEWTPES 134
Db 121 EFLGVMNTEWIIIES 134
RESULT 10
US-10-298-148-12
; Sequence 12, Application US/10298148
; Publication No. US2003017284A1
; GENERAL INFORMATION:
; APPLICANT: Cox III, George N
; TITLE OF INVENTION: Derivatives of Growth Hormone and Related Proteins
; FILE REFERENCE: 4152-1-PUS
; CURRENT APPLICATION NUMBER: US/10/298,148
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: US/09/462,941
; PRIOR FILING DATE: 2000-01-14
; PRIOR APPLICATION NUMBER: 60/052,516
; PRIOR FILING DATE: 1997-07-14
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 12
; LENGTH: 134
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-298-148-12
Query Match 61.8%; Score 430; DB 14; Length 134;
Best Local Similarity 64.9%; Pred. No. 5.3e-42;
Matches 87; Conservative 17; Mismatches 30; Indels 0; Gaps 0;
QY 1 MRMLNLSSLALGAAYSAFAVENPMRLVAETLLTSLTHTWLIGDGNLMIPTPKNKH 60
Db 1 MRMLHLSSLALGAAYVAIPTPTSAVKETLALLSTHRTLLIANETLRIPVPVKNH 60
QY 61 QLCIKVEFGIDTLKNQTAHGEAVDKLFQNLISLKEHIERQKKECAGERWRVTKFLDYIQ 120
Db 61 QLCTEEIFQGITLESQTVQGGTVVERLFFKNLSLIKKYIDGKKKCGERRRVNQFLDYIQ 120
QY 121 VFLGVINTEWTPES 134
Db 121 EFLGVMNTEWIIIES 134
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; APPLICANT: Staufenbiel, Matthias
; APPLICANT: Frey, Peter
; TITLE OF INVENTION: Molecular Antigen Array
; FILE REFERENCE: 1700.0190005
; CURRENT APPLICATION NUMBER: US/10/050,898
; CURRENT FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: US 60/262,379
; PRIOR FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: US 60/288,549
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: US 60/326,998
; PRIOR FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: US 60/331,045
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 350
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 233
; LENGTH: 134
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-050-898-233

Query Match 61.8%; Score 430; DB 14; Length 134;
Best Local Similarity 64.9%; Pred. No. 5.3e-42;
Matches 87; Conservative 17; Mismatches 30; Indels 0; Gaps 0;

Qy 1 MRMLNLSSLALGAAVVSFAFVENPMNRLVAETLTLLSTHRTWLTGDNLMIPTPENKNH 60
Db 1 MRMLHLSSLALGAAVVAIPTPTSAVKETLALLSTHRTLLIANETLRIPVPHKNH 60

Qy 61 QLCIKVEFGQIDTLKNQTAHGEAVDKLQNLSLIKEHIERQKRCAGRWRTKFLDYLO 120
Db 61 QLCTEEFGQIGTLESQTVGGTVRFLKNLSLIKYYIDGQKKCGEERRVNFQFLDYLO 120

Qy 121 VFLGVINTEWTPES 134
Db 121 EFLGVNTEWIIIES 134

RESULT 13
US-10-295-074-9
; Sequence 9, Application US/10295074
; Publication No. US20030185845A1
; GENERAL INFORMATION:
; APPLICANT: Pharmexa A/S
; TITLE OF INVENTION: NOVEL IMMUNOGENIC MIMETICS OF MULTIMER PROTEINS
; FILE REFERENCE: P1013DK00
; CURRENT APPLICATION NUMBER: US/10/295,074
; CURRENT FILING DATE: 2002-11-15
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 285
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: 2 human IL5 monomers joined by P30 and P2 epitopes
US-10-295-074-9

Query Match 61.8%; Score 430; DB 14; Length 285;
Best Local Similarity 64.9%; Pred. No. 1.5e-41;
Matches 87; Conservative 17; Mismatches 30; Indels 0; Gaps 0;

Qy 1 MRMLNLSSLALGAAVVSFAFVENPMNRLVAETLTLLSTHRTWLTGDNLMIPTPENKNH 60
Db 1 MRMLHLSSLALGAAVVAIPTPTSAVKETLALLSTHRTLLIANETLRIPVPHKNH 60

Qy 61 QLCIKVEFGQIDTLKNQTAHGEAVDKLQNLSLIKEHIERQKRCAGRWRTKFLDYLO 120
Db 61 QLCTEEFGQIGTLESQTVGGTVRFLKNLSLIKYYIDGQKKCGEERRVNFQFLDYLO 120

Qy 121 VFLGVINTEWTPES 134
Db 121 EFLGVNTEWIIIES 134

RESULT 13
US-10-295-074-9
; Sequence 9, Application US/10295074
; Publication No. US20030185845A1
; GENERAL INFORMATION:
; APPLICANT: Pharmexa A/S
; TITLE OF INVENTION: NOVEL IMMUNOGENIC MIMETICS OF MULTIMER PROTEINS
; FILE REFERENCE: P1013DK00
; CURRENT APPLICATION NUMBER: US/10/295,074
; CURRENT FILING DATE: 2002-11-15
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 285
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: 2 human IL5 monomers joined by P30 and P2 epitopes
US-10-295-074-9

Query Match 61.8%; Score 430; DB 14; Length 285;
Best Local Similarity 64.9%; Pred. No. 1.5e-41;
Matches 87; Conservative 17; Mismatches 30; Indels 0; Gaps 0;

Qy 1 MRMLNLSSLALGAAVVSFAFVENPMNRLVAETLTLLSTHRTWLTGDNLMIPTPENKNH 60
Db 1 MRMLHLSSLALGAAVVAIPTPTSAVKETLALLSTHRTLLIANETLRIPVPHKNH 60

Qy 61 QLCIKVEFGQIDTLKNQTAHGEAVDKLQNLSLIKEHIERQKRCAGRWRTKFLDYLO 120
Db 61 QLCTEEFGQIGTLESQTVGGTVRFLKNLSLIKYYIDGQKKCGEERRVNFQFLDYLO 120

Qy 121 VFLGVINTEWTPES 134
Db 121 EFLGVNTEWIIIES 134
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Db 121 EFLGVNTEWIIIES 134

RESULT 14
US-10-295-074-11
; Sequence 11, Application US/10295074
; Publication No. US20030185845A1
; GENERAL INFORMATION:
; APPLICANT: Pharmexa A/S
; TITLE OF INVENTION: NOVEL IMMUNOGENIC MIMETICS OF MULTIMER PROTEINS
; FILE REFERENCE: P1013DK00
; CURRENT APPLICATION NUMBER: US/10/295,074
; CURRENT FILING DATE: 2002-11-15
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 285
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: 2 human IL5 monomers joined by P2 and P30 epitopes
US-10-295-074-11

Query Match 61.8%; Score 430; DB 14; Length 285;
Best Local Similarity 64.9%; Pred. No. 1.5e-41;
Matches 87; Conservative 17; Mismatches 30; Indels 0; Gaps 0;

Qy 1 MRMLNLSSLALGAAVVSFAFVENPMNRLVAETLTLLSTHRTWLTGDNLMIPTPENKNH 60
Db 1 MRMLHLSSLALGAAVVAIPTPTSAVKETLALLSTHRTLLIANETLRIPVPHKNH 60

Qy 61 QLCIKVEFGQIDTLKNQTAHGEAVDKLQNLSLIKEHIERQKRCAGRWRTKFLDYLO 120
Db 61 QLCTEEFGQIGTLESQTVGGTVRFLKNLSLIKYYIDGQKKCGEERRVNFQFLDYLO 120

Qy 121 VFLGVINTEWTPES 134
Db 121 EFLGVNTEWIIIES 134

RESULT 15
US-10-295-074-15
; Sequence 15, Application US/10295074
; Publication No. US20030185845A1
; GENERAL INFORMATION:
; APPLICANT: Pharmexa A/S
; TITLE OF INVENTION: NOVEL IMMUNOGENIC MIMETICS OF MULTIMER PROTEINS
; FILE REFERENCE: P1013DK00
; CURRENT APPLICATION NUMBER: US/10/295,074
; CURRENT FILING DATE: 2002-11-15
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
; LENGTH: 287
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Two human IL5 monomers joined by a di-glycine linker and including
; OTHER INFORMATION: g terminally positioned tetanus toxoid P2 and P30 epitopes
US-10-295-074-15

Query Match 59.7%; Score 415.5; DB 14; Length 287;
Best Local Similarity 58.4%; Pred. No. 7.4e-40;
Matches 87; Conservative 17; Mismatches 30; Indels 15; Gaps 1;

Qy 1 MRMLNLSSLALGAAVVSFAFVENPMNRLVAETLTLLSTHRTWLTGDNLMIPTPENKNH 45
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Qy 46 GGNLMIPTPENKNHQLCKEIVFGQIDTLKNQTAHGEAVDKLQNLSLIKEHIERQKRC 105
Db 61 ANETLRIPVPHKNHQLCTEEIFQIGTLESQTVGGTVRFLKNLSLIKYYIDGQKKRC 120
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Qy 106 AGERRVTKELDYLOVFLGVNTENTPES 134
Db 121 GEERRVNQFLDYLOEFLGVNTENTWIES 149

Search completed: August 25, 2004, 00:21:34
Job time : 91.9478 secs

OM protein - protein search, using sw model
Run on: August 24, 2004, 23:55:53 ; Search time 26.3695 Seconds
(without alignments)
488.810 Million cell updates/sec

Title: US-10-787-392-5
Perfect score: 696
Sequence: 1 MRMLNLSLALGAAYVSFAF.....FLDYLVQLVGLVINTWTPES 134

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 78.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	551	79.2	134	JCS116	interleukin-5 precursor - bovine
2	430	61.8	134	A28477	interleukin-5 precursor - bovine
3	376	54.0	133	1 ICM85	interleukin-5 precursor - bovine
4	361	51.9	132	1 A48418	interleukin-5 precursor - bovine
5	83.5	12.0	1199	2 G69698	RNA polymerase (beta)
6	78.5	11.3	258	2 T47758	hypothetical protein
7	77.5	11.1	331	2 G83876	hypothetical protein
8	77	11.1	478	2 T33735	ATP-dependent deox
9	74.5	10.7	1232	2 B39432	hypothetical protein
10	73.5	10.6	253	2 T47757	hypothetical protein
11	72.5	10.4	207	2 C71914	phosphoserine phosphatase
12	72.5	10.4	451	2 S33816	kinase light chain
13	72.5	10.4	649	2 S33813	kinase light chain
14	72.5	10.4	677	2 S33814	kinase light chain
15	72.5	10.4	686	2 S33815	kinase light chain
16	72	10.3	253	2 C97331	arac-type DNA-binding protein
17	72	10.3	401	2 S28653	hypothetical protein
18	71	10.2	216	2 B69498	hypothetical protein
19	71	10.2	300	2 F84594	hypothetical protein
20	71	10.2	328	2 F64187	p-aminobenzoate synthase
21	71	10.2	446	2 S76228	hypothetical protein
22	71	10.2	461	2 T38698	nucleic acid protein - fib
23	71	10.2	544	2 T42932	virion tegument protein
24	70.5	10.1	1055	2 T10432	DNA-directed RNA polymerase
25	70	10.1	215	2 F45355	ORF2 protein - Aut
26	70	10.1	933	2 A59250	myosin - Acetabula
27	70	10.1	1871	2 D96898	probable DNA polymerase
28	70	10.1	1894	2 T02155	DNA-directed DNA polymerase
29	69.5	10.0	1188	2 JC4889	phosphatidylinositol 3-kinase

30 69 9.9 215 2 B72854
31 69 9.9 346 2 S66958
32 69 9.9 437 2 S50006
33 69 9.9 759 2 F46662
34 68.5 9.8 189 2 D89966
35 68.5 9.8 190 2 S23712
36 68.5 9.8 638 2 A82115
37 68.5 9.8 709 2 T32089
38 68.5 9.8 756 2 T12697
39 68.5 9.8 1102 2 S65235
40 68 9.8 215 2 T41780
41 68 9.8 304 2 B23431
42 68 9.8 414 2 G84311
43 68 9.8 416 2 T35282
44 68 9.8 529 2 S35306
45 68 9.8 767 1 COZPCD

ALIGNMENTS

RESULT 1

JCS116
interleukin-5 precursor - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 02-Feb-1997 #sequence_revision 27-Feb-1997 #text_change 20-Jun-2000
C:Accession: JCS116
R:Mertens, B.; Gobright, E.; Seow, H.F.
Gene 176, 273-274, 1996
A:Title: The nucleotide sequence of the bovine interleukin-5-encoding cDNA.
A:Reference number: JCS116; MUID:97075944; PMID:8918267
A:Accession: JCS116
A:Molecule type: mRNA
A:Residues: 1-134 <MER>
A:Cross-references: EMBL:Z67872; NID:g1113120; PIDN:CAA91779.1; PID:g1113121
A:Experimental source: lymphocytes
C:Comment: this protein plays a role in the eosinophilia associated with parasitic disease
C:Gene: IL-5
C:Superfamily: interleukin-5
C:Keywords: cytokine; glycoprotein; growth factor; homodimer; lymphokine; T-cell
F:1-15/Domain: signal sequence #status predicted <SIG>
F:20-134/Product: interleukin-5 #status predicted <MAT>
F:63/Disulfide bonds: interchain (to 105) #status predicted
F:76,90/Binding site: carbonyl site (Asn) (covalent) #status predicted
F:105/Disulfide bonds: interchain (to 63) #status predicted

Query Match 79.2%; Score 551; DB 2; Length 134;
Best Local Similarity 79.9%; Pred. No. 2.2e-46;
Matches 107; Conservative 15; Mismatches 12; Indels 0; Gaps 0;

QY 1 MRMLNLSLALGAAYVSFAFVPMNPLVAETLTLLSTHTWIGDNLMIPTENKQH 60

Db 1 MEMHLTLVALGAAYVCANAVSTMRNLVAETLTLLSSHTLLIGDNLMIPTQHTNH 60

QY 61 QLCICEVFGIDTLKQTAHGEVNDKLPONLSLKEHIEROKKRCAGBEWVTKFLDYLO 120

Db 61 QLCICEVFGIDTLKQTAHGEVNDKLPONLSLKEHIEROKKRCAGBEWVTKFLDYLO 120

QY 121 VFLGVINTEWTPES 134

Db 121 VFLGVINTEWTPES 134

RESULT 2

A28477
interleukin-5 precursor - human
N:Alternate names: B-cell growth factor II; cytotoxic T lymphocyte inducer; eosinophil
C:Species: Homo sapiens (man)
C:Date: 01-Dec-1989 #sequence_revision 07-Jul-1995 #text_change 22-Jun-1999
C:Accession: A28477; A33883; A28112; A39881; JX0106; S15775
R:Tanabe, T.; Konishi, M.; Mizuta, T.; Noma, T.; Honjo, T.
J. Biol. Chem. 262, 16580-16584, 1987

A;Title: Molecular cloning and structure of the human interleukin-5 gene.
 A;Reference number: A28477; MUID:8059042; PMID:2824500
 A;Accession: A28477
 A;Molecule type: DNA
 A;Residues: 1-134 <TAN>
 A;Cross-references: GB:J03478; NID:G186338; PIDN:AAA74469.1; PID:G386922
 R;Campbell, H.D.; Tucker, W.Q.J.; Hort, Y.; Martinson, M.E.; Mayo, G.; Clutterbuck, E.J.
 Proc. Natl. Acad. Sci. U.S.A. 84, 6629-6633, 1987
 A;Title: Molecular cloning, nucleotide sequence, and expression of the gene encoding human interleukin-5.
 A;Reference number: A33883; MUID:88016145; PMID:3498940
 A;Accession: A33883
 A;Molecule type: DNA
 A;Residues: 1-134 <CAM>
 A;Cross-references: GB:J02971; NID:G186340; PIDN:AAA98620.1; PID:G386923
 R;Azuma, C.; Tanabe, T.; Konishi, M.; Kinashi, T.; Noma, T.; Matsuda, F.; Yaoita, Y.; Tanabe, T.
 Nucleic Acids Res. 14, 9149-9158, 1986
 A;Title: Cloning of cDNA for human T-cell replacing factor (interleukin-5) and comparison of its nucleotide sequence with that of the mouse interleukin-5.
 A;Reference number: A26112; MUID:87066782; PMID:3024129
 A;Accession: A26112
 A;Molecule type: mRNA
 A;Residues: 1-134 <AZU>
 A;Cross-references: GB:X04698; NID:G33835; PIDN:CAA28390.1; PID:G33836
 R;Yokota, T.; Coffman, R.L.; Hagiwara, H.; Rennick, D.M.; Takebe, Y.; Yokota, K.; Gemmel, D.; Vries, J.; Lee, F.D.; Arai, N.; Arai, K.
 Proc. Natl. Acad. Sci. U.S.A. 84, 7388-7392, 1987
 A;Title: Isolation and characterization of lymphokine cDNA clones encoding mouse and human interleukin-5.
 A;Reference number: A39881; MUID:88041112; PMID:2823259
 A;Accession: A39881
 A;Status: not compared with conceptual translation
 A;Molecule type: mRNA
 A;Residues: 1-134 <YOK>
 R;Proudfoot, A.E.I.; Davies, J.G.; Turcatti, G.; Wingfield, P.T.
 FEBS Lett. 283, 61-64, 1991
 A;Title: Human interleukin-5 expressed in *Escherichia coli*: assignment of the disulfide bonds.
 A;Reference number: S15775; MUID:91243878; PMID:2037074
 A;Contents: annotation; disulfide bonds
 R;Minamide, Y.; Kodama, S.; Katayama, T.; Adachi, H.; Tanaka, S.; Tsujimoto, M.
 J. Biochem. 107, 292-297, 1990
 A;Title: Structure of recombinant human interleukin 5 produced by chinese hamster ovary cells.
 A;Reference number: JX0106; MUID:90299869; PMID:2361960
 A;Contents: annotation; disulfide bonds; glycosylation sites
 C;Genetics:
 A;Gene: GDB:115
 A;Cross-references: GDB:120097; OMIM:147850
 A;Map position: 5q31.1-5q31.1
 A;Introns: 48/3; 59/3; 102/3
 C;Superfamily: interleukin-5
 C;Keywords: cytokine; glycoprotein; growth factor; homodimer; lymphokine; T-cell
 F;1-19/Domain: signal sequence #status predicted <SIG>
 F;20-134/Product: interleukin-5 #status predicted <MAT>
 F;22/Binding site: carbohydrate (thr) (covalent) #status experimental
 F;47,90/Binding site: carbohydrate (asn) (covalent) #status predicted
 F;63/Disulfide bonds: interchain (to 105) #status experimental
 F;105/Disulfide bonds: interchain (to 63) #status experimental
 Query Match 61.8%; Score 430; DB 1; Length 134;
 Best Local Similarity 64.9%; Pred. No. 1.3e-34;
 Matches 87; Conservative 17; Mismatches 30; Indels 0; Gaps 0;
 Qy 1 MRMLNLSLLALGAAVYSAFAVENPMNRLVAETLLTSLTHTWLGDNLMIPENKQH 60
 Db 1 MRMLNLSLLALGAAVYSAFAVENPMNRLVAETLLTSLTHTWLGDNLMIPENKQH 60
 Qy 61 QLCIKVEFGQIDTLKQTAHGAVDKLFQNLISLKEHIERQKRCAGRWRTKFLDYLO 120
 Db 61 QLCITEEFQGGTLESQVGGTVERLFNLSLIKKYIDGQKKCGERRRVNQFDLYLO 120
 Qy 121 VFLGVINTEWTPES 134
 Db 121 EFLGVNTEWTEES 134

ICMS5
 interleukin-5 precursor - mouse
 N;Alternate names: B-cell growth factor II; cytotoxic T lymphocyte inducer; eosinophil d
 C;Species: Mus musculus (house mouse)
 C;Date: 30-Sep-1991 #sequence revision 30-Sep-1991 #text change 22-Jun-1999
 C;Accession: S00807; A38758; A24898; JS0077; PH0102; B39881
 R;Campbell, H.D.; Tucker, W.Q.J.; Hort, Y.; Martinson, M.E.; Tucker, W.Q.J.;
 Eur. J. Biochem. 174, 345-352, 1988
 A;Title: Isolation, structure and expression of cDNA and genomic clones for murine eosin
 n-5.
 A;Reference number: S00807; MUID:88254802; PMID:3133208
 A;Accession: S00807
 A;Molecule type: DNA
 A;Residues: 1-133 <CAM>
 A;Cross-references: EMBL:X06271; NID:952685; PIDN:CAA39607.1; PID:952686
 A;Accession: A38758
 A;Molecule type: mRNA
 A;Residues: 1-133 <CAM2>
 A;Cross-references: EMBL:X06270; NID:952687; PIDN:CAA39606.1; PID:952688
 R;Kinashi, T.; Harada, N.; Severinson, E.; Tanabe, T.; Sideras, P.; Konishi, M.; Azuma,
 Nature 324, 70-73, 1986
 A;Title: Cloning of complementary DNA encoding T-cell replacing factor and identity with
 A;Reference number: A24898; MUID:87065032; PMID:3024009
 A;Accession: A24898
 A;Molecule type: mRNA
 A;Residues: 1-133 <KIN>
 A;Cross-references: EMBL:X04601; NID:954898; PIDN:CAA28266.1; PID:954899
 R;Mizuta, T.R.; Tanabe, T.; Nakakubo, H.; Noma, T.; Honjo, T.
 Growth Factors 1, 51-57, 1988
 A;Title: Molecular cloning and structure of the mouse interleukin-5 gene.
 A;Reference number: JS0077; MUID:90180853; PMID:3078564
 A;Accession: JS0077
 A;Molecule type: DNA
 A;Residues: 1-133 <MIT>
 R;Takahashi, T.; Yamaguchi, N.; Mita, S.; Yamaguchi, Y.; Suda, T.; Tominaga, A.; Kikuchi
 Mol. Immunol. 27, 911-920, 1990
 A;Title: Structural comparison of murine T-cell (B151K12)-derived T-cell-replacing facto
 A;Reference number: PH0102; MUID:91015093; PMID:2215480
 A;Accession: PH0102
 A;Molecule type: protein
 A;Residues: 21-45; 'X', 47 <TAK>
 R;Yokota, T.; Coffman, R.L.; Hagiwara, H.; Rennick, D.M.; Takebe, Y.; Yokota, K.; Gemmel
 de Vries, J.; Lee, F.D.; Arai, N.; Arai, K.
 Proc. Natl. Acad. Sci. U.S.A. 84, 7388-7392, 1987
 A;Title: Isolation and characterization of lymphokine cDNA clones encoding mouse and hum
 A;Reference number: A39881; MUID:88041112; PMID:2823259
 A;Accession: B39881
 A;Status: preliminary; not compared with conceptual translation
 A;Molecule type: mRNA
 A;Residues: 1-14, 'AA', 15-133 <YOK>
 C;Genetics:
 A;Introns: 47/3; 58/3; 101/3
 C;Superfamily: interleukin-5
 C;Keywords: cytokine; glycoprotein; growth factor; homodimer; lymphokine; T-cell
 F;1-18/Domain: signal sequence #status predicted <SIG>
 F;19-133/Product: interleukin-5 #status predicted <MAT>
 F;46/Binding site: carbohydrate (asn) (covalent) #status experimental
 F;62/Disulfide bonds: interchain (to 104) #status predicted
 F;75,93/Binding site: carbohydrate (asn) (covalent) #status predicted
 F;105/Disulfide bonds: interchain (to 62) #status predicted
 Query Match 54.0%; Score 376; DB 1; Length 133;
 Best Local Similarity 56.8%; Pred. No. 2.2e-29;
 Matches 75; Conservative 21; Mismatches 34; Indels 2; Gaps 1;
 Qy 2 RMLNLSLLALGAAVYSAFAVENPMNRLVAETLLTSLTHTWLGDNLMIPENKQH 61
 Db 3 RMLNLSLLALGAAVYSAFAVENPMNRLVAETLLTSLTHTWLGDNLMIPENKQH 60
 Qy 62 LCICEVFGQIDTLKQTAHGAVDKLFQNLISLKEHIERQKRCAGRWRTKFLDYLO 121
 Db 61 LCICEIFQGLDILKQTVRGCTVEMLFQNLISLKEHIERQKRCAGRWRTKFLDYLO 120

QY 122 FLGVINTEWTP 133
Db 121 FLGVINTEWAME 132

RESULT 4
A48418
interleukin-5 precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: A48418; S37641
R:Uderia, K.; Li, W.Q.; Qin, Z.H.; Richter, G.; Raabe, T.; Diamantstein, T.; Blankenstein
Cytokine 3, 72-81, 1991
A:Title: The rat interleukin-5 gene: characterization and expression by retroviral gene
A:Reference number: A48418; MUID:91355638; PMID:1653053
A:Accession: A48418
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-132 <UBE>
A:Cross-references: EMBL:X54419; NID:G313254; PIDN:CAA38283.1; PID:G313255
A:Experimental source: cell line TR5-1
A>Note: sequence extracted from NCBI backbone (NCBI:63651, NCBI:63652)
C:Superfamily: interleukin-5
C:Keywords: cytokine; glycoprotein; growth factor; homodimer; lymphokine; T-cell
F:1-17/Domain: signal sequence #status predicted <SIG>
F:18-132/Product: interleukin-5 #status predicted <MAT>
F:45,74,88/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:61/Disulfide bonds: interchain (to 103) #status predicted
F:103/Disulfide bonds: interchain (to 61) #status predicted

Query Match 51.9%; Score 361; DB 1; Length 132;
Best Local Similarity 54.9%; Pred. No. 6.3e-28;
Matches 73; Conservative 21; Mismatches 37; Indels 2; Gaps 1;

QY 1 MRMLNLALLGAAVYSAFAVENPMNLVAETLLSHRTWLTGDNLMIPTEPNKH 60
Db 1 MRMLNLALLGAAVYSAFAVENPMNLVAETLLSHRTWLTGDNLMIPTEPNKH 58

QY 61 QLCIKVFQGITLKNQTAHGEAVDKLFQNLISLKEHIERQKRCAGRWRTKFLDYIQ 120
Db 59 QLCIGETFGDLIKNQTAVGGTVEILFQNLISLKYIDQKCEERKTRHFLDYIQ 118

QY 121 VELGVINTEWTP 133
Db 119 EFLGVINTEWAME 131

RESULT 5
G69698
RNA polymerase (beta' subunit) rpoC - Bacillus subtilis
C:Species: Bacillus subtilis
C>Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 02-Sep-2000
C:Accession: G69698
R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Allioni, G.; Azevedo, V.; Berte
C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Ch
A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Gallizzi, A.; Gall
lech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.
Koeter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,
A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maue
Y. M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetel
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon,
A:Authors: Schleich, S.; Schroeter, R.; Scofield, P.; Sekiguchi, J.; Sekowska, A.; Ser
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama,
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K
A:Authors: Yoshikawa, H.P.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A:Reference number: A69580; MUID:98044033; PMID:9384377
A:Accession: G69698
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-1199 <KUN>

A:Cross-references: GB:Z99104; GB:AL009136; NID:G2632267; PIDN:CAB11884.1; PID:e1182041;
A:Experimental source: strain 168
C:Genetics:
A:Gene: rpoC
C:Superfamily: Escherichia coli DNA-directed RNA polymerase beta' chain

Query Match 12.0%; Score 83.5; DB 2; Length 1199;
Best Local Similarity 27.1%; Pred. No. 8;
Matches 35; Conservative 20; Mismatches 41; Indels 33; Gaps 6;

QY 1 MRMLNLALLGAAVYSAFAVENPMNLVAETLLSHRTWLTGDNLMIPTEPNKH 59
Db 114 MGLVLDMSPRALEEYVFASVVTDPAN-----TPLEKK 147

QY 60 HOLCIKEVFQGITLKN--QTAHG-EAVDKLFQNLISLKE--HIERQKRCAGB-RWRVT 113
Db 148 QLLSEKEVAYLDKYNKFKQASMGAEALHKLQIDLDVKEVDMLKEELKTSQGRRTAI 207

QY 114 KFLDYLOVF 122
Db 208 KRLEVLEAF 216

RESULT 6
T47758
hypothetical protein F2413.60 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 28-Jul-2000
C:Accession: T47758
R:Nyakatura, G.; Rartmann, B.; Dauner, D.; Sterr, W.; Holland, R.; Weichselgartner, M.;
submitted to the Protein Sequence Database, February 2000
A:Reference number: Z24475
A:Accession: T47758
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-258 <NVA>
A:Cross-references: EMBL:AL138655
A:Experimental source: cultivar Columbia; BAC clone F2413
C:Genetics:
A:Map position: 3
A:Introns: 109/3
A>Note: F2413.60
C:Superfamily: Arabidopsis thaliana hypothetical protein F2413.60

Query Match 11.3%; Score 78.5; DB 2; Length 258;
Best Local Similarity 26.8%; Pred. No. 4;
Matches 22; Conservative 15; Mismatches 38; Indels 7; Gaps 2;

QY 28 RLVAETLLSHRTWLTGDNLMIPTEPNKHQLCIKVFQGITD---TLKNQTAHGEA 83
Db 161 KAVANYIVTSVATR---LGDNEVMVQISSKHNFISNVLSGLEEDRFVLVDMSSSRSQ 217

QY 84 VDKLFQNLISLKEHIERQKRC 105
Db 218 GERLFYTLHLQVEKIENYKLC 239

RESULT 7
G83876
hypothetical protein BH1815 [imported] - Bacillus halodurans (strain C-125)
C:Species: Bacillus halodurans
C>Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
C:Accession: G83876
R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hir
Nucleic Acids Res. 28, 4317-4331, 2000
A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A:Reference number: AB3650; MUID:20512582; PMID:11058132
A:Accession: G83876
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-331 <STO>
A:Cross-references: GB:AP001513; GB:BA000004; NID:g10174345; PIDN:BA05534.1; GSPDB:GN0
A:Experimental source: strain C-125

C:Genetics:
A:Gene: BH1815

Query Match 11.1%; Score 77.5; DB 2; Length 331;
Best Local Similarity 26.7%; Pred. No. 6.8;
Matches 27; Conservative 20; Mismatches 43; Indels 11; Gaps 4;

QY 7 LSLIA--LGAAYSAFAVENPMLVAETLLTLLTHTWLGDNLMIPTPENKQHLQ 63

DB 86 LRLADALTATFASKETEOMINKKLTSHRLADEL-----DNRLVLP-PDRGNRE-- 137

QY 64 IKVEFOGIDTLKNQTAHGEAVDKLFQNLISLKEHIERQKR 104

DB 138 VOELIKTWLHLDVKEGEVIRYQYGVNLTKEFTLENGR 178

RESULT 8

T33735

hypothetical protein H34C03.1 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 04-Mar-2000

C:Accession: T33735

R:Kalicki, J.; Gibson, A.

submitted to the EMBL Data Library, October 1998

A:Description: The sequence of C. elegans cosmid H34C03.

A:Reference number: Z21394

A:Accession: T33735

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-478 <KAL>

A:Cross-references: EMBL:AF100862; PIDN:AAC68976.1; GSFDB:GN00022; CESP:H34C03.1

A:Experimental source: strain Bristol N2; clone H34C03

C:Genetics:

A:Gene: CESP:H34C03.1

A:Map position: 4

A:Introns: 57/1; 103/2; 185/3; 283/2; 347/3; 426/3

C:Superfamily: Caenorhabditis elegans hypothetical protein H34C03.1

Query Match 11.1%; Score 77; DB 2; Length 478;
Best Local Similarity 27.3%; Pred. No. 12;
Matches 33; Conservative 20; Mismatches 46; Indels 22; Gaps 5;

QY 6 NLSLALGAAYSAFAVENPMLVAETLLT-----LSTHTWLGDNLMIPTP----- 55

DB 261 NKSLELGNWQQTALALEAILERLESESVTQSEVSAHKTFLVVAEPAPQPVKKIDV 320

QY 56 -----ENKNHQLCIKEVFOG-----IDTLKNQTAHGEAVDKLFQNLISLKEHI--ERQKR 104

DB 321 EVKNQDKNEVIEKGTERTDIDWVFGTPLSEA-DKLSASKSAVARDVLLDSEGR 379

QY 105 C 105

DB 380 C 380

RESULT 9

B39432

ATP-dependent deoxyribonuclease chain A adda - Bacillus subtilis

C:Alternate names: ATP-dependent exonuclease synthesis protein Adda

C:Species: Bacillus subtilis

C>Date: 21-Feb-1992 #sequence_revision 21-Feb-1992 #text_change 02-Feb-2001

C:Accession: B39432; H69582

R:Kooistra, J.; Venema, G.

J. Bacteriol. 173, 3644-3655, 1991

A:Title: Cloning, sequencing, and expression of Bacillus subtilis genes involved in ATP-

A:Reference number: A39432; MUID:91267926; PMID:1646786

A:Accession: B39432

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-1232 <KOO>

A:Cross-references: GB:M63489; NID:g142438; PIDN:AAA22201.1; PID:g142440

R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter

C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chd

A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler
iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.
Koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,
A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel
Y. M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon,
A:Authors: Schleich, S.; Schroeter, R.; Scoffone, P.; Sekiguchi, J.; Sekowska, A.; Seror
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama,
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K
A:Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A:Reference number: A69580; MUID:98044033; PMID:9384377
A:Accession: H69582
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-1232 <KUN>
A:Cross-references: GB:Z99109; GB:AL009126; NID:g2633260; PIDN:CAB12903.1; PID:e1183065;
A:Experimental source: strain 168
C:Genetics:
A:Gene: adda
C:Keywords: nucleotide binding; P-loop
F:30-37/Region: nucleotide-binding motif A (P-loop)

Query Match 10.7%; Score 74.5; DB 2; Length 1232;
Best Local Similarity 22.2%; Pred. No. 62;
Matches 24; Conservative 24; Mismatches 37; Indels 23; Gaps 4;

QY 22 VENPMRLVATLTLTLLTHTWLG--DGNLMIPTPENKQHLQCIKEVFOGIDTLKNQTA 79

DB 633 IDNPF-----QDIFLASVLRSPVIGADENELSLRLNKKAPY-----YEAMKDYLA 679

QY 80 HGEAVDKLFQNLISLKEHIERQK-----KRCAGERWRVTKFDYL 119

DB 680 AGDRSDELYQKLNTFYGHQKWRFAFKNSHVSSELIWEVYRTKMYDIV 727

RESULT 10

T47757

hypothetical protein F24I3.50 - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C>Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 28-Jul-2000

C:Accession: T47757

R:Nyakatura, G.; Fartmann, B.; Dauner, D.; Sterr, W.; Holland, R.; Weichselgartner, M.;

submitted to the Protein Sequence Database, February 2000

A:Reference number: Z24475

A:Accession: T47757

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-253 <NYA>

A:Cross-references: EMBL:AL138655

A:Experimental source: cultivar Columbia; BAC clone F24I3

C:Genetics:

A:Map position: 3

A:Introns: 104/3

A>Note: F24I3.50

C:Superfamily: Arabidopsis thaliana hypothetical protein F24I3.60

Query Match 10.6%; Score 73.5; DB 2; Length 253;
Best Local Similarity 27.1%; Pred. No. 12;
Matches 23; Conservative 15; Mismatches 34; Indels 13; Gaps 3;

QY 28 RLVAETLLTHTWLGDNLMIPTPENKQHLQCIKEVFOGID-----TLKNQTAH 80

DB 156 KAVASYLSTVSATR---LGNENVMVQSSSKIHNFISNVLGGIEDGFLVDVSSRSQ 212

QY 81 GEAVDKLFQNLISLKEHIERQKRC 105

DB 213 GE---RLFYTLHLQVENNDYKINC 234

RESULT 11

C71914
phosphoserine phosphatase - Helicobacter pylori (strain J99)
C:Species: Helicobacter pylori
A:Variety: strain J99
C:Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 22-Jun-1999
C:Accession: C71914
R:Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.;
Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.;
Nature 397, 176-180, 1999
A:Title: Genomic sequence comparison of two unrelated isolates of the human gastric path
A:Reference number: A71800; MUID:99120557; PMID:9923682
A:Accession: C71914
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-207 <ARN>
A:Cross-references: GB:AE001491; GB:AE001439; NID:g4155127; PIDN:AAD06170.1; PID:g415514
A:Experimental source: strain J99
C:Genetics:
A:Gene: serB
C:Superfamily: phosphoserine phosphatase

Query Match 10.4%; Score 72.5; DB 2; Length 207;
Best Local Similarity 29.8%; Pred. No. 12;
Matches 31; Conservative 14; Mismatches 34; Indels 25; Gaps 5;

QY 9 LLALGRAVVSAPAVE-NPMRLVA-----ETLTLLSTHETWLTGNGNLM 51
Db 109 LNLDAAFNLIIVENNALNGLVTGHWMFYSKGEVLLALQRLINLSKORTLVVGGAND 168
QY 52 IPTPENKNHOLCIKEVFGQIDTTLKNQTAHGEAVDKLFQNLSLIK 95
Db 169 LSMFKAH----IKIAFNAKELKQHATH--CIDK--PNLALIK 204

RESULT 12
S33816
kinesin light chain isoform 4 - sea urchin (Strongylocentrotus purpuratus)
C:Species: Strongylocentrotus purpuratus (purple urchin)
C:Date: 08-Dec-1993 #sequence_revision 01-Dec-1995 #text_change 09-Sep-1997
C:Accession: S33816
R:Wedaman, K.P.; Knight, A.E.; Kendrick-Jones, J.; Scholey, J.M.
J. Mol. Biol. 231, 155-158, 1993
A:Title: Sequences of sea urchin kinesin light chain isoforms.
A:Reference number: S33813; MUID:93267648; PMID:8496962
A:Accession: S33816
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-451 <WED>
A:Cross-references: EMBL:L08258; NID:g161531; PID:g161532

Query Match 10.4%; Score 72.5; DB 2; Length 451;
Best Local Similarity 25.9%; Pred. No. 30;
Matches 21; Conservative 19; Mismatches 30; Indels 11; Gaps 3;

QY 46 GGNLMIPTPENKNHQLC--IKEVFGQIDTTLKNQTAHGEAVDKLFQNLSLIKHEIERQKK 103
Db 15 GQGNL-----SQEQIITGTREVIGLEQLKNE--HNDILNSLYQSLKMLKDKDTFGDSN 65

QY 104 RCAGERNVTKFLDYLOVFLG 124
Db 66 LVEKTDIIKSLSLSLGLG 86

RESULT 13
S33813
kinesin light chain - sea urchin (Strongylocentrotus purpuratus)
C:Species: Strongylocentrotus purpuratus (purple urchin)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Sep-1997
C:Accession: S33813
R:Wedaman, K.P.; Knight, A.E.; Kendrick-Jones, J.; Scholey, J.M.
J. Mol. Biol. 231, 155-158, 1993
A:Title: Sequences of sea urchin kinesin light chain isoforms.
A:Reference number: S33813; MUID:93267648; PMID:8496962

Query Match 10.4%; Score 72.5; DB 2; Length 451;
Best Local Similarity 25.9%; Pred. No. 30;
Matches 21; Conservative 19; Mismatches 30; Indels 11; Gaps 3;

QY 46 GGNLMIPTPENKNHQLC--IKEVFGQIDTTLKNQTAHGEAVDKLFQNLSLIKHEIERQKK 103
Db 15 GQGNL-----SQEQIITGTREVIGLEQLKNE--HNDILNSLYQSLKMLKDKDTFGDSN 65

QY 104 RCAGERNVTKFLDYLOVFLG 124
Db 66 LVEKTDIIKSLSLSLGLG 86

RESULT 14
S33814
kinesin light chain - sea urchin (Strongylocentrotus purpuratus)
C:Species: Strongylocentrotus purpuratus (purple urchin)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Sep-1997
C:Accession: S33814
R:Wedaman, K.P.; Knight, A.E.; Kendrick-Jones, J.; Scholey, J.M.
J. Mol. Biol. 231, 155-158, 1993
A:Title: Sequences of sea urchin kinesin light chain isoforms.
A:Reference number: S33813; MUID:93267648; PMID:8496962
A:Accession: S33814
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-677 <WED>
A:Cross-references: EMBL:L10234; NID:g161527; PID:g161528

Query Match 10.4%; Score 72.5; DB 2; Length 677;
Best Local Similarity 25.9%; Pred. No. 48;
Matches 21; Conservative 19; Mismatches 30; Indels 11; Gaps 3;

QY 46 GGNLMIPTPENKNHQLC--IKEVFGQIDTTLKNQTAHGEAVDKLFQNLSLIKHEIERQKK 103
Db 15 GQGNL-----SQEQIITGTREVIGLEQLKNE--HNDILNSLYQSLKMLKDKDTFGDSN 65

QY 104 RCAGERNVTKFLDYLOVFLG 124
Db 66 LVEKTDIIKSLSLSLGLG 86

RESULT 15
S33815
kinesin light chain isoform 3 - sea urchin (Strongylocentrotus purpuratus)
C:Species: Strongylocentrotus purpuratus (purple urchin)
C:Date: 08-Dec-1993 #sequence_revision 01-Dec-1995 #text_change 01-Dec-2000
C:Accession: S33815; S36727
R:Wedaman, K.P.; Knight, A.E.; Kendrick-Jones, J.; Scholey, J.M.
J. Mol. Biol. 231, 155-158, 1993
A:Title: Sequences of sea urchin kinesin light chain isoforms.
A:Reference number: S33813; MUID:93267648; PMID:8496962
A:Accession: S33815
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-686 <WED>
A:Cross-references: EMBL:L10235
R:Wedaman, K.P.; Knight, A.E.; Kendrick-Jones, J.; Scholey, J.M.
submitted to the EMBL Data Library, February 1993
A:Reference number: S36727
A:Accession: S36727
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-568, A', 570-686 <WE2>
A:Cross-references: EMBL:L10235; NID:g161529; PID:g161530

Query Match 10.4%; Score 72.5; DB 2; Length 686;

A:Accession: S33813
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-649 <WED>
A:Cross-references: EMBL:L10233; NID:g161525; PID:g161526

Query Match 10.4%; Score 72.5; DB 2; Length 649;
Best Local Similarity 25.9%; Pred. No. 46;
Matches 21; Conservative 19; Mismatches 30; Indels 11; Gaps 3;

QY 46 GGNLMIPTPENKNHQLC--IKEVFGQIDTTLKNQTAHGEAVDKLFQNLSLIKHEIERQKK 103
Db 15 GQGNL-----SQEQIITGTREVIGLEQLKNE--HNDILNSLYQSLKMLKDKDTFGDSN 65

QY 104 RCAGERNVTKFLDYLOVFLG 124
Db 66 LVEKTDIIKSLSLSLGLG 86

RESULT 14
S33814
kinesin light chain - sea urchin (Strongylocentrotus purpuratus)
C:Species: Strongylocentrotus purpuratus (purple urchin)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Sep-1997
C:Accession: S33814
R:Wedaman, K.P.; Knight, A.E.; Kendrick-Jones, J.; Scholey, J.M.
J. Mol. Biol. 231, 155-158, 1993
A:Title: Sequences of sea urchin kinesin light chain isoforms.
A:Reference number: S33813; MUID:93267648; PMID:8496962
A:Accession: S33814
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-677 <WED>
A:Cross-references: EMBL:L10234; NID:g161527; PID:g161528

Query Match 10.4%; Score 72.5; DB 2; Length 677;
Best Local Similarity 25.9%; Pred. No. 48;
Matches 21; Conservative 19; Mismatches 30; Indels 11; Gaps 3;

QY 46 GGNLMIPTPENKNHQLC--IKEVFGQIDTTLKNQTAHGEAVDKLFQNLSLIKHEIERQKK 103
Db 15 GQGNL-----SQEQIITGTREVIGLEQLKNE--HNDILNSLYQSLKMLKDKDTFGDSN 65

QY 104 RCAGERNVTKFLDYLOVFLG 124
Db 66 LVEKTDIIKSLSLSLGLG 86

RESULT 15
S33815
kinesin light chain isoform 3 - sea urchin (Strongylocentrotus purpuratus)
C:Species: Strongylocentrotus purpuratus (purple urchin)
C:Date: 08-Dec-1993 #sequence_revision 01-Dec-1995 #text_change 01-Dec-2000
C:Accession: S33815; S36727
R:Wedaman, K.P.; Knight, A.E.; Kendrick-Jones, J.; Scholey, J.M.
J. Mol. Biol. 231, 155-158, 1993
A:Title: Sequences of sea urchin kinesin light chain isoforms.
A:Reference number: S33813; MUID:93267648; PMID:8496962
A:Accession: S33815
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-686 <WED>
A:Cross-references: EMBL:L10235
R:Wedaman, K.P.; Knight, A.E.; Kendrick-Jones, J.; Scholey, J.M.
submitted to the EMBL Data Library, February 1993
A:Reference number: S36727
A:Accession: S36727
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-568, A', 570-686 <WE2>
A:Cross-references: EMBL:L10235; NID:g161529; PID:g161530

Query Match 10.4%; Score 72.5; DB 2; Length 686;

GenCore version 5.1.6
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QM protein - protein search, using sw model

Run on: August 24, 2004, 23:41:12 ; Search time 15.0683 Seconds
(without alignments)
463.052 Million cell updates/sec

Title: US-10-787-382-5
Perfect score: 696
Sequence: 1 MRMLNLSLALCAAYVSAP.....FLDYQLVFLGVINTEWTPES 134

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	696	100.0	134	1 IL5_CANFA	Q95J76 felis famil
2	591	84.9	134	1 IL5_FELCA	O77515 felis silve
3	567	81.5	134	1 IL5_HORSE	O02699 equus cabal
4	551	79.2	134	1 IL5_BOVIN	P52173 bos taurus
5	536	77.0	132	1 IL5_SHEEP	Q28586 ovis aries
6	430	61.8	134	1 IL5_HUMAN	P05113 homo sapien
7	429	61.6	134	1 IL5_CERTO	P46685 cercocobus
8	426	61.2	134	1 IL5_MACMU	P48093 macaca mula
9	414.5	59.6	135	1 IL5_CAVPO	O08957 cavia porce
10	388	55.7	132	1 IL5_MERUN	Q62575 meriones un
11	388	55.7	132	1 IL5_SIGHI	Q9519 sigmodon hi
12	376	54.0	133	1 IL5_MOUSE	P04401 mus musculu
13	372	53.4	139	1 IL5_MACEU	Q9xt91 macropus eu
14	361	51.9	132	1 IL5_RAT	Q08125 rattus norv
15	98.5	14.2	590	1 MP44 MYXVL	Q9q8q1 myxoma viru
16	83.5	12.0	1199	1 RPOC_BACSU	P37871 bacillus su
17	77	11.1	437	1 SECV_STRGB	O59912 streptomyc
18	74.5	10.7	1232	1 ADDA_BACSU	P23478 bacillus su
19	72.5	10.4	686	1 KLC_STRFU	Q05090 strongyloce
20	72	10.3	401	1 Y148 METSM	P22344 methanobrev
21	71	10.2	216	1 YJ87_ARCFU	O28292 archaeoglob
22	71	10.2	328	1 YB70_HARIN	O57537 haemophilus
23	71	10.2	461	1 TIPI1_SCHPO	P79055 schizosacch
24	70.5	10.1	1055	1 RPOC_PEDAC	P77917 pediococcus
25	69	9.9	215	1 Y034_NPVAC	P21287 autographa
26	69	9.9	346	1 UFEL1_YEAST	P41834 saccharomyc
27	68.5	9.8	349	1 EGC2_VIBVU	Q8d4q0 vibrio vuln
28	68.5	9.8	439	1 ARLY1_THETN	Q8r7c3 thermoaer
29	68	9.8	169	1 HSCB1_BUCBP	Q89a17 buchnera ap
30	68	9.8	529	1 CRTI1_MYXPA	O02861 myxococcus
31	68	9.8	767	1 CC10_SCHPO	P01123 schizosacch
32	67.5	9.7	247	1 Y179_ARCFU	Q30058 archaeoglob
33	67	9.6	189	1 INAC_BOVIN	P05009 bos taurus

34	67	9.6	317	1 SVGA_LACLA	Q9cgl1 lactococcus
35	67	9.6	437	1 SECV_STRCO	P46785 streptomyc
36	67	9.6	437	1 SECV_STRLI	P49977 streptomyc
37	66.5	9.6	767	1 CUL1_SCHPO	O13790 schizosacch
38	66	9.5	119	1 RPOZ_CAUCR	P58066 caulobacter
39	66	9.5	360	1 HIS8_LACLA	Q02135 lactococcus
40	66	9.5	864	1 SYL_WIGBR	Q8d333 wiggleswort
41	66	9.5	1197	1 EVGS_ECO57	P58402 escherichia
42	65.5	9.4	248	1 NAG1_CANAL	Q04802 candida alb
43	65.5	9.4	756	1 CYTM_SOLTU	P37842 solanum tub
44	65.5	9.4	889	1 SECV_DROME	Q3vvg4 drosophila
45	65.5	9.4	3859	1 TRAP_HUMAN	Q3y4a5 homo sapien

ALIGNMENTS

RESULT 1
IL5_CANFA
ID IL5_CANFA STANDARD; PRT; 134 AA.
AC Q95J76;
DT 15-MAR-2004 (Rel. 43, Created)
DT 15-MAR-2004 (Rel. 43, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Interleukin-5 precursor (IL-5) (T-cell replacing factor) (TRF)
DE (Eosinophil differentiation factor).
GN IL5.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21334408; PubMed=1140633;
RA Yang S., Sellins K.S., Weber E., McCall C.;
RT "Canine interleukin-5: molecular characterization of the gene and
expression of biologically active recombinant protein.";
RL J. Interferon Cytokine Res. 21:361-367(2001).
CC -!- FUNCTION: Factor that induces terminal differentiation of late-
developing B-cells to immunoglobulin secreting cells (By
similarity).
CC -!- SUBUNIT: Homodimer; disulfide-linked (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the IL-5 family.
CC
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CC
CC EMBL; AF331920; AAL10716.1; -;
CC EMBL; AF331919; AAL10715.1; -;
CC InterPro; IPR009079; 4_helix_cytokine.
CC InterPro; IPR000186; Interleukin_5.
CC Pfam; PF02025; IL5; 1.
CC PRINTS; PR00432; INTERLEUKIN5.
CC ProDom; PD006721; Interleukin_5; 1.
CC Cytokine; Growth factor; Glycoprotein; Signal.
CC SIGNAL 1 21
CC CHAIN 22 134
CC INTERLEUKIN-5.
CC FT DISULFID 63 63
CC INTERCHAIN (WITH C-63) (BY SIMILARITY).
CC FT DISULFID 105 105
CC INTERCHAIN (WITH C-63) (BY SIMILARITY).
CC FT CARBOHYD 76 76
CC N-LINKED (GLCNAC...) (POTENTIAL).
CC FT CARBOHYD 90 90
CC N-LINKED (GLCNAC...) (POTENTIAL).
CC SQ SEQUENCE 134 AA; 15307 MW; 003C86D94D6FF4C6 CRC64;
Query Match 100.0%; Score 696; DB 1; Length 134;
Best Local Similarity 100.0%; Pred. No. 5.3e-62;
Matches 134; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 MRMLNLSSLALGAAYSAFAVENPMRLVAETLLTLLSTHRTWLIGDGNLMIPPTENKH 60
DB 1 MRMLNLSSLALGAAYSAFAVENPMRLVAETLLTLLSTHRTWLIGDGNLMIPPTENKH 60
QY 61 QLCIKEVFGQIDTLKNTQTAHGEAVDKLFQNLISLKEHIERQKRCACGERWRVTKFDLYLQ 120
DB 61 QLCIKEVFGQIDTLKNTQTAHGEAVDKLFQNLISLKEHIERQKRCACGERWRVTKFDLYLQ 120
QY 121 VFLGVINTEWTPES 134
DB 121 VFLGVINTEWTPES 134
RESULT 2
IL5_FELCA STANDARD; PRT; 134 AA.
AC 077515; 062740;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Interleukin-5 precursor (IL-5) (T-cell replacing factor) (TRF)
DE (Eosinophil differentiation factor).
GN IL5
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_TaxID=9685;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98452715; PubMed=9781459;
RA Padric P.A., Qin Y., Wells T.N.C., Solway J., Camoretti-Mercado B.;
RT "Sequence and structural analysis of feline interleukin-5 cDNA.";
RL Am. J. Vet. Res. 59:1263-1269(1998).
RN [2]
RP SEQUENCE OF 12-128 FROM N.A.
RA Harley R., Day M.J., Gruffydd-Jones T.J., Harbours D.A., Helps C.R.;
RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Factor that induces terminal differentiation of late-
CC developing B-cells to immunoglobulin secreting cells (By
CC similarity).
CC -!- SUBUNIT: Homodimer; disulfide-linked (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the IL-5 family.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC
CC EMBL; AF025436; AAC64505.1; -.
CC EMBL; AF051372; AAC05752.1; -.
CC HSSP; P05113; 1HUL.
CC InterPro: IPR000186; Interleukin_5.
CC Pfam; PF02025; IL5; 1.
CC PRINTS; PR00432; INTERLEUKINS.
CC ProDom; PD06721; Interleukin_5; 1.
CC Cytokine; Growth factor; Glycoprotein; Signal.
CC SIGNAL 1 19
CC CHAIN 20 134
CC INTERLEUKIN-5.
CC BY SIMILARITY.
CC FT DISULFID 63 63
CC INTERCHAIN (WITH C-105) (BY SIMILARITY).
CC FT DISULFID 105 105
CC INTERCHAIN (WITH C-63) (BY SIMILARITY).
CC FT CARBOHYD 76 76
CC N-LINKED (GLCNAC. .) (POTENTIAL).
CC FT CARBOHYD 90 90
CC N-LINKED (GLCNAC. .) (POTENTIAL).
CC FT CONFLICT 104 105
CC KC -> NF (IN REF. 2).
CC FT CONFLICT 108 111
CC ERWR -> KWK (IN REF. 2).
CC FT CONFLICT 114 114
CC K -> N (IN REF. 2).
CC FT CONFLICT 117 117
CC D -> N (IN REF. 2).
CC FT CONFLICT 121 121
CC V -> F (IN REF. 2).
CC FT CONFLICT 125 126
CC VI -> LL (IN REF. 2).
CC SEQUENCE 134 AA; 15224 MW; 87D18DB8F8CAC820 CRC64;

```

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Query Match 84.9%; Score 591; DB 1; Length 134;
Best Local Similarity 85.1%; Pred. No. 1.3e-51;
Matches 114; Conservative 11; Mismatches 9; Indels 0; Gaps 0;
QY 1 MRMLNLSSLALGAAYSAFAVENPMRLVAETLLTLLSTHRTWLIGDGNLMIPPTENKH 60
DB 1 MRMLNLSSLALGAAYSAFAVENPMRLVAETLLTLLSTHRTWLIGDGNLMIPPTENKH 60
QY 61 QLCIKEVFGQIDTLKNTQTAHGEAVDKLFQNLISLKEHIERQKRCACGERWRVTKFDLYLQ 120
DB 61 QLCIKEVFGQIDTLKNTQTAHGEAVDKLFQNLISLKEHIERQKRCACGERWRVTKFDLYLQ 120
QY 121 VFLGVINTEWTPES 134
DB 121 VFLGVINTEWTPES 134
RESULT 3
IL5_HORSE STANDARD; PRT; 134 AA.
AC 003699;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Interleukin-5 precursor (IL-5) (T-cell replacing factor) (TRF)
DE (Eosinophil differentiation factor).
GN IL5
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP SEQUENCE FROM N.A.
RA Vandergrift E.V., Horchov D.W.;
RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Factor that induces terminal differentiation of late-
CC developing B-cells to immunoglobulin secreting cells (By
CC similarity).
CC -!- SUBUNIT: Homodimer; disulfide-linked (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the IL-5 family.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; U91947; AAB51382.1; -.
CC HSSP; P05113; 1HUL.
CC InterPro: IPR000186; Interleukin_5.
CC Pfam; PF02025; IL5; 1.
CC PRINTS; PR00432; INTERLEUKINS.
CC ProDom; PD06721; Interleukin_5; 1.
CC Cytokine; Growth factor; Glycoprotein; Signal.
CC SIGNAL 1 19
CC CHAIN 20 134
CC INTERLEUKIN-5.
CC BY SIMILARITY.
CC FT DISULFID 63 63
CC INTERCHAIN (WITH C-105) (BY SIMILARITY).
CC FT DISULFID 105 105
CC INTERCHAIN (WITH C-63) (BY SIMILARITY).
CC FT CARBOHYD 76 76
CC N-LINKED (GLCNAC. .) (POTENTIAL).
CC FT CARBOHYD 90 90
CC N-LINKED (GLCNAC. .) (POTENTIAL).
CC SQ SEQUENCE 134 AA; 15081 MW; 2914840E3E7A006D CRC64;
Query Match 81.5%; Score 567; DB 1; Length 134;
Best Local Similarity 83.5%; Pred. No. 3.2e-49;
Matches 111; Conservative 10; Mismatches 12; Indels 0; Gaps 0;
QY 1 MRMLNLSSLALGAAYSAFAVENPMRLVAETLLTLLSTHRTWLIGDGNLMIPPTENKH 60
DB 1 MRMLNLSSLALGAAYSAFAVENPMRLVAETLLTLLSTHRTWLIGDGNLMIPPTENKH 60

```

Qy 61 QLCICEVFGQIDTLKNOTAAGEAVDKLFQNLISLKEHIERQKRCAGERWRVTKFDLYLQ 120
Db 61 QLCICEVFGQIDTLKNOTAAGEAVDKLFQNLISLKEHIERQKRCAGERWRVTKFDLYLQ 120
Qy 121 VFLGVINTEWTPES 133
Db 121 EFLGVINTEWTPES 133

RESULT 4
IL5_BOVIN
ID IL5_BOVIN STANDARD; PRT; 134 AA.
AC P21773;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Interleukin-5 precursor (IL-5) (T-cell replacing factor) (TRF)
DE (Eosinophil differentiation factor).
GN IL5.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RX MEDLINE=97075944; PubMed=8918267;
RA Mertens B., Gibrignt E., Seow H.F.;
RT "The nucleotide sequence of the bovine interleukin-5 encoding cDNA";
RL Gene 176:273-274 (1996).
CC -1- FUNCTION: Factor that induces terminal differentiation of late-
developing B-cells to immunoglobulin secreting cells (By
similarity).
CC -1- SUBUNIT: Homodimer; disulfide-linked.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the IL-5 family.
CC
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CC
CC EMBL; Z67872; CAA91779.1; -.
CC PIR; JCS116; JCS116.
CC HSSP; P05113; 1HUL.
CC InterPro; IPR000186; Interleukin_5.
CC Pfam; PF02025; IL5; 1.
CC PRINTS; PR00432; INTERLEUKINS.
CC ProDom; PD006721; Interleukin_5; 1.
KW Cytokine; Growth factor; Glycoprotein; Signal.
FT SIGNAL 1 21 BY SIMILARITY.
FT CHAIN 22 134 INTERLEUKIN-5.
FT DISULFID 63 63 INTERCHAIN (WITH C-105) (BY SIMILARITY).
FT DISULFID 105 105 INTERCHAIN (WITH C-63) (BY SIMILARITY).
FT CARBOHYD 76 76 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 90 90 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 134 AA; 15229 MW; 0B3A2328EE7431F4 CRC64;

Query Match 79.2%; Score 551; DB 1; Length 134;
Best Local Similarity 79.8%; Pred. No. 1.2e-47;
Matches 107; Conservative 15; Mismatches 12; Indels 0; Gaps 0;

Qy 1 MRMLNLSLALGAAYSAFAVENPMLVAETLLSTHRTWLIGDGNLMITPENKH 60
Db 1 MRMLHTLVALGAAYCANAVESTMRLVAETLLSSRTLLIGDGNLMITPQHTNH 60
Qy 61 QLCICEVFGQIDTLKNOTAAGEAVDKLFQNLISLKEHIERQKRCAGERWRVTKFDLYLQ 120

Db 61 QLCICEVFGQIDTLKNOTAAGEAVDKLFQNLISLKEHIERQKRCAGERWRVTKFDLYLQ 120
Qy 121 VFLGVINTEWTPES 134
Db 121 VFLGVINTEWTPES 134

RESULT 5
IL5_SHEEP
ID IL5_SHEEP STANDARD; PRT; 132 AA.
AC Q28586;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Interleukin-5 precursor (IL-5) (T-cell replacing factor) (TRF)
DE (Eosinophil differentiation factor).
GN IL5.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RA Bryson C.E., Viney E., Brandon M., Boyd A.W.;
RL Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Seow H.-F., David M.-J., McWaters P.G., Hurst L., Wood P.R.;
RT "Cloning of ovine interleukin-5 cDNA";
RL Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Factor that induces terminal differentiation of late-
developing B-cells to immunoglobulin secreting cells (By
similarity).
CC -1- SUBUNIT: Homodimer; disulfide-linked (By similarity).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the IL-5 family.
CC
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CC
CC EMBL; U17053; AAS60629.1; -.
CC EMBL; U17052; AAS60629.1; JOINED.
CC HSSP; U35038; AAC99991.1; -.
CC HSSP; P05113; 1HUL.
CC InterPro; IPR000186; Interleukin_5.
CC Pfam; PF02025; IL5; 1.
CC PRINTS; PR00432; INTERLEUKINS.
CC ProDom; PD006721; Interleukin_5; 1.
KW Cytokine; Growth factor; Glycoprotein; Signal.
FT SIGNAL 1 19 BY SIMILARITY.
FT CHAIN 20 132 INTERLEUKIN-5.
FT DISULFID 61 61 INTERCHAIN (WITH C-103) (BY SIMILARITY).
FT DISULFID 103 103 INTERCHAIN (WITH C-61) (BY SIMILARITY).
FT CARBOHYD 74 74 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 88 88 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 132 AA; 14974 MW; D783F2B720E249D9 CRC64;

Query Match 77.0%; Score 536; DB 1; Length 132;
Best Local Similarity 78.8%; Pred. No. 3.6e-46;
Matches 104; Conservative 15; Mismatches 13; Indels 0; Gaps 0;

Qy 3 MLNLSLALGAAYSAFAVENPMLVAETLLSTHRTWLIGDGNLMITPENKH 62
Db 1 MHLRUTLVALGAAYCANAVESTMRLVAETLLSTHRTWLIGDGNLMITPQHTNH 60
Qy 63 CIKEVFGQIDTLKNOTAAGEAVDKLFQNLISLKEHIERQKRCAGERWRVTKFDLYLQ 122

Db 61 CIEEFQIDTLKQTAQDAVKKIPRNLSIKKEYIDLOKRCGGGRWRVKQFLDYLOVF 120
QY 123 LGVINTWTPES 134
121 LGVINTWTPES 132
Db 121 LGVINTWTPES 132

RESULT 6
IL5_HUMAN
ID IL5_HUMAN STANDARD; PRT; 134 AA.
AC POS13; Q13840;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Interleukin-5 precursor (IL-5) (T-cell replacing factor) (TRF)
DE (Eosinophil differentiation factor) (B cell differentiation factor I).
GN IL5
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP MEDLINE=87066782; PubMed=3024129;
RA Azuma C., Tanabe T., Konishi M., Kinashi T., Noma T., Matsuda F.,
RA Yaota Y., Takatsu K., Hammarstrom L., Smith C.I.E., Severinson E.,
RA Honjo T.;
RT "Cloning of cDNA for human T-cell replacing factor (interleukin-5)
RT and comparison with the murine homologue."
RL Nucleic Acids Res. 14:9149-9158(1986).
RN [2]
RP SEQUENCE FROM N.A.
RA MEDLINE=88059042; PubMed=2824500;
RA Tanabe T., Konishi M., Mizuta T., Noma T., Honjo T.;
RT "Molecular cloning and structure of the human interleukin-5 gene."
RL J. Biol. Chem. 262:16580-16584(1987).
RN [3]
RP SEQUENCE FROM N.A.
RA MEDLINE=88016145; PubMed=3498940;
RA Campbell H.D., Tucker W.Q.J., Hott Y., Martinson M.E., Mayo G.,
RA Clutterbuck E.J., Sanderson C.J., Young I.G.;
RT "Molecular cloning, nucleotide sequence, and expression of the gene
RT encoding human eosinophil differentiation factor (interleukin 5)."
RL Proc. Natl. Acad. Sci. U.S.A. 84:6629-6633(1987).
RN [4]
RP SEQUENCE FROM N.A.
RA MEDLINE=88041112; PubMed=2823259;
RA Yokota T., Coffman R.L., Hagiwara H., Rennick D.M., Takebe Y.,
RA Yokota K., Gemmell L., Shrader B., Yang G., Meyerson P., Luh J.,
RA Hoy P., Pene J., Briere F., Spits H., Banchereau J., de Vries J.,
RA Lee F.D., Arai N., Arai K.;
RT "Isolation and characterization of lymphokine cDNA clones encoding
RT mouse and human IgA-enhancing factor and eosinophil
RT colony-stimulating factor activities: relationship to interleukin
RT 5.";
RL Proc. Natl. Acad. Sci. U.S.A. 84:7388-7392(1987).
RN [5]
RP SEQUENCE FROM N.A.
RA Honjo T., Takatsu K., Severinson E.;
RL Submitted (FEB-1992) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A.
RA Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Poel C.L., Yi Q.,
RA Nickerson D.A.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
RN [7]
RP SEQUENCE OF 20-134, AND DISULFIDE BONDS.
RA MEDLINE=90299868; PubMed=2361960;
RA Minamitake Y., Kodama S., Katayama T., Adachi H., Tanaka S.,
RA Tsujimoto M.;
RT "Structure of recombinant human interleukin 5 produced by Chinese
RT hamster ovary cells."
RL J. Biochem. 107:292-297(1990).

RN [8]
RP DISULFIDE BONDS.
RX MEDLINE=91243878; PubMed=2037074;
RA Proudfoot A.E.I., Davies J.G., Turcatti G., Wingfield P.T.;
RT "Human interleukin-5 expressed in Escherichia coli: assignment of the
RT disulfide bridges of the purified unglycosylated protein."
RL FEBS Lett. 283:61-64(1991).
RN [9]
RP X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS).
RX MEDLINE=93247642; PubMed=8483502;
RA Milburn M.V., Hassell A.M., Lambert M.H., Jordan S.R.,
RA Proudfoot A.E.I., Graber P., Wells T.N.C.;
RT "A novel dimer configuration revealed by the crystal structure at
RT 2.4-A resolution of human interleukin-5."
RL Nature 363:172-176(1993).
CC CC
CC -!- FUNCTION: Factor that induces terminal differentiation of late-
CC developing B-cells that immunoglobulin secreting cells.
CC -!- SUBUNIT: Homodimer; disulfide-linked.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the IL-5 family.
CC -!- DATABASE: NAME=R&D Systems' cytokine mini-reviews: IL5;
CC WWW="http://www.rndsystems.com/asp/g_sitebuilder.asp?bodyId=207".
CC
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CC
CC
CC EMBL; X04688; CAA28390.1; -
CC EMBL; J03478; AAN74469.1; -
CC EMBL; J02971; AAN98620.1; -
CC EMBL; X12705; CAA31210.1; -
CC EMBL; X12706; CAA31211.1; -
CC EMBL; AF353265; AAK19759.1; -
CC PIR; A28477; A28477.
CC PDB; 1HUL; 07-DEC-95.
CC Genew; HGNC:5016; IL5.
CC MIM; 147850; -
CC GO; GO:0005576; C:extracellular; TAS.
CC GO; GO:0005137; F:interleukin-5 receptor binding; TAS.
CC GO; GO:0009626; P:hypersensitive response; TAS.
CC GO; GO:0006954; P:inflammatory response; TAS.
CC InterPro; IPR000186; Interleukin_5.
CC Pfam; PF02025; IL5; 1.
CC PRINTS; PR00432; INTERLEUKINS.
CC ProDom; PD006721; Interleukin_5; 1.
KW Cytokine; Growth factor; Glycoprotein; Signal; 3D-structure.
FT SIGNAL 1 19
FT CHAIN 20 134 INTERLEUKIN-5.
FT DISULFID 63 63 INTERCHAIN (WITH C-105).
FT DISULFID 105 105 INTERCHAIN (WITH C-63).
FT CARBOHYD 22 22 O-LINKED.
FT CARBOHYD 47 47 N-LINKED (GLCNAC. . .).
FT CONFLICT 88 88 F -> L (IN REF. 5; CAA31210).
FT HELIX 26 38
FT TURN 39 40
FT TURN 41 45
FT TURN 46 46
FT STRAND 51 54
FT HELIX 60 62
FT HELIX 64 77
FT TURN 82 82
FT HELIX 83 103
FT TURN 104 105
FT STRAND 108 111
FT HELIX 112 128
FT TURN 129 129
SQ SEQUENCE 134 AA; 15238 MW; DC984467179556A3 CRC64;
Query Match 61.8%; Score 430; DB 1; Length 134;


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Best Local Similarity 64.9%, Pred. No. 1.2e-35;
Matches 87; Conservative 17; Mismatches 30; Indels 0; Gaps 0;

QY 1 MRMLNLSSLALGAAVSAFAVENPMNRLVAETLLTLLSTHRTWLTGDNLMIPENKNH 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 MRMLNLSSLALGAAVSAFAVENPMNRLVAETLLTLLSTHRTWLTGDNLMIPENKNH 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 QLCIKVEFGQIDTLKNQTAHGEAVDKLPQNLISLKEHIEROKKRCAGERNVTKFLDYIQ 120
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 QLCIKVEFGQIDTLKNQTAHGEAVDKLPQNLISLKEHIEROKKRCAGERNVTKFLDYIQ 120
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 121 VFLGVINTEWTPES 134
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 121 EFLGVNTEWTEIES 134
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 7
IL5_CERTO STANDARD; PRT; 134 AA.
AC P46685;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DE 10-OCT-2003 (Rel. 42, Last annotation update)
DE Interleukin-5 precursor (IL-5) (T-cell replacing factor) (TRF)
DE (Eosinophil differentiation factor).
GN IL5.
OS Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Cercopithecidae;
OC Cercopithecinae; Cercopithecidae;
OC NCBI_TaxID=9531;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FUJ;
RX MEDLINE=96003435; PubMed=7561102;
RA Villinger F.J., Brar S.S., Mayne A.E., Chikkala N., Ansari A.A.;
RT "Comparative sequence analysis of cytokine genes from human and
RT nonhuman primates.";
RL J. Immunol. 155:3946-3954(1995).
CC -!- FUNCTION: Factor that induces terminal differentiation of late-
CC developing B-cells to immunoglobulin secreting cells (By
CC similarity).
CC -!- SUBUNIT: Homodimer; disulfide-linked (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the IL-5 family.
CC
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CC
CC EMBL; L26033; AAA9971.1; -.
CC HSPF; P05113; IHUL.
CC InterPro; IPR000186; Interleukin_5.
CC Pfam; PF02025; IL5; 1.
CC PRINTS; PR00432; INTERLEUKIN5.
CC ProDom; PD006721; Interleukin 5; 1.
CC Cytokine; Growth factor; Glycoprotein; Signal.
FT SIGNAL 1 19
FT CHAIN 20 134
FT DISULFID 63 63
FT INTERCHAIN (WITH C-105) (BY SIMILARITY).
FT DISULFID 105 105
FT INTERCHAIN (WITH C-63) (BY SIMILARITY).
FT CARBOHYD 22 22
FT O-LINKED (BY SIMILARITY).
FT CARBOHYD 47 47
FT N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 90 90
FT N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 134 AA; 15339 MW; 7BDD491C437981ED CRC64;

Query Match 61.6%; Score 429; DB 1; Length 134;
Best Local Similarity 64.2%; Pred. No. 1.5e-35;
Matches 86; Conservative 20; Mismatches 28; Indels 0; Gaps 0;
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QY 1 MRMLNLSSLALGAAVSAFAVENPMNRLVAETLLTLLSTHRTWLTGDNLMIPENKNH 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 MRMLNLSSLALGAAVSAFAVENPMNRLVAETLLTLLSTHRTWLTGDNLMIPENKNH 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 QLCIKVEFGQIDTLKNQTAHGEAVDKLPQNLISLKEHIEROKKRCAGERNVTKFLDYIQ 120
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 QLCIKVEFGQIDTLKNQTAHGEAVDKLPQNLISLKEHIEROKKRCAGERNVTKFLDYIQ 120
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 121 VFLGVINTEWTPES 134
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 121 EFLGVNTEWTEIES 134
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 8
IL5_MACMU STANDARD; PRT; 134 AA.
AC P48093;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DE 10-OCT-2003 (Rel. 42, Last annotation update)
DE Interleukin-5 precursor (IL-5) (T-cell replacing factor) (TRF)
DE (Eosinophil differentiation factor).
GN IL5.
OS Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Cercopithecidae;
OC Cercopithecinae; Cercopithecidae;
OC NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RX MEDLINE=96003435; PubMed=7561102;
RA Villinger F.J., Brar S.S., Mayne A.E., Chikkala N., Ansari A.A.;
RT "Comparative sequence analysis of cytokine genes from human and
RT nonhuman primates.";
RL J. Immunol. 155:3946-3954(1995).
CC -!- FUNCTION: Factor that induces terminal differentiation of late-
CC developing B-cells to immunoglobulin secreting cells (By
CC similarity).
CC -!- SUBUNIT: Homodimer; disulfide-linked (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the IL-5 family.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; U19848; AAA86710.1; -.
CC HSPF; P05113; IHUL.
CC InterPro; IPR000186; Interleukin_5.
CC Pfam; PF02025; IL5; 1.
CC PRINTS; PR00432; INTERLEUKIN5.
CC ProDom; PD006721; Interleukin 5; 1.
CC Cytokine; Growth factor; Glycoprotein; Signal.
FT SIGNAL 1 19
FT CHAIN 20 134
FT DISULFID 63 63
FT INTERCHAIN (WITH C-105) (BY SIMILARITY).
FT DISULFID 105 105
FT INTERCHAIN (WITH C-63) (BY SIMILARITY).
FT CARBOHYD 22 22
FT O-LINKED (BY SIMILARITY).
FT CARBOHYD 47 47
FT N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 90 90
FT N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 134 AA; 15150 MW; DC985ECF4B86A3 CRC64;

Query Match 61.2%; Score 426; DB 1; Length 134;
Best Local Similarity 64.9%; Pred. No. 2.9e-35;
Matches 87; Conservative 16; Mismatches 31; Indels 0; Gaps 0;
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```
QY 121 VFLGVINTEWTP 133
DB 119 EFLGVSTWTEWME 131

RESULT 11
ID IL5_SIGHI STANDARD; PRT; 132 AA.
AC O9ES19;
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Interleukin-5 precursor (IL-5) (T-cell replacing factor) (TRF)
DE (Eosinophil differentiation factor)
DE (Eosinophil differentiation factor)
GN IL5
OS Sigmogon hispid (Hispid cotton rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;
OC Sigmogon.
OX NCBI_TaxID=42415;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20510033; PubMed=11054577;
RA Howard S., Jacquet A., Haumont M., Daminet V., Milican F., Glineur F.,
RA Bollen A.;
RT "Cloning, expression and purification of recombinant cotton rat
RT Interleukin-5";
RL Gene 257:149-135 (2000).
CC -!- FUNCTION: Factor that induces terminal differentiation of late-
CC developing B-cells to immunoglobulin secreting cells.
CC -!- SUBUNIT: Homodimer; disulfide-linked.
CC -!- SIMILARITY: Belongs to the IL-5 family.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
EMBL: AF148211; AGL6722.1; -
DR HSP; P05113; IHUL.
DR InterPro: IPR000186; Interleukin_5.
DR Pfam: PF02025; IL5; 1.
DR PRINTS; PR00432; INTERLEUKIN5.
DR ProDom; PD006721; Interleukin_5; 1.
KW Cytokine; Growth factor; Glycoprotein; Signal.
FT SIGNAL 1 19 BY SIMILARITY.
FT CHAIN 20 132 INTERLEUKIN-5.
FT DISULFID 61 61 INTERCHAIN (WITH C-103) (BY SIMILARITY).
FT DISULFID 103 103 INTERCHAIN (WITH C-61) (BY SIMILARITY).
FT CARBOHYD 45 45 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 74 74 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 88 88 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 132 AA; 15434 MW; B328B81B2371F5E9 CRC64;

Query Match 55.7%; Score 388; DB 1; Length 132;
Best Local Similarity 59.4%; Pred. No. 1.7e-31;
Matches 79; Conservative 19; Mismatches 33; Indels 2; Gaps 1;

QY 1 MRMLNLSLALGAAYVSAFVAPENMNLVAETLLSTHRTWLTIGDNLMIPTPENKH 60
DB 1 MRMLNLSLITL--ACVWTFVAPVPHVTKETLIQLSHRALLTSNETVRLPVPTRKH 58
QY 61 QLCKEYFQGIIDTKNTAHGEAVDKLFQNLSLIKHEIRQKRCAGRWVTKFDYILQ 120
DB 59 QLCKEYFQGIIDTKNTAHGEAVDKLFQNLSLIKHEIRQKRCAGRWVTKFDYILQ 118
QY 121 VFLGVINTEWTP 133
DB 119 EFLGVSTWTEWME 131
```

```
DB 119 EFLGVSTWTEWME 131

RESULT 12
ID IL5_MOUSE STANDARD; PRT; 133 AA.
AC P04401;
DT 20-MAR-1987 (Rel. 04, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Interleukin-5 precursor (IL-5) (T-cell replacing factor) (TRF) (B-cell
DE growth factor II) (BCGF-II) (Eosinophil differentiation factor)
DE (Cytotoxic T lymphocyte inducer).
GN IL5 OR IL-5.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88254802; PubMed=3133208;
RA Campbell H.D., Sanderson C.J., Wang Y., Hori Y., Martinson M.E.,
RA Tucker W.O.J., Stellwagen A., Strath M., Young I.G.;
RT "Isolation, structure and expression of cDNA and genomic clones for
RT murine eosinophil differentiation factor. Comparison with other
RT eosinophilopoietic lymphokines and identity with interleukin-5";
RL Eur. J. Biochem. 174:345-352 (1988).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=87065032; PubMed=3024009;
RA Kinashi T., Harada N., Severinson E., Tanabe T., Sideras P.,
RA Konishi M., Azuma C., Tomimaga A., Bergstedt-Lindqvist S.,
RA Takahashi M., Matsuda F., Yacita Y., Takatsu K., Honjo T.;
RT "Cloning of complementary DNA encoding T-cell replacing factor and
RT identity with B-cell growth factor II";
RL Nature 324:70-73 (1986).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=90180853; PubMed=3078564;
RA Mizuta T.R., Tanabe T., Nakakubo H., Noma T., Honjo T.;
RT "Molecular cloning and structure of the mouse interleukin-5 gene";
RL Growth Factors 1:51-57 (1988).
CC -!- FUNCTION: Factor that induces terminal differentiation of late-
CC developing B-cells to immunoglobulin secreting cells.
CC -!- SUBUNIT: Homodimer; disulfide-linked.
CC -!- SIMILARITY: Belongs to the IL-5 family.
CC -----
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CC -----
EMBL: X06270; CAA29606.1; -
DR EMBL; X06271; CAA29607.1; -
DR EMBL; X04601; CAA28266.1; -
DR PIR; S00807; ICMSS.
DR HSP; P05113; IHUL.
DR MGD; MGI:96557; IL5.
DR InterPro: IPR000186; Interleukin_5.
DR Pfam; PF02025; IL5; 1.
DR PRINTS; PR00432; INTERLEUKIN5.
DR ProDom; PD006721; Interleukin_5; 1.
KW Cytokine; Growth factor; Glycoprotein; Signal.
FT SIGNAL 1 20
FT CHAIN 21 133 INTERLEUKIN-5.
FT DISULFID 62 62 INTERCHAIN (WITH C-104) (BY SIMILARITY).
FT DISULFID 104 104 INTERCHAIN (WITH C-62) (BY SIMILARITY).
FT CARBOHYD 46 46 N-LINKED (GLCNAC...) (POTENTIAL).
```

Query Match	53.4%;	Score 372;	DB 1;	Length 139;	
Best Local Similarity	55.1%;	Pred. No. 6.8e-30;			
Matches	76;	Conservative 23;	Mismatches 35;	Indels 4;	Gaps 1;
Qy	1	MRMLNLSLALGAAVVSFAFVENPMNRIVAEETLLSTHRTWLIGDGNLMIPTENKQH	60		
Db	2	MKILVCLPLLTLYAGCVYGIATGNPVSRLVTETLSLITAHRTLLIGNGLRISIPQNH	61		
Qy	61	QLCIKEVFGIDITLKNQTAHGEAVDKLFQNLSLIKEHIEBQKRCACGERWRVTKFLDYIQ	120		
Db	62	PLCIEBIFQGIETLKNQTAENNVVEIFQNLSSLKGYITAKEKQCGGERRRVEQFLDYILE	121		
Qy	121	VFLGVI-----NTEWTPES	134		
Db	122	EFLRTINIEWTEWTVES	139		

```

RESULT 14
IL5 RAT
ID IL5 RAT STANDARD; PRT; 132 AA.
AC Q08125;
DC 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 01-OCT-2003 (Rel. 42, Last annotation update)
DE Interleukin-5 precursor (IL-5) (T-cell replacing factor) (TRF) (B-cell
DE growth factor II) (BCGF-II) (Eosinophil differentiation factor)
DE (Cytotoxic T lymphocyte inducer).
GN IL5 OR IL-5.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_Taxid=10116;
[1]
SEQUENCE FROM N.A.
RP STRAIN=Lewis;
RC MEDLINE=91355638; PubMed=1635053;
RA Ueberla K.T., Li W., Guin Z., Richter G., Raabe T.,
RA Diamantstein T., Blanckenstein T.;
RT "The rat interleukin-5 gene: characterization and expression by
RT retroviral gene transfer and polymerase chain reaction.";
RL cytokine 3:72-81(1991).
CC -!- FUNCTION: Factor that induces terminal differentiation of late-
CC developing B-cells to immunoglobulin secreting cells.
CC -!- SUBUNIT: Homodimer; disulfide-linked.
CC -!- SURCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the IL-5 family.
-----
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-----
CC EMBL; X54419; CAA39283.1; -.
DR DR PIR; A48418; A48418.
DR HSSP; P05113; 1HUL.
DR InterPro; IPR000186; Interleukin_5.
DR PFam; PF02025; IL5; 1.
DR PRINTS; PR00432; INTERLEUKINS.
DR ProDom; PD006721; Interleukin_5; 1.
KW Cytokine; Growth factor; Glycoprotein; Signal.
FT SIGNAL 1 19
FT CHAIN 20 132
FT FT DISULFID 61 61 INTERCHAIN (WITH C-103) (BY SIMILARITY).
FT FT DISULFID 103 103 INTERCHAIN (WITH C-61) (BY SIMILARITY).
FT FT CARBOHYD 45 45 N-LINKED (GLCNAC. .) (POTENTIAL).
FT FT CARBOHYD 74 74 N-LINKED (GLCNAC. .) (POTENTIAL).
FT FT CARBOHYD 88 88 N-LINKED (GLCNAC. .) (POTENTIAL).
FT SEQUENCE 132-AA; 15207 MW; 214A928B4C047031 CRC64;
SQ
Query Watch 51.9%; Score 361; DB 1; Length 132;

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Db          279 YKKIRLCYGGDFLMNVYLSFFCIRHDIIFDYLTIVNTD 315

Search completed: August 25, 2004, 00:02:57
Job time : 17.0683 secs

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[illegible]

Search completed: August 25, 2004, 00:02:57
Job time : 17.0683 secs

[illegible]

```

RESULT 15
MP44_MXVVL
ID MP44_MXVVL STANDARD; PRT; 590 AA.
AC Q9Q8G1;
16-OCT-2001. (Rel. 40, Created)
16-OCT-2001. (Rel. 40, Last sequence update)
10-OCT-2003. (Rel. 42, Last annotation update)
DT Probable metalloendopeptidase GI-type (EC 3.4.24.-).
GN M045U.
OS Myxoma virus (strain Lausanne).
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Leporipoxvirus.
OC NCBI_TaxID=31530;
RN [1]
RP SEQUENCE FROM N.A.
MEDLINE=20032073; PubMed=10562494;
Cameron C., Hota-Mitchell S., Chen L., Barrett J., Cao J.X.,
Macaulay C., Miller D., Evans D., McFadden G.;
"The complete DNA sequence of myxoma virus.";
Virology 264:238-318(1999).
RT RL
CC -!- FUNCTION: Seems to be involved in viral proteins maturation by
CC cleavage at Ala-Gly-|-Xaa motifs [By similarity].
CC -!- COFACTOR: Binds 1 zinc ion [potential].
CC -!- SIMILARITY: Belongs to peptidase family M44.
CC -----
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CC -----
EMBL AF170726; AAF14933.1; -.
MEROPS; M44.001; -.
InterPro; IPR005072; Peptidase_M44.
Pfam; PF03410; Peptidase_M44; 1.
Hydrolase; Metalloprotease; Zinc.
METAL . 41 ZINC (CATALYTIC) (POTENTIAL).
ACT SITE 44 44 POTENTIAL.
FT ACT SITE 44 44 POTENTIAL.
FT FT METAL 45 45 ZINC (CATALYTIC) (POTENTIAL).
SEQUENCE 590 AA; 63224 MW; 1DEE178930C75884 CRC64;
SQ

```

Query Match	14.3%	Score 98.5	DB 1	Length 590	
Best Local Similarity	26.3%	Pred. No. 0.045			
Matches	41	Conservative 23	Mismatches 38	Indels 55	Gaps 8
QY	7	LSLLALGAAVSFAVENPNRLVAEPLTLLSTHRTWLIGDGNLIMPTP-----ENK	58		
Db	180	LSLLA-----NTEGRUPACELTPTCVRT-IIGKTIIMPSPFYTMVVRVPS	226		
QY	59	NHO-----LCIKVEFQGITDLKNQTAGEAVD-KLFQNLSLIKH-----I	98		
Db	227	LHNILSILCLYEIYHLVDY-----ETVDNKLVTFTSFIEHSDYERFLQSGRLNLTI	278		
QY	99	ERQKQCAGERWVRTKFLDYLQV-----ELGVINTE	129		

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 24, 2004, 23:54:03 ; Search time 78.0321 Seconds
(without alignments)
541.821 Million cell updates/sec

Title: US-10-787-382-5
Perfect score: 696
Sequence: 1 MRMLNLSLLALGAAYVSAP.....FLDYQLVGLGVINTWTPES 134

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues
Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPREMBL 25:
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	696	100.0	134	6 Q95J76	Q95J76 canis famil
2	586	84.2	134	6 Q9TSD7	Q9TSD7 felis silve
3	578	83.0	134	6 Q9MYM5	Q9MYM5 sus scrofa
4	571	82.0	118	6 Q9TV10	Q9TV10 canis famil
5	448	64.4	134	6 Q9MKH1	Q9MKH1 saimiri sci
6	354	50.9	132	11 Q9R2C9	Q9R2C9 rattus norv
7	109.5	15.7	40	6 Q9XT92	Q9XT92 smnthopsis
8	81.5	11.7	488	13 Q7ZUA6	Q7ZUA6 gallus gall
9	80.5	11.6	485	13 Q7Z221	Q7Z221 gallus gall
10	79.5	11.4	610	5 Q9NA53	Q9NA53 caenorhabdi
11	79	11.4	676	8 Q7YKV5	Q7YKV5 mapania par
12	78.5	11.3	258	10 Q9M1K0	Q9M1K0 arabidopsis
13	78.5	11.3	463	11 Q91WC6	Q91WC6 mus musculu
14	78.5	11.3	490	11 Q9JIT0	Q9JIT0 mus musculu
15	77.5	11.1	331	16 Q9KBV9	Q9KBV9 bacillus ha
16	77	11.1	478	5 Q9TYV7	Q9TYV7 caenorhabdi

17	76.5	11.0	158	5 O96575	O96575 leucophaea
18	75.5	10.8	284	4 Q8NDP7	Q8NDP7 homo sapien
19	75.5	10.8	490	4 Q8WVF7	Q8WVF7 homo sapien
20	75.5	10.8	490	4 Q96QZ5	Q96QZ5 homo sapien
21	75	10.8	292	17 Q8PUD3	Q8PUD3 methanosarc
22	74.5	10.7	313	16 Q8PNY3	Q8PNY3 xanthomonas
23	74	10.6	241	8 Q8SKZ3	Q8SKZ3 myosotis ra
24	74	10.6	241	8 Q8SKY6	Q8SKY6 myosotis di
25	74	10.6	302	16 Q83IU2	Q83IU2 enterococcu
26	74	10.6	395	5 Q9VKL1	Q9VKL1 shewaphila
27	73.5	10.6	253	10 Q9M1K1	Q9M1K1 arabidopsis
28	73.5	10.6	1293	16 Q8EYF1	Q8EYF1 shewaphila
29	73	10.5	241	8 Q8SKY3	Q8SKY3 myosotis ma
30	73	10.5	248	10 Q8RVK0	Q8RVK0 helianthus
31	73	10.5	313	16 Q8PCA2	Q8PCA2 xanthomonas
32	73	10.5	623	10 Q7XSA0	Q7XSA0 oryza sativ
33	73	10.5	661	11 Q921P5	Q921P5 mus musculu
34	73	10.5	664	11 Q8K2B3	Q8K2B3 mus musculu
35	73	10.5	827	10 Q8W3A1	Q8W3A1 oryza sativ
36	72.5	10.4	207	16 Q9ZLI2	Q9ZLI2 helicobacte
37	72.5	10.4	229	16 Q9CLP5	Q9CLP5 pasteurella
38	72.5	10.4	310	17 Q8ZS22	Q8ZS22 pyrobaculum
39	72.5	10.4	313	2 O64666	O64666 xanthomonas
40	72.5	10.4	418	10 Q8S1N1	Q8S1N1 oryza sativ
41	72.5	10.4	510	10 Q8GW74	Q8GW74 arabidopsis
42	72.5	10.4	645	5 Q81HQ8	Q81HQ8 plasmodium
43	72	10.3	253	16 Q97DG5	Q97DG5 clostridium
44	72	10.3	296	17 Q8TQV4	Q8TQV4 methanosarc
45	72	10.3	562	12 Q7TH69	Q7TH69 lycoris pot

ALIGNMENTS

RESULT 1

Q95J76 PRELIMINARY; PRT; 134 AA.
ID Q95J76
AC Q95J76;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Interleukin-5.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-21334408; PubMed-11440633;
RA Yang S., Sellins K.S., Weber E., McCall C.;
RT "Canine interleukin-5: molecular characterization of the gene and
expression of biologically active recombinant protein.";
J. Interferon Cytokine Res. 21:361-367(2001).
RL EMBL; AF331920; AAL10716.1; -.
DR EMBL; AF331919; AAL10715.1; -.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005137; F:interleukin-5 receptor binding; IEA.
DR GO; GO:0005955; P:immune response; IEA.
DR InterPro; IPR000186; Interleukin_5.
DR PRINTS; PR00432; INTERLEUKIN5.
DR PRODOM; PD006721; Interleukin_5; 1.
SQ SEQUENCE 134 AA; 15307 MW; 003C86D94D6FF4C6 CRC64;

Query Match 100.0%; Score 696; DB 6; Length 134;
Best Local Similarity 100.0%; Pred. No. 1.5e-63;
Matches 134; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MRMLNLSLLALGAAYVSAPFNENRNLVAETLTLLSTHRTWLICDGNLMPTPENKXH	60
Db	1	MRMLNLSLLALGAAYVSAPFNENRNLVAETLTLLSTHRTWLICDGNLMPTPENKXH	60
QY	61	QLCICEVFOGIDTLKNQTAHGEAVDKFNLSLIKEHIERQKRCAGERWRTKFLDYQLQ	120

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Db 61 QLCIKVEFGQIDTLKNQTAHGEAVDKLFQNLSLIKHEIERQKRCAGRWRTKFLDYIQ 120
QY 121 VFLGVINTEWTPES 134
Db 121 VFLGVINTEWTPES 134

RESULT 2
Q9TSD7
ID Q9TSD7 PRELIMINARY; PRT; 134 AA.
AC Q9TSD7;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Interleukin 5.
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_TaxID=9685;
RN [1]
RP SEQUENCE FROM N.A.
RA Vandegrift E., Hughes K.J., O'Reilly K.L.;
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF068770; AAC27616.1; -.
DR HSSP; POS113; 1HUL.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005137; F:interleukin-5 receptor binding; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR000186; Interleukin_5.
DR Pfam; PF02025; IL5; 1.
DR PRINTS; PR00432; INTERLEUKINS.
DR ProDom; PD005721; Interleukin_5; 1.
DR ProDom; PD006721; Interleukin_5; 1.
SQ SEQUENCE 134 AA; 15176 MW; 9A118B78F8C820 CRC64;

Query Match 84.2%; Score 586; DB 6; Length 134;
Best Local Similarity 85.0%; Pred. No. 3e-52;
Matches 113; Conservative 11; Mismatches 9; Indels 0; Gaps 0;

QY 1 MEMLNLSLLALGAAYVSFAVENPMNRLVAETLLSTHRTWLIGDGNLMPTPENKH 60
Db 1 MEMLNLSLLALGAAYVSFAVENPMNRLVAETLLSTHRTWLIGDGNLMPTPENKH 60
QY 61 QLCIKVEFGQIDTLKNQTAHGEAVDKLFQNLSLIKHEIERQKRCAGRWRTKFLDYIQ 120
Db 61 QLCIEEVEFGQIDTLKNQTAHGEAVDKLFQNLSLIKHEIERQKRCAGRWRTKFLDYIQ 120
QY 121 VFLGVINTEWTPES 133
Db 121 VFLGVINTEWTPES 133

RESULT 3
Q9TSD7
ID Q9TSD7 PRELIMINARY; PRT; 134 AA.
AC Q9TSD7;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Interleukin-5.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=20130134; PubMed=10663563;
RA Sylvain H., Matvienko O., leonchiks A., Alving K., van der Ploeg I.;
RT "Molecular cloning, expression, and purification of pig interleukin-5."
RL Immunogenetics 51:59-64 (2000).
RN [2]

```

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RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Johnsen C.K., Grondahl-Hansen J., Johansen R., Jungersen G.,
RA Heegaard P.M.H.;
RT "Sus scrofa mRNA for interleukin-5."
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ010088; CAB70611.2; -.
DR EMBL; AJ133452; CAB36328.1; -.
DR HSSP; POS113; 1HUL.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005137; F:interleukin-5 receptor binding; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR000186; Interleukin_5.
DR Pfam; PF02025; IL5; 1.
DR PRINTS; PR00432; INTERLEUKINS.
DR ProDom; PD006721; Interleukin_5; 1.
SQ SEQUENCE 134 AA; 15191 MW; B485D562A028A899 CRC64;

Query Match 83.0%; Score 578; DB 6; Length 134;
Best Local Similarity 85.1%; Pred. No. 2e-51;
Matches 114; Conservative 8; Mismatches 12; Indels 0; Gaps 0;

QY 1 MEMLNLSLLALGAAYVSFAVENPMNRLVAETLLSTHRTWLIGDGNLMPTPENKH 60
Db 1 MEMLNLSLLALGAAYVSFAVENPMNRLVAETLLSTHRTWLIGDGNLMPTPENKH 60
QY 61 QLCIKVEFGQIDTLKNQTAHGEAVDKLFQNLSLIKHEIERQKRCAGRWRTKFLDYIQ 120
Db 61 QLCIEEVEFGQIDTLKNQTAHGEAVDKLFQNLSLIKHEIERQKRCAGRWRTKFLDYIQ 120
QY 121 VFLGVINTEWTPES 134
Db 121 VFLGVINTEWTPES 134

RESULT 4
Q9TSD7
ID Q9TSD7 PRELIMINARY; PRT; 118 AA.
AC Q9TSD7;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Interleukin-5 (Fragment).
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RA German A.J., Helps C.R., Harley R., Hall E.J., Day M.J.;
RT "Cloning and sequencing of canine interleukin-5."
RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF091133; AAD46991.1; -.
DR HSSP; POS113; 1HUL.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005137; F:interleukin-5 receptor binding; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR000186; Interleukin_5.
DR Pfam; PF02025; IL5; 1.
DR PRINTS; PR00432; INTERLEUKINS.
DR ProDom; PD005721; Interleukin_5; 1.
DR ProDom; PD006721; Interleukin_5; 1.
FT NON TER 1
FT NON TER 118
SQ SEQUENCE 118 AA; 13507 MW; 36A5563DD67C968C CRC64;

Query Match 82.0%; Score 571; DB 6; Length 118;
Best Local Similarity 93.8%; Pred. No. 8.9e-51;
Matches 106; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 18 SAFAVENPMNRLVAETLLSTHRTWLIGDGNLMPTPENKHOLCIKEVFGQIDTLKNQ 77
Db 6 SAFAVENPMNRLVAETLLSTHRTWLIGDGNLMPTPENKHOLCIKEVFGQIDTLKNQ 65

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QY 78 TARGEAVDKLFONLSLKEHIEROKKRCACERWRTKFLDYQLQVFLGVNTW 130
DB 66 TARGEAVDKLFONLSLKEHIEROKKRCACERWRTKFLDYQLQVFLGVNTW 118

RESULT 5
Q8MKH1 PRELIMINARY; PRT; 134 AA.
AC Q8MKH1; 2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Interleukin-5.
OS Saimiri sciureus (Common squirrel monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Cebinae; Saimiri.
OX NCBI_TaxID=9521;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=2197273; PubMed=11976788;
RA Herold J.M., Laverne A., Kazanji M.;
RT "Molecular cloning, characterization, and quantification of squirrel
RT monkey (Saimiri sciureus) Th1 and Th2 cytokines."
RL Immunogenetics 54:20-29(2002).
DR EMBL; AF294756; AAK92043.1; -.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005137; F:interleukin-5 receptor binding; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR000186; Interleukin_5.
DR Pfam; PFO2025; IL5; 1.
DR PRINTS; PR00432; INTERLEUKINS.
DR ProDom; PD006721; Interleukin_5; 1.
SQ SEQUENCE 134 AA; 15210 MW; EAFACASDB48767C CRC64;

Query Match 64.48; Score 448; DB 6; Length 134;
Best Local Similarity 67.98; Pred. No. 4.3e-38;
Matches 91; Conservative 13; Mismatches 30; Indels 0; Gaps 0;

QY 1 MRMLNLSSLALGAAYVSFAVENPMNRLVAETLTLLSTHRTWLTGDNLMIPENKNH 60
DB 1 MRMLNLSSLALGAAYVSFAVENPMNRLVAETLTLLSTHRTWLTGDNLMIPENKNH 58
QY 61 QLCIKVEFGIDTLKNQTAHGEAVDKLFONLSLKEHIEROKKRCACERWRTKFLDYQL 120
DB 59 QLCIKVEFGIDTLKNQTAHGEAVDKLFONLSLKEHIEROKKRCACERWRTKFLDYQL 118
QY 121 VFLGVNTWTPES 134
DB 119 EFLGVNTWTPES 131

RESULT 6
Q9R2C9 PRELIMINARY; PRT; 132 AA.
AC Q9R2C9; 2002 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Interleukin-5 precursor.
GN IL-5.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=Lou M;
RA Pierrot C.;
RT "Cloning, expression of rat IL-5 and production of neutralizing
RT antiserum: comparative study of IL-5 activity expressed in E.coli and
RT baculovirus system."
RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ011299; CAA09587.1; -.

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DR HSSP; P05113; 1HUL.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005137; F:interleukin-5 receptor binding; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR000186; Interleukin_5.
DR Pfam; PFO2025; IL5; 1.
DR PRINTS; PR00432; INTERLEUKINS.
DR ProDom; PD006721; Interleukin_5; 1.
KW Signal.
FT CHAIN 1 17 POTENTIAL.
FT CHAIN 18 132 INTERLEUKIN-5.
SQ SEQUENCE 132 AA; 15191 MW; 814A87CBAC04702B CRC64;

Query Match 50.9%; Score 354; DB 11; Length 132;
Best Local Similarity 54.1%; Pred. No. 1.9e-28;
Matches 72; Conservative 21; Mismatches 38; Indels 2; Gaps 1;

QY 1 MRMLNLSSLALGAAYVSFAVENPMNRLVAETLTLLSTHRTWLTGDNLMIPENKNH 60
DB 1 MRMLNLSSLALGAAYVSFAVENPMNRLVAETLTLLSTHRTWLTGDNLMIPENKNH 58
QY 61 QLCIKVEFGIDTLKNQTAHGEAVDKLFONLSLKEHIEROKKRCACERWRTKFLDYQL 120
DB 59 QLCIKVEFGIDTLKNQTAHGEAVDKLFONLSLKEHIEROKKRCACERWRTKFLDYQL 118
QY 121 VFLGVNTWTPES 133
DB 119 EFLGVNTWTPES 131

RESULT 7
Q9XT92 PRELIMINARY; PRT; 40 AA.
AC Q9XT92; 2002 (TREMBlrel. 12, Created)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Interleukin-5 (Fragment).
GN IL5.
OS Smnithopsis macroura (Stripe-faced dunnart).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Metatheria; Dasyuromorphia; Dasyuridae; Smnithopsis.
OX NCBI_TaxID=9302;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99432005; PubMed=10501836;
RA Hawken R.J., Maccarone P., Todter R., Marshall Graves J.A.,
RA Maddox J.F.;
RT "Isolation and characterization of marsupial IL5 genes."
RL Immunogenetics 49:942-948(1999).
DR EMBL; AF064208; AAD37461.1; -.
DR HSSP; P05113; 1HUL.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005137; F:interleukin-5 receptor binding; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR000186; Interleukin_5.
DR Pfam; PFO2025; IL5; 1.
DR PRINTS; PR00432; INTERLEUKINS.
DR ProDom; PD006721; Interleukin_5; 1.
FT NON_TER 1 1
FT NON_TER 40 40
SQ SEQUENCE 40 AA; 4695 MW; 54B93064203EA70B CRC64;

Query Match 15.7%; Score 109.5; DB 6; Length 40;
Best Local Similarity 53.8%; Pred. No. 0.00056;
Matches 21; Conservative 9; Mismatches 8; Indels 1; Gaps 1;

QY 71 IDTLKNQTAHGEAVDKLFONLSLKEHIEROKKRCACER 109
DB 1 IETLKNQTAEDNVVERIFQNFSLKEHITTKKQC-GE 38

RESULT 8

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Q7ZUA6
ID Q7ZUA6 PRELIMINARY; PRT; 488 AA.
AC Q7ZUA6
DT 01-JUN-2003 (TReMBLrel. 24, Created)
DT 01-JUN-2003 (TReMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE LMbr1.
GN LMbr1.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RA Konaguchi C., Yamamoto Y., Nishimatsu S., Nohno T.;
RT "Expression of Lmbr1 in the chick limb bud."
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB105057; BAC65224.1; -
DR InterPro; IPR008075; Lipocalin1_recep.
DR InterPro; IPR006876; LMbr1.
DR Pfam; PF04791; LMbr1; 1
DR PRINTS; PR01692; LIPOCALIN1MR.
DR SEQUENCE 488 AA; 55083 MW; 7553C35EA44F0E7A CRC64;
Query Match 11.7%; Score 81.5; DB 13; Length 488;
Best Local Similarity 23.0%; Pred. No. 8.5;
Matches 34; Conservative 27; Mismatches 36; Indels 51; Gaps 6;
QY 3 MLNLSLLALGAAYVSFAVENPMRLVAETLTLLSTHRTW-----LIGDGNL 50
Db 152 MLILALLILGIVWVASALIDN-----DAASMESLYDLWEFYLPYLYSCISLMGCLLL 204
QY 51 MIPTP-----ENKNHQL-----CIKEVFOGI-DTLKNQTAHG 81
Db 205 LLCTPGLSRMFTVWGQLLVKPTILEDLDEQWYITLBEALQKLNKISSTLENQTVF- 263
QY 82 EAVDKLFQNLKIEHIERQKRCAGER 109
Db 264 --LERELEKVKCKTNLERRKASAWER 289
Query Match 11.4%; Score 79.5; DB 5; Length 610;
Best Local Similarity 23.9%; Pred. No. 18;
Matches 32; Conservative 24; Mismatches 51; Indels 27; Gaps 6;
ID Q7ZZZ1 PRELIMINARY; PRT; 485 AA.
AC Q7ZZZ1
DT 01-JUN-2003 (TReMBLrel. 24, Created)
DT 01-JUN-2003 (TReMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE LMbr1 (Fragment).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Huang Y.Q., Deng X.M., Li N.;
RT "A Novel Candidate Gene for Chicken Polydactyly."
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY251537; AAP04355.1; -
DR InterPro; IPR008075; Lipocalin1_recep.
DR InterPro; IPR006876; LMbr1.
DR Pfam; PF04791; LMbr1; 1
DR PRINTS; PR01692; LIPOCALIN1MR.
FT NON_TER 1
SQ SEQUENCE 485 AA; 54711 MW; 3A70CBFF25C08E9 CRC64;
Query Match 11.6%; Score 80.5; DB 13; Length 485;
Best Local Similarity 23.0%; Pred. No. 11;
Matches 34; Conservative 27; Mismatches 36; Indels 51; Gaps 6;

QY 3 MLNLSLLALGAAYVSFAVENPMRLVAETLTLLSTHRTW-----LIGDGNL 50
Db 149 MLILALLILGIVWVASALIDN-----DAASMESLYDLWEFYLPYLYSCISLMGCLLL 201
QY 51 MIPTP-----ENKNHQL-----CIKEVFOGI-DTLKNQTAHG 81
Db 202 LLCTPGLSRMFTVWGQLLVKPTILEDLDEQWYITLBEALQKLNKISSTLENQTVF- 260
QY 82 EAVDKLFQNLKIEHIERQKRCAGER 109
Db 261 --LEGELEKVKCKTNLERRKASAWER 286
RESULT 10
Q9NA53
ID Q9NA53 PRELIMINARY; PRT; 610 AA.
AC Q9NA53
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-MAR-2003 (TReMBLrel. 23, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE Hypothetical protein Y73F8A.19.
GN Y73F8A.19.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA Matthews L.;
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=99069613; PubMed=9851916;
RA none;
RT "Genome sequence of the nematode C.elegans: A platform for
investigating biology."
RL Science 282:2012-2018(1998).
DR EMBL; AL132862; CAB60545.2; -
DR WormPep; Y73F8A.19; CE32997.
KW Hypothetical protein.
SQ SEQUENCE 610 AA; 69313 MW; F797871430B6FC74 CRC64;
Query Match 11.4%; Score 79.5; DB 5; Length 610;
Best Local Similarity 23.9%; Pred. No. 18;
Matches 32; Conservative 24; Mismatches 51; Indels 27; Gaps 6;
ID Q9NA53 PRELIMINARY; PRT; 676 AA.
AC Q9NA53
DT 01-OCT-2003 (TReMBLrel. 25, Created)
DT 01-OCT-2003 (TReMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE NADH dehydrogenase subunit F (Fragment).
GN NDHF.
OS Mpania paradoxa.
OC Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Cyperaceae; Mpania.
OX NCBI_TaxID=205740;

```
RN
RP SEQUENCE FROM N.A.
RA Givnish T.J., Pires J.C., Graham S.W., McPherson M., Prince L.M.,
RA Patterson T.B., Rai H., Roalson E.H., Evans T.M., Hahn W.J.,
RA Millam K.C., Molvray M., Kores P.J., O'Brien H., Hall J.C.,
RA Kress W.J., Sytoma K.J.;
RT "A monocot-wide phylogeny based on the highly informative cpDNA gene
RT ndhF: evidence for widespread concerted convergence.";
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY129256; AAN05045.1; -
KW Chloroplast.
FT NON TER 1
FT NON TER 676
FT NON TER 676
SQ SEQUENCE 676 AA; 76485 MW; 7B225B10D13A3C39 CRC64;

Query Match 11.4%; Score 79; DB 8; Length 676;
Best Local Similarity 25.4%; Pred. No. 23;
Matches 35; Conservative 13; Mismatches 40; Indels 50; Gaps 6;

QY 3 MLNLSLLGAAVYSAFAVENPMNLVAETLLSTHRTWLIGDGNLMPTPENKNH-- 60
DB 519 MLFPLLLLVFTVFGISGIGHFERGI--DLILS--KWLISSTNLF--ESSNYCV 569
QY 61 -----QCIKEVFQGITLKNQTAHGEAVDKLFQNLSLIKEHIEROK 102
DB 570 NSVEFLKNTIFSVAIFGLCIAIFYG-----SVYSFFQNLIFYNSFLKRGV 617
QY 103 KRCAGERWRYTKFLDYIQ 120
DB 618 KR-----SFLDQIQ 626

RESULT 12
Q9MIKO
ID Q9MIKO PRELIMINARY; PRT; 258 AA.
AC Q9MIKO
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein (Putative bHLH transcription factor).
GN F24I3.60.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
CX NCBI_TaxID=3702;
[1]
RP SEQUENCE FROM N.A.
RA Nyakatura G., Fartmann B., Dauner D., Sterr W., Holland R.,
RA Weichselgartner M., Mewes H.W., Lemcke K., Mayer K.F.X., Quetier F.,
RA Salaroubat M.;
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
[2]
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
[3]
RP SEQUENCE FROM N.A.
RA Jakoby M.J., Heim M.A., Bailey P., Martin C., Weissshaar B.;
RA "Basic-helix-loop-helix (bHLH) transcription factors in Arabidopsis
RA thaliana.";
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE BASIC HELIX-LOOP-HELIX (bHLH) FAMILY OF
CC TRANSCRIPTION FACTORS.
DR EMBL; ALA38655; CAB72168.1; -
DR EMBL; AF488577; AAM10941.1; -
DR PIR; T47758; T47758.
DR InterPro; IPR001092; HLH_basic.
DR Pfam; PF00010; HLH; 1.
DR SMART; SM00353; HLH; 1.
DR PROSITE; PS00888; HLH_2; 1.
KW Hypothetical protein.
SQ SEQUENCE 258 AA; 29004 MW; 2AE6CBF05422D3E0 CRC64;
```

```
Query Match 11.3%; Score 78.5; DB 10; Length 258;
Best Local Similarity 26.8%; Pred. No. 8;
Matches 22; Conservative 15; Mismatches 38; Indels 7; Gaps 2;

QY 28 RLVAETLLSTHRTWLIGDGNLMPTPENKNHQLCIKEVFQGITLKNQTAHGEA 83
DB 161 KAVANYISTVSATR---LGDNEVAVQISSKIHNFISNVLSGLEDRFVLVDMSRSSQ 217
QY 84 VKLQFQNLSLIKEHIEROKKRC 105
DB 218 GERLFYTLHLQVKIENYKLNK 239

RESULT 13
Q9IWC6
ID Q9IWC6 PRELIMINARY; PRT; 463 AA.
AC Q9IWC6
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Similar to limb region 1.
GN LMBR1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CX NCBI_TaxID=10090;
[1]
RP SEQUENCE FROM N.A.
RA TISSUE=Eye, and Retina;
RA Strausberg R.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC016110; AAH16110.1; -
DR MGI; 1861746; Lmbri.
DR InterPro; IPR008075; Lipocalin1_recep.
DR InterPro; IPR006876; LMBR1.
DR Pfam; PF04791; LMBR1; 1.
DR PRINTS; PRO1692; LIPOCALINMR.
SQ SEQUENCE 463 AA; 52005 MW; 8A115C8C5384A0C6 CRC64;

Query Match 11.3%; Score 78.5; DB 11; Length 463;
Best Local Similarity 22.8%; Pred. No. 16;
Matches 33; Conservative 31; Mismatches 36; Indels 45; Gaps 7;

QY 3 MLNLSLLGAAVYSAFAVENPMNLVAETLLSTHRTWLIGDGNL 50
DB 126 VLLLLALLLGWVWVASALID-----SDAASMESLYDLWEFYLPYLSILMGCLLL 178
QY 51 XIPTPENKNH-----QCIKEVFQGITLKNQTAHGEA-----V 84
DB 179 LLCTPVGLSRMFTVMGQLLVKPAILEDDEQIYMTLEEEALQRLHGLSSSVENVNML 238
QY 85 DXLFQNLSLIKEHIEROKKRCAGER 109
DB 239 EQELENVKILTKLERKKASAWER 263

RESULT 14
Q9JIT0
ID Q9JIT0 PRELIMINARY; PRT; 490 AA.
AC Q9JIT0
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE LMBR1 long form.
GN LMBR1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CX NCBI_TaxID=10090;
[1]
RP SEQUENCE FROM N.A.
RA STRAIN=B10.D2/nsn.
RC
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Search completed: August 25, 2004, 00:05:31
Job time : 83.0321 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 24, 2004, 23:40:07 ; Search time 83.1325 Seconds
(without alignments)
390.857 Million cell updates/sec

Title: US-10-787-382-10
Perfect score: 610
Sequence: 1 PAVENPMRLVAETLLTLLST.....FLDYQLQVFLGVINTEWTPES 115

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:.*
1: Geneseqp1980s:.*
2: Geneseqp1990s:.*
3: Geneseqp2000s:.*
4: Geneseqp2001s:.*
5: Geneseqp2002s:.*
6: Geneseqp2003as:.*
7: Geneseqp2003bs:.*
8: Geneseqp2004s:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	610	100.0	115	3 AAY58220	Canine ma
2	610	100.0	134	3 AAY58219	Canine in
3	601	98.5	134	4 AAB72615	Canine in
4	487	79.8	132	2 AAW08479	Ovine IL-
5	357	58.5	113	1 AAP93152	Sequence
6	357	58.5	287	6 AAO30459	hIL5.36 v
7	356	58.4	112	1 AAP80279	Pleiotrop
8	356	58.4	115	1 AAP81038	Sequence
9	356	58.4	115	3 AAB45489	Human int
10	356	58.4	115	5 ABG94295	Human mat
11	356	58.4	115	5 ABG80607	Human mat
12	356	58.4	115	6 AAO30453	Human C-I
13	356	58.4	123	5 ABG94353	Human IL-
14	356	58.4	123	5 ABG80665	Human IL-
15	356	58.4	134	2 AAB92802	Human int
16	356	58.4	134	4 AAB72617	Human int
17	356	58.4	134	5 ABG94294	Human int
18	356	58.4	134	5 ABG80606	Human pre
19	356	58.4	134	5 AAU10353	Interleuk
20	356	58.4	136	5 ABG94352	Human C-I
21	356	58.4	136	5 ABG80664	Human ILn
22	356	58.4	138	5 ABG94351	Human C-I
23	356	58.4	138	5 ABG80663	Human ILn
24	356	58.4	285	6 AAO30457	hIL5-P30-
25	356	58.4	285	6 AAO30458	hIL5-P2-P

26	356	58.4	287	6 AAO30460	hIL5.37 v
27	352	57.7	134	5 AAU10354	Interleuk
28	351	57.5	121	2 AAW3436	Human int
29	347	56.9	115	2 AAW05273	N-termina
30	347	56.9	115	2 AAW72948	Truncated
31	347	56.9	133	1 AAP71064	Murine eo
32	347	56.9	133	1 AAP82969	B cell di
33	347	56.9	133	1 AAP82969	B cell re
34	347	56.9	133	2 AAR96963	T cell re
35	347	56.9	133	2 AAW72949	T cell re
36	347	56.9	133	4 AAB72618	Murine in
37	347	56.9	134	5 ABG94349	Mouse C-I
38	347	56.9	134	5 ABG80661	Mouse IL-
39	346	56.7	134	1 AAP81056	Sequence
40	344	56.4	136	5 ABG94348	Mouse C-I
41	344	56.4	136	5 ABG80660	Mouse IL-
42	343	56.2	84	4 AAB72616	Canine in
43	343	56.2	113	2 AAW05274	N-termina
44	343	56.2	113	5 ABG94296	Mouse int
45	343	56.2	113	5 ABG80608	Mouse mat

ALIGNMENTS

RESULT 1
AAY58220
ID AAY58220 standard; protein; 115 AA.
XX
AC AAY58220;
XX
XX 14-MAR-2000 (first entry)
DT
XX Canine mature interleukin-5 (IL-5).
DE
XX Interleukin-5; IL-5; antibody; canine; inhibitor; immune response;
KW immunoregulation; tumour; cancer; autoimmune disease; vaccine.
XX
OS Canis familiaris.
XX
XX WO9961618-A2.
PN
XX
XX 02-DEC-1999.
PD
XX
XX 28-MAY-1999; 99WO-US011942.
PF
XX
XX 29-MAY-1998; 98US-0087306P.
PR
XX
XX (HESK-) HESKA CORP.
PA
XX
XX Sim G, Yang S, Dreitz MJ, Wonderling RS;
PI
XX WPI; 2000-072623/06.
DR
XX N-PSDB; AAZ55550, AAZ55551.
N-PSDB;
XX
XX Nucleic acids encoding immunoregulatory proteins from cats or dogs,
PT useful for treating or preventing e.g. tumors or autoimmune disease.
PT
XX
XX Claim 3h; Page 227; 264pp; English.

Sequences AAY58219-Y58220 represent encoded and mature canine interleukin-5 (IL-5). The invention relates to canine IL-4, canine or feline ILT-3 ligand, canine or feline CD40, canine or feline CD154 (CD40 ligand), canine IL-5, canine IL-13, feline interferon-alpha (IFN-alpha), and feline granulocyte macrophage colony-stimulating factor (GM-CSF), and nucleotides which encode these immunoregulatory proteins. The proteins, their associated nucleic acids, specific antibodies and inhibitors may be used as vaccines for therapeutic or prophylactic regulation of an immune response in animals (particularly cats, dogs, horses and humans). They may be used to treat autoimmune or infectious diseases including allergies, tumours, inflammation and graft rejection, and to increase the response from a co-administered antigen. The nucleotide sequences can also be used for the recombinant production of a protein, while

CC nucleotide fragments are useful as probes, as amplification primers and
 CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).
 CC The proteins may be used to raise antibodies and to screen for modulators
 CC of activity, while the antibodies may be used in detection, and in drug
 CC targeting
 XX SQ Sequence 115 AA;

Query Match 100.0%; Score 610; DB 3; Length 115;
 Best Local Similarity 100.0%; Pred. No. 1.8e-64;
 Matches 115; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 FAVENPNRLVAETLLSTHRTWLIGDGNLMIPTPENKNHQLCIKEVFGIDTLKNQTA 60
 DB 1 FAVENPNRLVAETLLSTHRTWLIGDGNLMIPTPENKNHQLCIKEVFGIDTLKNQTA 60
 QY 61 HGEAVDKLFQNLISLKEHIERQKRCAGRWRTKFLDYQLVFLGVINTEWTPES 115
 DB 61 HGEAVDKLFQNLISLKEHIERQKRCAGRWRTKFLDYQLVFLGVINTEWTPES 115

RESULT 2
 AAY58219
 ID AAY58219 standard; protein; 134 AA.
 XX AC AAY58219;
 XX DT 14-MAR-2000 (first entry)
 XX DE Canine interleukin-5 (IL-5).
 XX KW Interleukin-5; IL-5; antibody; canine; inhibitor; immune response;
 XX KW immunoregulation; tumour; cancer; autoimmune disease; vaccine.
 XX OS Canis familiaris.
 XX PN W09961618-A2.
 XX PD 02-DEC-1999.
 XX PF 28-MAY-1999; 99WO-US011942.
 XX PR 29-MAY-1998; 98US-0087306P.
 XX PA (HESK-) HESKA CORP.
 XX PI Sim G, Yang S, Dreitz MJ, Wonderling RS;
 DR WI: 2000-072623/06
 DR N-PSDB; AAZ55546, AAZ55547, AAZ55548, AAZ55549.
 XX PT Nucleic acids encoding immunoregulatory proteins from cats or dogs,
 XX useful for treating or preventing e.g. tumors or autoimmune disease.
 XX PS Claim 3h; Page 224; 264pp; English.

XX Sequences AAY58219-Y58220 represent encoded and mature canine interleukin
 CC -5 (IL-5). The invention relates to canine IL-4, canine or feline ILT-3
 CC ligand, canine or feline CD40, canine or feline CD154 (CD40 ligand),
 CC canine IL-5, canine IL-13, feline interferon-alpha (IFN-alpha) and feline
 CC granulocyte macrophage colony-stimulating factor (GM-CSF), and nucleotides
 CC which encode these immunoregulatory proteins. The proteins, their
 CC associated nucleic acids, specific antibodies and inhibitors may be used
 CC as vaccines for therapeutic or prophylactic regulation of an immune
 CC response in animals (particularly cats, dogs, horses and humans). They
 CC may be used to treat autoimmune or infectious diseases including
 CC allergies, tumours, inflammation and graft rejection, and to increase the
 CC response for a co-administered antigen. The nucleotide sequences can
 CC also be used for the recombinant production of a protein, while
 CC nucleotide fragments are useful as probes, as amplification primers and
 CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).
 CC The proteins may be used to raise antibodies and to screen for modulators
 CC of activity, while the antibodies may be used in detection, and in drug

CC targeting
 XX SQ Sequence 134 AA;
 Query Match 100.0%; Score 610; DB 3; Length 134;
 Best Local Similarity 100.0%; Pred. No. 2.2e-64;
 Matches 115; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 FAVENPNRLVAETLLSTHRTWLIGDGNLMIPTPENKNHQLCIKEVFGIDTLKNQTA 60
 DB 20 FAVENPNRLVAETLLSTHRTWLIGDGNLMIPTPENKNHQLCIKEVFGIDTLKNQTA 79
 QY 61 HGEAVDKLFQNLISLKEHIERQKRCAGRWRTKFLDYQLVFLGVINTEWTPES 115
 DB 80 HGEAVDKLFQNLISLKEHIERQKRCAGRWRTKFLDYQLVFLGVINTEWTPES 134

RESULT 3
 AAB72615
 ID AAB72615 standard; protein; 134 AA.
 XX AC AAB72615;
 XX DT 04-MAY-2001 (first entry)
 XX DE Canine interleukin-5 protein #1.
 XX KW Dog; interleukin-5; IL-5; allergy; cancer; gene therapy;
 XX KW inflammatory reaction.
 XX OS Canis sp.
 XX PN W0200111049-A2.
 XX PD 15-FEB-2001.
 XX PF 09-AUG-2000; 2000WO-US021651.
 XX PR 10-AUG-1999; 99US-00371615.
 XX PA (IDEX-) IDEXX LAB INC.
 XX PI Guo H, Lawton R, Mermer B, Aiyappa AP;
 XX WPI; 2001-191542/19.
 XX DR N-PSDB; AAF74300.
 XX PT Novel canine interleukin 5 polynucleotide and polypeptides are used for
 XX generating antibodies which are useful in treating allergies in dogs.
 XX PS Claim 29; Page 46-47; 48pp; English.

XX The present invention provides the protein and coding sequences of the
 CC canine interleukin-5 (IL-5) protein. This can be used to treat allergies,
 CC cancer and inflammatory reactions in dogs. The present sequence is one
 CC version of the IL-5 protein shown in the specification
 XX SQ Sequence 134 AA;
 Query Match 98.5%; Score 601; DB 4; Length 134;
 Best Local Similarity 99.1%; Pred. No. 2.6e-63;
 Matches 114; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 FAVENPNRLVAETLLSTHRTWLIGDGNLMIPTPENKNHQLCIKEVFGIDTLKNQTA 60
 DB 20 FAVENPNRLVAETLLSTHRTWLIGDGNLMIPTPENKNHQLCIKEVFGIDTLKNQTA 79
 QY 61 HGEAVDKLFQNLISLKEHIERQKRCAGRWRTKFLDYQLVFLGVINTEWTPES 115
 DB 80 HGEAVDKLFQNLISLKEHIERQKRCAGRWRTKFLDYQLVFLGVINTEWTPES 134
 RESULT 4

AAW08479
ID AAW08479 standard; protein; 132 AA.
XX AC
XX AAW08479;
XX DT 17-OCT-2003 (revised)
XX DT 24-SEP-1997 (first entry)
XX DE
XX DE Ovine IL-5.
XX KW Cytokine; ovine; sheep; interleukin-5; interleukin-12; IL-5; IL-12;
XX KW livestock; cow; stress; transport; vaccine adjuvant; veterinary; cancer;
XX KW immunosuppression; allergy; reproductive system; growth; early maturity;
XX KW antibody; diagnosis; immunopotentiator;
XX KW early haematopoietic progenitor cell; cytotoxic cell; thymocyte;
XX KW secretion; IgM; IgA; bacterial endotoxin; gamma-interferon.
XX OS
XX OS Ovis aries.
XX PN WO9700321-A1.
XX PD
XX PD 03-JAN-1997.
XX PF 14-JUN-1996; 96WO-AU000360.
XX PR 14-JUN-1995; 95AU-00003502.
XX PR 27-OCT-1995; 95AU-00006244.
XX XX
XX PA (CSIR) COMMONWEALTH SCI & IND RES ORG.
XX PI Seow H, Wood P;
XX DR WPI: 1997-077528/07.
XX DR N-PSDB; AAT50755, AAT50756.
XX XX
XX PT Nucleic acid encoding ovine interleukin-5 or -12 - used as vaccine
XX PT adjuvants and to treat or prevent microbial infections in livestock.
XX PS Claim 31; Page 39-40; 78pp; English.
XX CC This protein sequence represents ovine interleukin-5 (IL-5). Ovine IL-5
CC or IL-12 are used to treat and/or prevent infections in livestock (esp.
CC cows and sheep), particularly where the animals are stressed, e.g. during
CC transport. IL-5 and IL-12 can also be used as adjuvants in vaccines for
CC veterinary use (partic. weakly immunogenic subunit or synthetic peptide
CC vaccines). They may also be used to treat cancer, immunosuppression and
CC allergy, to enhance/suppress the reproductive system and to promote
CC growth or early maturity. Optionally interleukin can be delivered from
CC constructs or delivery cells and antibodies are useful in enzyme
CC immunoassays for rapid diagnosis of infection. The interleukins are
CC immunopotentiators, especially IL-5 promotes growth of early
CC haematopoietic progenitor cells and generation of cytotoxic cells from
CC thymocytes, also it stimulates production and secretion of IgM and IgA
CC (in synergism with bacterial endotoxin). IL-12 induces production of
CC gamma-interferon by, and proliferation of, T and NK cells and increases
CC the (non-)specific cytolytic lymphocyte response. The genetic constructs
CC can also be used for in vitro production of IL-5 or -12. (updated on 17-
XX OCT-2003 to standardise OS field)
XX SQ Sequence 132 AA;
Query Match 79.8%; Score 487; DB 2; Length 132;
Best Local Similarity 80.7%; Pred. No. 9.9e-50;
Matches 92; Conservative 13; Mismatches 9; Indels 0; Gaps 0;
QY 2 AVENMRLVAETLLTSLTHTWLTGNGNLMIPPTENKHNQICKEVFGQIDTLKNQTAH 61
DB 19 AVESTMRLVAETLLTSLTHTWLTGNGNLMIPPTQHTNHNQICKEVFGQIDTLKNQTAQ 78
QY 62 GEAVDKLPONLSLKEHIERQKRCAGRWRTKFLDYLOVFLGVINTEWTPES 115
DB 79 GDAVKIFRNLISLKEIDYQKRCGGRWRVQFLDYLOVFLGVINTEWTPES 132

RESULT 5
AAP93152
ID AAP93152 standard; protein; 113 AA.
XX AC
XX AAP93152;
XX DT 15-MAR-1992 (first entry)
XX DE
XX DE Sequence of human interleukin-5 (IL-5).
XX KW B-cell growth factor; lymphokine; B-cell stimulating factor 2.
XX OS Homo sapiens.
XX PN GB2217328-A.
XX PD
XX PD 25-OCT-1989.
XX PF 12-APR-1988; 85GB-00008524.
XX PR 12-APR-1988; 85GB-00008524.
XX PA (BREI-) BRITISH BIO-TECHN L.
XX PI Edwards RM;
XX XX
XX DR WPI: 1989-311767/43.
XX DR N-PSDB; AAN91647.
XX XX
XX PT Synthetic gene encoding human interleukin-5 - has restriction sites at
XX PT frequent intervals to facilitate manipulation.
XX PS Disclosure; Fig 3a; 2lpp; English.
XX CC AAN91647 has restriction sites for HindIII, BspMI, NcoI, SpeI, BspMI.
XX CC ApuII, XmaI, ClaI, Ball, PstI, DraII, BamHI and EcoRI. IL5 acts as a B-
XX CC cell growth and differentiation factor
XX SQ Sequence 113 AA;
Query Match 58.5%; Score 357; DB 1; Length 113;
Best Local Similarity 61.9%; Pred. No. 2.5e-34;
Matches 70; Conservative 17; Mismatches 26; Indels 0; Gaps 0;
QY 3 VENPMNRLVAETLLTSLTHTWLTGNGNLMIPPTENKHNQICKEVFGQIDTLKNQTAH 62
DB 1 MEIPTSALVKETLALLSTHTLTLTANETLRIPVPHKHNQICKEVFGQIDTLKNQTAH 60
QY 63 EAVDKLPONLSLKEHIERQKRCAGRWRTKFLDYLOVFLGVINTEWTPES 115
DB 61 GTVERLFKNLSLIRKYIDGQKCGERRVQNQFLDYLOVFLGVINTEWTPES 113
RESULT 6
AAO30459
ID AAO30459 standard; protein; 287 AA.
XX AC
XX AAO30459;
XX DT 22-SEP-2003 (first entry)
XX DE hIL5.36 variant protein.
XX KW Multimeric protein; interleukin 5; IL5; TNFalpha; inflammatory disease;
XX KW tumour necrosis factor alpha; gene therapy; arthritis; interleukin 5;
XX KW IL5; epitope; human; tetanus toxoid; chimeric; variant; mutant; mutein.
XX OS Homo sapiens.
XX OS Unidentified.
XX OS Chimeric.
XX PF Key Location/Qualifiers

29. 2004

repetitive antigen array. The invention also comprises a coat protein capable of forming a capsid which comprises mutant Obeta coat proteins having an amino acid sequence selected from five amino acid sequences fully defined in the specification. The compounds of the invention may have antimicrobial, antiallergic, immunomodulatory, cytostatic, antiviral, antidiabetic, or hypoglycaemic activities and may be used in immunisation and as a vaccine. The present sequence represents a protein sequence used to create the compositions of the invention

Sequence 115 AA;

Query Match 58.4%; Score 356; DB 5; Length 115;
Best Local Similarity 62.5%; Pred. No. 3.4e-34;
Matches 70; Conservative 16; Mismatches 26; Indels 0; Gaps 0;

QY 4 ENPMRLVAETLLSTHRTWLGDNLMPTPENKHQLCIKVEFGIDTLKNOTAHGE 63

Db 4 EIPTSALVKETLALLSTHRTWLGDNLMPTPENKHQLCIKVEFGIDTLKNOTAHGE 63

QY 64 AVDKLFQNLSTLKEHIERQKRCAGRWRTKFDLYLQVFLGVINTEWTPES 115

Db 64 TVERLFKNLSLIKYYIDGQKKCGEERRVNVQFLDYLQVFLGVINTEWTPES 115

RESULT 11

ABG80607

ID ABG80607 standard; protein; 115 AA.

AC ABG80607;

DT 29-NOV-2002 (first entry)

DE Human mature Interleukin 5.

Molecular antigen array; vaccine; antigen; antimicrobial; molecular-scaffold; amyloid beta; Abeta 1-42; influenza; graft versus host disease; IGF-mediated allergic reaction; anaphylaxis; adult respiratory distress syndrome; ARDS; Crohn's disease; allergic asthma; acute lymphoblastic leukaemia; non-Hodgkin's lymphoma; Grave's disease; systemic lupus erythematosus; osteoporosis; inflammatory immune disease; myasthenia gravis; multiple sclerosis; angioimmunoproliferative disease lymphadenopathy; Alzheimer's disease; rheumatoid arthritis; diabetes; infectious disease; factor Xa; enterokinase; cysteine-containing linker.

Homo sapiens.

W0200256907-A2.

25-JUL-2002.

21-JAN-2002; 2002WO-IB000168.

19-JAN-2001; 2001US-0262379P.

04-MAY-2001; 2001US-0288549P.

05-OCT-2001; 2001US-0326998P.

07-NOV-2001; 2001US-0331045P.

(CYTO-) CYTOS BIOTECHNOLOGY AG.

(NOVS) NOVARTIS PHARMA AG.

(MAUR) MAURER P.

(LECH) LECHNER F.

(ORTM) ORTMANN R.

(LUJO) LUEGEND R.

(STAU) STAUFENBIEL M.

(FREV) FREY P.

Maurer P, Lechner F, Ortmann R, Luegend R, Staufenbiel M, Frey P;

Renner WA, Bachmann M, Tiesot A, Sebbel P, Piossek C;

WPI; 2002-636514/69.

PT Molecular antigen array used in the production of vaccines for infectious diseases.

XX Disclosure; Page 399; 418pp; English.

XX The invention relates to a composition comprising: (a) a non-natural molecular scaffold comprising: (i) a core particle selected from: (1) a core particle of a non-natural origin; and (2) a core particle of natural origin; and (ii) an organiser comprising at least one first attachment site, where the organiser is connected to the core particle by at least one covalent bond; (b) an antigen or antigenic determinant with at least one second attachment site, where the antigen or antigenic determinant is amyloid beta peptide (Abeta 1-42) or its fragment, and where the second attachment site is selected from: (i) an attachment site not naturally occurring with the antigen or antigenic determinant; and (ii) an attachment site naturally occurring with the antigen or antigenic determinant, where the second attachment site is capable of association through at least one non-peptide bond to the first attachment site; and where the antigen or antigenic determinant and the scaffold interact through the association to form an ordered and repetitively occurring array. Also included is a process for producing a non-naturally occurring ordered and repetitive antigen array. The composition is used in immunisation and as a vaccine for diseases such as influenza, graft versus host disease, IGF-mediated allergic reactions, anaphylaxis, adult respiratory distress syndrome (ARDS), Crohn's disease, allergic asthma, acute lymphoblastic leukaemia, non-Hodgkin's lymphoma, Grave's disease, systemic lupus erythematosus, inflammatory immune diseases, myasthenia gravis, immunoproliferative disease lymphadenopathy, angioimmunoproliferative lymphadenopathy, immunoblastic lymphadenopathy, rheumatoid arthritis, diabetes, multiple sclerosis, Alzheimer's disease, osteoporosis and infectious diseases. The present sequence is an antigen for use in the array of the invention. The antigen is modified to possess a cleavage site (enterokinase or factor Xa) and a Cysteine-containing N- or C-terminal linker peptide which serves as the attachment point to a virus like particle or bacterial protein (the scaffold protein)

Sequence 115 AA;

Query Match 58.4%; Score 356; DB 5; Length 115;

Best Local Similarity 62.5%; Pred. No. 3.4e-34;

Matches 70; Conservative 16; Mismatches 26; Indels 0; Gaps 0;

QY 4 ENPMRLVAETLLSTHRTWLGDNLMPTPENKHQLCIKVEFGIDTLKNOTAHGE 63

Db 4 EIPTSALVKETLALLSTHRTWLGDNLMPTPENKHQLCIKVEFGIDTLKNOTAHGE 63

QY 64 AVDKLFQNLSTLKEHIERQKRCAGRWRTKFDLYLQVFLGVINTEWTPES 115

Db 64 TVERLFKNLSLIKYYIDGQKKCGEERRVNVQFLDYLQVFLGVINTEWTPES 115

RESULT 12

AAO30453

ID AAO30453 standard; protein; 115 AA.

AC AAO30453;

DT 22-SEP-2003 (first entry)

XX Human mature interleukin 5 (IL5) protein.

DE Multimeric protein; interleukin 5; IL5; TNFalpha; inflammatory disease; tumour necrosis factor alpha; gene therapy; arthritis; interleukin 5; IL5; human.

Homo sapiens.

W02003042244-A2.

22-MAY-2003.

15-NOV-2002; 2002WO-DK000764.

PR 16-NOV-2001; 2001DK-00001702.
PR 16-NOV-2001; 2001US-0331575P.
PA (PHAR-) PHARMEXA AS.
PA (KLYS/) KLYSNER S.
PA (NIEL/) NIELSEN F S.
PA (BRAT/) BRATT T.
PA (VOLD/) VOLDBOEG B.
PA (MOUR/) MOURITSEN S.
XX
XX Klynsner S, Nieleen FS, Bratt T, Voldborg B, Mouritsen S;
XX WPI; 2003-449558/42.
XX
XX New immunogenic analogue of a polymeric protein, useful for preparing a
XX composition for treating inflammatory diseases e.g. arthritis.
XX Disclosure; Page 105; 196pp; English.
XX
XX The invention relates to immunogenic analogues of multimeric proteins
XX such as immunogenic variants of interleukin 5 (IL5) and tumour necrosis
XX factor alpha (TNF, TNFalpha) and methods for production of immunogenic
XX analogues. The immunogenic analogue is useful for preparing a composition
XX for treating inflammatory diseases, e.g., arthritis. It is also used in
XX gene therapy. The present sequence is human mature IL5 protein. This
XX sequence is used to illustrate the method of the invention
XX
XX Sequence 115 AA;
XX
XX Query Match 58.4%; Score 356; DB 6; Length 115;
XX Best Local Similarity 62.5%; Pred. No. 3.4e-34;
XX Matches 70; Conservative 16; Mismatches 26; Indels 0; Gaps 0;
XX
QY 4 ENPMRLVAETLLSTHRTWLGDMIMPTENKHNQHCICEVFGIDTLKNQAHGE 63
Db 4 EPTSAVKETALLSTHRTLLIANETLRIPVPHKHQOLCTEIFQIGITLESQTVQGG 63
QY 64 AVDKLFQNLSLIKHIERQKRCAGERRVTKFDLYQLVFLGVINTWPTES 115
Db 64 TVERLFKNLSLTKYIDGKKCKGERRRVNQFLDYQLQFLGVNNTWIEIES 115
RESULT 13
ABG94353
ID ABG94353 standard; protein; 123 AA.
XX
XX AC ABG94353;
XX
XX 10-DEC-2002 (first entry)
XX
XX Human C-IL-5-S protein.
XX
XX Human; mouse; rat; antimicrobial; antiallergic; immunomodulatory;
XX cytostatic; antiviral; antidiabetic; hypoglycaemic; antigen array;
XX vaccine; infectious disease.
XX
XX Homo sapiens.
XX
XX WO200256905-A2.
XX
XX 25-JUL-2002.
XX
XX 21-JAN-2002; 2002WO-1B000166.
XX
XX 19-JAN-2001; 2001US-0262379P.
XX 04-MAY-2001; 2001US-0288549P.
XX 05-OCT-2001; 2001US-0328998P.
XX 07-NOV-2001; 2001US-0331045P.
XX
XX (CYTO-) CYTOS BIOTECHNOLOGY AG.
XX
XX Renner WA, Bachmann M, Tissot A, Maurer P, Lechner F, Sebbel P;
XX Piossek C;

XX WPI; 2002-627351/67.
XX
XX Molecular antigen array used in the production of vaccines for infectious
XX diseases.
XX
XX Example 10; Page 440; 441pp; English.
XX
XX This invention relates to a novel ordered and repetitive antigen array
XX used in the production of vaccines for infectious diseases. The invention
XX also discloses a composition comprising a non-natural molecular scaffold
XX comprising a core particle selected from a core particle of a non-natural
XX origin and a core particle of natural origin and an organiser comprising
XX at least one first attachment site, where the organiser is connected to
XX the core particle by at least one covalent bond. Also disclosed is an
XX antigen or antigenic determinant with at least one second attachment
XX site, where the antigen or antigenic determinant is amyloid beta peptide
XX (Abeta1-42) or its fragment and where the second attachment site is
XX selected from an attachment site not naturally occurring with the antigen
XX or antigenic determinant and an attachment site naturally occurring with
XX the antigen or antigenic determinant, where the second attachment site is
XX capable of association through at least one non-peptide bond to the first
XX attachment site and where the antigen or antigenic determinant and the
XX scaffold interact through the association to form an ordered and
XX repetitive antigen array. The invention also comprises a coat protein
XX capable of forming a capsid which comprises mutant beta coat proteins
XX having an amino acid sequence selected from five amino acid sequences
XX fully defined in the specification. The compounds of the invention may
XX have antimicrobial, antiallergic, immunomodulatory, cytostatic,
XX antiviral, antidiabetic, or hypoglycaemic activities and may be used in
XX immunisation and as a vaccine. The present sequence represents a protein
XX sequence used to create the compositions of the invention
XX
XX Sequence 123 AA;
XX
XX Query Match 58.4%; Score 356; DB 5; Length 123;
XX Best Local Similarity 62.5%; Pred. No. 3.7e-34;
XX Matches 70; Conservative 16; Mismatches 26; Indels 0; Gaps 0;
XX
QY 4 ENPMRLVAETLLSTHRTWLGDMIMPTENKHNQHCICEVFGIDTLKNQAHGE 63
Db 12 EPTSAVKETALLSTHRTLLIANETLRIPVPHKHQOLCTEIFQIGITLESQTVQGG 71
QY 64 AVDKLFQNLSLIKHIERQKRCAGERRVTKFDLYQLVFLGVINTWPTES 115
Db 72 TVERLFKNLSLTKYIDGKKCKGERRRVNQFLDYQLQFLGVNNTWIEIES 123
RESULT 14
ABG80665
ID ABG80665 standard; protein; 123 AA.
XX
XX AC ABG80665;
XX
XX 29-NOV-2002 (first entry)
XX
XX Human IL-5/ N-terminal cysteine containing linker, human C-IL-5-S.
XX
XX Molecular antigen array; vaccine; antigen; antimicrobial; mutant;
XX molecular scaffold; amyloid beta; Abeta 1-42; influenza; mitein;
XX graft versus host disease; IGS-mediated allergic reaction; anaphylaxis;
XX adult respiratory distress syndrome; ARDS; Crohn's disease;
XX allergic asthma; acute lymphoblastic leukaemia; non-Hodgkin's lymphoma;
XX Grave's disease; systemic lupus erythematosus; osteoporosis;
XX inflammatory immune disease; myasthenia gravis; multiple sclerosis;
XX immunoproliferative disease lymphadenopathy; Alzheimer's disease;
XX angioimmunoproliferative lymphadenopathy; immunoblastic lymphadenopathy;
XX rheumatoid arthritis; diabetes; infectious disease; factor Xa;
XX enterokinase; cysteine-containing linker.
XX
XX Homo sapiens.
XX
XX Synthetic.

PN WO200256907-A2.
 XX 25-JUL-2002.
 PD 21-JAN-2002; 2002WO-IB000168.
 XX 19-JAN-2001; 2001US-0262379P.
 PR 04-MAY-2001; 2001US-0288549P.
 PR 05-OCT-2001; 2001US-0326998P.
 PR 07-NOV-2001; 2001US-0331045P.
 XX (CYTO-) CYTOS BIOTECHNOLOGY AG.
 PA (NOVS) NOVARTIS PHARMA AG.
 PA (MAUR) MAURER P.
 PA (LECH) LECHNER F.
 PA (ORTM) ORTMANN R.
 PA (LUEO) LUEOEND R.
 PA (STAU) STAUFENBIEL M.
 PA (FREY) FREY P.
 XX Maurer P, Lechner F, Ortmann R, Lueoend R, Staufenbiel M, Frey P;
 PI Renner WA, Bachmann M, Tissot A, Sebbel P, Piossek C;
 XX WPI; 2002-636514/68.
 DR Molecular antigen array used in the production of vaccines for infectious
 PT diseases.
 PT Disclosure; Page 417; 418pp; English.
 XX The invention relates to a composition comprising: (a) a non-natural
 CC molecular scaffold comprising: (i) a core particle selected from: (1) a
 CC core particle of a non-natural origin; and (2) a core particle of natural
 CC origin; and (ii) an organiser comprising at least one first attachment
 CC site, where the organiser is connected to the core particle by at least
 CC one covalent bond; (b) an antigen or antigenic determinant with at least
 CC one second attachment site, where the antigen or antigenic determinant is
 CC amyloid beta peptide (Abeta 1-42) or its fragment, and where the second
 CC attachment site is selected from: (i) an attachment site not naturally
 CC occurring with the antigen or antigenic determinant; and (ii) an
 CC attachment site naturally occurring with the antigen or antigenic
 CC determinant, where the second attachment site is capable of association
 CC through at least one non-peptide bond to the first attachment site; and
 CC where the antigen or antigenic determinant and the scaffold interact
 CC through the association to form an ordered and repetitive antigen array.
 CC Also included is a process for producing a non-naturally occurring
 CC ordered and repetitive antigen array. The composition is used in
 CC immunisation and as a vaccine for diseases such as influenza, graft
 CC versus host disease, IgE-mediated allergic reactions, anaphylaxis, adult
 CC respiratory distress syndrome (ARDS), Crohn's disease, allergic asthma,
 CC acute lymphoblastic leukaemia, non-Hodgkin's lymphoma, Grave's disease,
 CC systemic lupus erythematosus, inflammatory immune diseases, myasthenia
 CC gravis, immunoproliferative disease lymphadenopathy, immunoblastic lymphadenopathy,
 CC angioimmunoproliferative lymphadenopathy, immunoblastic lymphadenopathy,
 CC rheumatoid arthritis, diabetes, multiple sclerosis, Alzheimer's disease,
 CC osteoporosis and infectious diseases. The present sequence is a modified
 CC antigen for use in the array of the invention. The antigen is modified to
 CC possess a cleavage site (enterokinase or factor Xa) and a Cysteine-
 CC containing N- or C-terminal linker peptide which serves as the attachment
 CC point to a virus like particle or bacterial protein (the scaffold
 CC protein)
 XX Sequence 123 AA;
 SQ Query Match 58.4%; Score 356; DB 5; Length 123;
 Best Local Similarity 62.5%; Pred. No. 3.7e-34;
 Matches 70; Conservative 16; Mismatches 26; Indels 0; Gaps 0;
 QY 4 ENPMRLVAETLLTLLSHRTWLGDNLMIPPEKNHQLCKEIVFGQIDTLKNQTAHGE 63
 Db 12 EIPTSALVKETALLSTHRTLLIANETLRIPVPVKNHQLCTEETFGIGTLESQVQGG 71
 QY 64 AVDKLFQNLSLIKEHIEROKRCAGERRWRTKFLDYQLQVFLGVNTEWTPES 115

Db 72 TVERLFPKLSLIKKYIDGQKKCGERRRVNQFLDYQLQVFLGVNTEWTPES 123
 RESULT 15
 AAR92802
 ID AAR92802 standard; protein; 134 AA.
 XX AAR92802;
 AC AAR92802;
 XX 24-MAY-1996 (first entry)
 DT Human interleukin-5.
 XX Human interleukin-5.
 DE Cytokine; mutein; interleukin-5; agonist; antagonist; diagnosis; therapy;
 KW cancer; inflammation; degenerative disease.
 XX Homo sapiens.
 OS WO9604306-A2.
 XX 15-FEB-1996.
 PD 31-JUL-1995; 95WO-US008950.
 PF 01-AUG-1994; 94US-00284393.
 PR (SCHE) SCHERING CORP.
 XX Zurawski SM, Zurawski G;
 PI WPI; 1996-129335/13.
 DR Mutein(s) of human and murine cytokine(s), esp. interleukin(s) and murine
 PT P600 contg. amino acid substitutions - useful for the diagnosis and
 PT treatment of cancer, inflammation, etc.
 XX Disclosure; Page 43; 52pp; English.
 XX Muteins of human interleukin-5 (AAR92802) and other cytokines (see also
 CC AAR92790-801) are obtd. by site-directed mutagenesis of natural cytokine
 CC sequences at positions identified as critical for activity. The muteins
 CC are useful in the screening of cytokine and cytokine receptor levels, and
 CC in the diagnosis or treatment of e.g. inflammation, cancer, and
 CC degenerative disorders
 XX Sequence 134 AA;
 SQ Query Match 58.4%; Score 356; DB 2; Length 134;
 Best Local Similarity 62.5%; Pred. No. 4.2e-34;
 Matches 70; Conservative 16; Mismatches 26; Indels 0; Gaps 0;
 QY 4 ENPMRLVAETLLTLLSHRTWLGDNLMIPPEKNHQLCKEIVFGQIDTLKNQTAHGE 63
 Db 23 EIPTSALVKETALLSTHRTLLIANETLRIPVPVKNHQLCTEETFGIGTLESQVQGG 82
 QY 64 AVDKLFQNLSLIKEHIEROKRCAGERRWRTKFLDYQLQVFLGVNTEWTPES 115
 Db 83 TVERLFPKLSLIKKYIDGQKKCGERRRVNQFLDYQLQVFLGVNTEWTPES 134
 Search completed: August 25, 2004, 00:02:24
 Job time : 83.1325 secs

Result No.	Score		Query Match	Length	DB	ID	Description
1	610	100.0	115	4	US-09-322-409-86	Sequence 86, Appl	
2	610	100.0	115	4	US-09-451-527-86	Sequence 86, Appl	
3	610	100.0	134	4	US-09-322-409-81	Sequence 81, Appl	
4	610	100.0	134	4	US-09-451-527-81	Sequence 81, Appl	
5	601	98.5	134	4	US-09-371-615A-2	Sequence 2, Appl	
6	356	58.4	134	1	US-08-284-393B-13	Sequence 13, Appl	
7	356	58.4	134	3	US-08-759-628-9	Sequence 9, Appl	
8	356	58.4	134	4	US-09-371-615A-7	Sequence 7, Appl	
9	356	58.4	134	4	US-09-462-941-12	Sequence 12, Appl	
10	356	58.4	134	5	PCT-US95-08950-13	Sequence 13, Appl	
11	356	58.4	134	6	5324640-2	Patent No. 5324640	
12	351	57.5	121	4	US-09-180-864-2	Sequence 2, Appl	
13	347	56.9	133	4	US-09-371-615A-8	Sequence 8, Appl	
14	72.5	11.9	686	4	US-09-914-259-33	Sequence 33, Appl	
15	72	11.8	15	5	PCT-US94-06655-4	Sequence 4, Appl	
16	71	11.6	323	4	US-09-134-000C-5535	Sequence 5535, Appl	
17	69.5	11.4	976	3	US-08-560-005-2	Sequence 2, Appl	
18	69.5	11.4	976	3	US-09-195-868-14	Sequence 14, Appl	
19	69.5	11.4	976	3	US-09-418-540-2	Sequence 2, Appl	
20	69.5	11.4	976	4	US-09-969-528-2	Sequence 2, Appl	
21	69.5	11.4	1187	3	US-08-654-962B-8	Sequence 8, Appl	
22	69.5	11.4	1187	3	US-09-311-743-8	Sequence 8, Appl	
23	69.5	11.4	1189	3	US-09-195-868-15	Sequence 15, Appl	
24	69.5	11.4	1229	3	US-09-195-868-28	Sequence 28, Appl	
25	67.5	11.1	968	1	US-08-434-730-14	Sequence 14, Appl	
26	67.5	11.1	1185	3	US-08-664-962B-2	Sequence 2, Appl	
27	67.5	11.1	1185	3	US-09-311-743-2	Sequence 2, Appl	

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; CURRENT FILING DATE: 1999-12-01
; EARLIER APPLICATION NUMBER: 09/322,409
; EARLIER FILING DATE: 1999-05-28
; EARLIER APPLICATION NUMBER: 60/087,306
; EARLIER FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 86
; LENGTH: 115
; TYPE: PRT
; ORGANISM: Canis familiaris
US-09-451-527-86

Query Match      100.0%; Score 610; DB 4; Length 115;
Best Local Similarity 100.0%; Pred. No. 4e-71;
Matches 115; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FAVENPNRLVAETLTLLSTHRTWLIGDGNLMPTPENKQHQLCIKEVFQGITLKNQTA 60
Db 1 FAVENPNRLVAETLTLLSTHRTWLIGDGNLMPTPENKQHQLCIKEVFQGITLKNQTA 60

Qy 61 HGEAVDKLFQNLSLIKHEIERQKRCAGRWRTKFLDYQLQVFLGVINTWTPES 115
Db 61 HGEAVDKLFQNLSLIKHEIERQKRCAGRWRTKFLDYQLQVFLGVINTWTPES 115

RESULT 3
US-09-322-409-81
; Sequence 81, Application US/09322409
; Patent No. 6471957
; GENERAL INFORMATION:
; APPLICANT: Sim, Gek-kee
; APPLICANT: Yang, Shumin
; APPLICANT: Dreitz, Matthew J.
; APPLICANT: Wonderling, Ramani S.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; FILE REFERENCE: IM-2-C1
; CURRENT APPLICATION NUMBER: US/09/322,409
; EARLIER FILING DATE: 1999-05-28
; EARLIER APPLICATION NUMBER: 60/087,306
; EARLIER FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 154
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 81
; LENGTH: 134
; TYPE: PRT
; ORGANISM: Canis familiaris
US-09-322-409-81

Query Match      100.0%; Score 610; DB 4; Length 134;
Best Local Similarity 100.0%; Pred. No. 5e-71;
Matches 115; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FAVENPNRLVAETLTLLSTHRTWLIGDGNLMPTPENKQHQLCIKEVFQGITLKNQTA 60
Db 1 FAVENPNRLVAETLTLLSTHRTWLIGDGNLMPTPENKQHQLCIKEVFQGITLKNQTA 60

Qy 61 HGEAVDKLFQNLSLIKHEIERQKRCAGRWRTKFLDYQLQVFLGVINTWTPES 115
Db 61 HGEAVDKLFQNLSLIKHEIERQKRCAGRWRTKFLDYQLQVFLGVINTWTPES 115

RESULT 4
US-09-451-527-81
; Sequence 81, Application US/09451527
; Patent No. 6482403
; GENERAL INFORMATION:
; APPLICANT: Sim, Gek-kee
; APPLICANT: Yang, Shumin
; APPLICANT: Dreitz, Matthew J.
; APPLICANT: Wonderling, Ramani S.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
```

```
; TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF
; FILE REFERENCE: IM-2-C2
; CURRENT APPLICATION NUMBER: US/09/451,527
; CURRENT FILING DATE: 1999-12-01
; EARLIER APPLICATION NUMBER: 09/322,409
; EARLIER FILING DATE: 1999-05-28
; EARLIER APPLICATION NUMBER: 60/087,306
; EARLIER FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 81
; LENGTH: 134
; TYPE: PRT
; ORGANISM: Canis familiaris
US-09-451-527-81

Query Match      100.0%; Score 610; DB 4; Length 134;
Best Local Similarity 100.0%; Pred. No. 5e-71;
Matches 115; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FAVENPNRLVAETLTLLSTHRTWLIGDGNLMPTPENKQHQLCIKEVFQGITLKNQTA 60
Db 20 FAVENPNRLVAETLTLLSTHRTWLIGDGNLMPTPENKQHQLCIKEVFQGITLKNQTA 79

Qy 61 HGEAVDKLFQNLSLIKHEIERQKRCAGRWRTKFLDYQLQVFLGVINTWTPES 115
Db 80 HGEAVDKLFQNLSLIKHEIERQKRCAGRWRTKFLDYQLQVFLGVINTWTPES 134

RESULT 5
US-09-371-615A-2
; Sequence 2, Application US/09371615A
; Patent No. 6537781
; GENERAL INFORMATION:
; APPLICANT: IDEXX LABORATORIES
; TITLE OF INVENTION: METHODS AND COMPOSITIONS CONCERNING
; FILE REFERENCE: CANINE INTERLEUKIN 5
; FILE REFERENCE: 03604001700US00
; CURRENT APPLICATION NUMBER: US/09/371,615A
; CURRENT FILING DATE: 1999-08-10
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 134
; TYPE: PRT
; ORGANISM: Canis familiaris
US-09-371-615A-2

Query Match      98.5%; Score 601; DB 4; Length 134;
Best Local Similarity 99.1%; Pred. No. 7.3e-70;
Matches 114; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FAVENPNRLVAETLTLLSTHRTWLIGDGNLMPTPENKQHQLCIKEVFQGITLKNQTA 60
Db 20 FAVENPNRLVAETLTLLSTHRTWLIGDGNLMPTPENKQHQLCIKEVFQGITLKNQTA 79

Qy 61 HGEAVDKLFQNLSLIKHEIERQKRCAGRWRTKFLDYQLQVFLGVINTWTPES 115
Db 80 HGEAVDKLFQNLSLIKHEIERQKRCAGRWRTKFLDYQLQVFLGVINTWTPES 134

RESULT 6
US-08-284-393B-13
; Sequence 13, Application US/08284393B
; Patent No. 5696234
; GENERAL INFORMATION:
; APPLICANT: Zurawski, Sandra M.
; APPLICANT: Zurawski, Gerard
; TITLE OF INVENTION: MUTINS OF MAMMALIAN CYTOKINES
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
```

```
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/08/284,393B
; APPLICATION NUMBER: US/08/284,393B
; FILING DATE: 01-AUG-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,030
; REFERENCE/DOCKET NUMBER: DX0389
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-852-9196
; TELEFAX: 415-496-1200
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 134 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-284-393B-13

Query Match 58.4%; Score 356; DB 1; Length 134;
Best Local Similarity 62.5%; Pred. No. 3.7e-38;
Matches 70; Conservative 16; Mismatches 26; Indels 0; Gaps 0;

QY 4 ENPMRLVAETLLSTHRTWLIGDGNLMITPENKQHQLCIKEVFQGITLKNQTAHGE 63
DB 23 EIPTSALVKETALLSTHRTLLIANETLRIPVPVHKHQLCTEETIFQGITLESQTVQGG 82
QY 64 AVDKLFQNLSLIKHEIRQKRCACGERWRVTKFLDYQLQVFLGVINTEWTPES 115
DB 83 TVERLFKNLSLIKXKIDGKKCGEERRRVNQFLDYQLQVFLGVNTEWIES 134

RESULT 7
US-08-759-628-9
; Sequence 9, Application US/08/759628
; Patent No. 6225446
; GENERAL INFORMATION:
; APPLICANT: Altmann, Scott W.
; APPLICANT: Rock, Fernando L.
; APPLICANT: Bazan, J. Fernando
; APPLICANT: Kastelein, Robert A.
; TITLE OF INVENTION: MUTATIONAL VARIANTS OF MAMMALIAN PROTEINS
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/759,628
; FILING DATE: 05-DEC-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION NUMBER: US 60/008,574
; FILING DATE: 06-DEC-1995
; ATTORNEY/AGENT INFORMATION:
```

```
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,030
; REFERENCE/DOCKET NUMBER: DX0552Q
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-852-9196
; TELEFAX: 415-496-1200
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 134 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 20-134
; OTHER INFORMATION: /note= "Peptide of Figure 1"
; US-08-759-628-9

Query Match 58.4%; Score 356; DB 3; Length 134;
Best Local Similarity 62.5%; Pred. No. 3.7e-38;
Matches 70; Conservative 16; Mismatches 26; Indels 0; Gaps 0;

QY 4 ENPMRLVAETLLSTHRTWLIGDGNLMITPENKQHQLCIKEVFQGITLKNQTAHGE 63
DB 23 EIPTSALVKETALLSTHRTLLIANETLRIPVPVHKHQLCTEETIFQGITLESQTVQGG 82
QY 64 AVDKLFQNLSLIKHEIRQKRCACGERWRVTKFLDYQLQVFLGVINTEWTPES 115
DB 83 TVERLFKNLSLIKXKIDGKKCGEERRRVNQFLDYQLQVFLGVNTEWIES 134

RESULT 8
US-09-371-615A-7
; Sequence 7, Application US/09371615A
; Patent No. 6537781
; GENERAL INFORMATION:
; APPLICANT: IDEXX LABORATORIES
; TITLE OF INVENTION: METHODS AND COMPOSITIONS CONCERNING
; FILE OF INVENTION: CANINE INTERLEUKIN 5
; FILE REFERENCE: 03604001700US00
; CURRENT APPLICATION NUMBER: US/09/371,615A
; CURRENT FILING DATE: 1999-08-10
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 134
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Interleukin 5
; US-09-371-615A-7

Query Match 58.4%; Score 356; DB 4; Length 134;
Best Local Similarity 62.5%; Pred. No. 3.7e-38;
Matches 70; Conservative 16; Mismatches 26; Indels 0; Gaps 0;

QY 4 ENPMRLVAETLLSTHRTWLIGDGNLMITPENKQHQLCIKEVFQGITLKNQTAHGE 63
DB 23 EIPTSALVKETALLSTHRTLLIANETLRIPVPVHKHQLCTEETIFQGITLESQTVQGG 82
QY 64 AVDKLFQNLSLIKHEIRQKRCACGERWRVTKFLDYQLQVFLGVINTEWTPES 115
DB 83 TVERLFKNLSLIKXKIDGKKCGEERRRVNQFLDYQLQVFLGVNTEWIES 134

RESULT 9
US-09-462-941-12
; Sequence 12, Application US/09462941
; Patent No. 6608183
; GENERAL INFORMATION:
; APPLICANT: Cox III, George N
; APPLICANT: Bolder Biotechnology, Inc.
```

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; TITLE OF INVENTION: Derivatives of Growth Hormone and Related Proteins
; FILE REFERENCE: 4152-1-FUS
; CURRENT APPLICATION NUMBER: US/09/462,941
; CURRENT FILING DATE: 2000-01-14
; PRIOR APPLICATION NUMBER: 60/052,516
; PRIOR FILING DATE: 1997-07-14
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 134
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-462-941-12

Query Match      58.4%; Score 356; DB 4; Length 134;
Best Local Similarity 62.5%; Pred. No. 3.7e-38;
Matches 70; Conservative 16; Mismatches 26; Indels 0; Gaps 0;

QY 4 ENPMNRLVAETLTLLSTHRTWLIGDGNLMPTPENKXHQLCIKVEFGQIDTLKXQTAHGE 63
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Db 23 EIPTSALVKETLALLSTHRTLLIANETLRIPVPVKKHQLCITEIFOGIGTLESQTVQGG 82
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 64 AVDKLFQNLSLIKHIERQKRCACGERWRVTKFLDYQLQVFLGVINTWTPES 115
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 83 TVERLFKNLSLIKKYIDGQKKCGEERRRVNQFLDYQLQVFLGVNNTWIIIES 134
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 10
PCT-US95-08950-13
; Sequence 13, Application PC/TUS9508950
; GENERAL INFORMATION:
; APPLICANT: Zurawski, Sandra M.
; APPLICANT: Zurawski, Gerard
; TITLE OF INVENTION: MUTINS OF MAMMALIAN CYTOKINES
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/08950
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/284,393
; FILING DATE: 01-AUG-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: DX0389
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-852-9196
; TELEFAX: 415-496-1200
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 134 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US95-08950-13

Query Match      58.4%; Score 356; DB 5; Length 134;
Best Local Similarity 62.5%; Pred. No. 3.7e-38;
Matches 70; Conservative 16; Mismatches 26; Indels 0; Gaps 0;
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QY 4 ENPMNRLVAETLTLLSTHRTWLIGDGNLMPTPENKXHQLCIKVEFGQIDTLKXQTAHGE 63
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Db 23 EIPTSALVKETLALLSTHRTLLIANETLRIPVPVKKHQLCITEIFOGIGTLESQTVQGG 82
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 64 AVDKLFQNLSLIKHIERQKRCACGERWRVTKFLDYQLQVFLGVINTWTPES 115
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 83 TVERLFKNLSLIKKYIDGQKKCGEERRRVNQFLDYQLQVFLGVNNTWIIIES 134
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 11
5324640-2
; Patent No. 5324640
; APPLICANT: Honjo, Tasuku/Takatsu, Kiyoshi;Severinson, Eva
; TITLE OF INVENTION: HUMAN B-CELL DIFFERENTIATION FACTOR AND
; PROCESS OF PRODUCING SAID FACTOR
; NUMBER OF SEQUENCES: 2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/99,467
; FILING DATE: 21-SEP-1987
; SEQ ID NO:2:
; LENGTH: 134
5324640-2

Query Match      58.4%; Score 356; DB 6; Length 134;
Best Local Similarity 62.5%; Pred. No. 3.7e-38;
Matches 70; Conservative 16; Mismatches 26; Indels 0; Gaps 0;

QY 4 ENPMNRLVAETLTLLSTHRTWLIGDGNLMPTPENKXHQLCIKVEFGQIDTLKXQTAHGE 63
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 23 EIPTSALVKETLALLSTHRTLLIANETLRIPVPVKKHQLCITEIFOGIGTLESQTVQGG 82
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 64 AVDKLFQNLSLIKHIERQKRCACGERWRVTKFLDYQLQVFLGVINTWTPES 115
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 83 TVERLFKNLSLIKKYIDGQKKCGEERRRVNQFLDYQLQVFLGVNNTWIIIES 134
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RESULT 12
US-09-180-864-2
; Sequence 2, Application US/09180864
; Patent No. 6465616
; GENERAL INFORMATION:
; APPLICANT: Lobe, Angel
; APPLICANT: Vadas, Matthew
; APPLICANT: Shannon, Frances
; APPLICANT: Bastiras, Stan
; APPLICANT: Hey, Allan W
; TITLE OF INVENTION: AN INTERLEUKIN-5 ANTAGONIST
; FILE REFERENCE: 9972Z
; CURRENT APPLICATION NUMBER: US/09/180,864
; CURRENT FILING DATE: 1999-04-12
; PRIOR APPLICATION NUMBER: 08/591,438
; PRIOR FILING DATE: 1994-07-28
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 121
; TYPE: PRT
; ORGANISM: modified IL-5
US-09-180-864-2

Query Match      57.5%; Score 351; DB 4; Length 121;
Best Local Similarity 61.6%; Pred. No. 1.4e-37;
Matches 69; Conservative 16; Mismatches 27; Indels 0; Gaps 0;

QY 4 ENPMNRLVAETLTLLSTHRTWLIGDGNLMPTPENKXHQLCIKVEFGQIDTLKXQTAHGE 63
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Db 10 EIPTSALVKETLALLSTHRTLLIANETLRIPVPVKKHQLCITEIFOGIGTLESQTVQGG 69
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 64 AVDKLFQNLSLIKHIERQKRCACGERWRVTKFLDYQLQVFLGVINTWTPES 115
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 70 TVERLFKNLSLIKKYIDGQKKCGEERRRVNQFLDYQLQVFLGVNNTWIIIES 121
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
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RESULT 13

US-09-371-615A-8
; Sequence 8, Application US/09371615A
; Patent No. 6537781

; GENERAL INFORMATION:
; APPLICANT: IDEXX LABORATORIES
; TITLE OF INVENTION: METHODS AND COMPOSITIONS CONCERNING

; TITLE OF INVENTION: CANINE INTERLEUKIN 5

; FILE REFERENCE: 036040017000S00

; CURRENT APPLICATION NUMBER: US/09/371.615A

; CURRENT FILING DATE: 1999-08-10

; NUMBER OF SEQ ID NOS: 8

; SOFTWARE: FastSEQ for Windows Version 3.0

; SEQ ID NO 8

; LENGTH: 133

; TYPE: PRT

; ORGANISM: Mus musculus

; FEATURE:

; OTHER INFORMATION: Interleukin 5

US-09-371-615A-8

Query Match

Best Local Similarity 56.9%; Score 347; DB 4; Length 133;

Mismatches 66; Conservative 18; Mismatches 29; Indels 0; Gaps 0;

QY 2 AVENPMRLVAETLTLLSTHRTWLTGDNLMIPENKHOLCIKEVFGIDTLKNOTAH 61

DB 20 AMIPKSTVVKELTQLSARALTSNETWRLPVPFHKHQLCIGIFQGLDILKQTVR 79

QY 62 GEAVDKLFQNLISKEHIEFKQKRCAGRWRTKFLDYLVQVFLGVINTEWTP 114

DB 80 GGTVMFLFQNLISLTKYIDRQKCGERRRTRQFLDYLVQVFLGVINTEW 132

RESULT 14

US-09-914-259-33

; Sequence 33, Application US/09914259

; Patent No. 6495336

; GENERAL INFORMATION:

; APPLICANT: Makowski, Lee

; APPLICANT: Hyman, Paul

; APPLICANT: Williams, Mark

; TITLE OF INVENTION: STAGED ASSEMBLY OF NANOSTRUCTURES

; FILE REFERENCE: 8471-010-999

; CURRENT APPLICATION NUMBER: US/09/914.259

; CURRENT FILING DATE: 2000-11-21

; NUMBER OF SEQ ID NOS: 180

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 33

; LENGTH: 686

; TYPE: PRT

; ORGANISM: Strongylocentrotus purpuratus

US-09-914-259-33

Query Match

Best Local Similarity 11.9%; Score 72.5; DB 4; Length 686;

Mismatches 21; Conservative 19; Mismatches 30; Indels 11; Gaps 3;

QY 27 GDGNLMIPENKHOLC--IKEVFGIDTLKNOTAHGEAVDKLFQNLISKEHIERQKK 84

DB 15 GQGNL-----SQEQIITGTREVIKGLEQKNE--HNDILNSLYSLKWLKDTGDSN 65

QY 85 RCAGERWRVTKFLDYLVQVFLG 105

DB 66 LVEKTDIEKSLSLGLG 86

RESULT 15

PCT-US94-06655-4

; Sequence 4, Application PC/TUS9406655

; GENERAL INFORMATION:

; APPLICANT: Chaiken, Irwin

APPLICANT: Graddis, Thomas
APPLICANT: Myszka, David
TITLE OF INVENTION: Coiled-Coil Stem Loop Templates

NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:

ADDRESSEE: SmithKline Beecham Corporation

STREET: Corporate Patents / P.O. Box 1539

CITY: King of Prussia

STATE: PA

COUNTRY: USA

ZIP: 19406-0939

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US94/06655

FILING DATE:

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Sutton, Jeffrey A.

REGISTRATION NUMBER: 34028

REFERENCE/DOCKET NUMBER: PS0164

TELECOMMUNICATION INFORMATION:

TELEPHONE: (215) 270-5024

TELEFAX: (215) 270-5090

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 15 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

FEATURE:

NAME/KEY: Region

LOCATION: 1..15

OTHER INFORMATION: /note="Corresponds to amino acids

93-107 of human Interleukin 5 (helix D)."

PCT-US94-06655-4

Query Match

Best Local Similarity 11.8%; Score 72; DB 5; Length 15;

Mismatches 13; Conservative 1; Mismatches 1; Indels 0;

Gaps 0;

QY 97 LDYLVQVFLGVINTEW 111

DB 1 LDYLVQVFLGVINTEW 15

Search completed: August 25, 2004, 00:07:16

Job time : 21.7831 secs

Blank Sheet

OM protein - protein search, using sw model
Run on: August 25, 2004, 00:05:39 ; Search time 78.0522 Seconds
(without alignments)
463.015 Million cell updates/sec

Title: US-10-787-382-10
Perfect score: 610
Sequence: 1 FAVENPMNRLVAETLLST.....FLDYQLVFLGVINTEWTPSS 115

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1295152 seqs, 31425058 residues

Total number of hits satisfying chosen parameters: 1295152

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA.*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
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- 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US09D_PUBCOMB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	610	100.0	115	9	US-09-755-633-10
2	610	100.0	115	14	US-10-218-654-86
3	610	100.0	115	14	US-10-262-439-86
4	610	100.0	134	9	US-09-755-633-5
5	610	100.0	134	14	US-10-218-654-81
6	610	100.0	134	14	US-10-262-439-81
7	358	58.7	115	16	US-10-658-834A-588
8	357	58.5	115	16	US-10-658-834A-569
9	357	58.5	287	14	US-10-295-074-13
10	356	58.4	115	14	US-10-289-454-234
11	356	58.4	115	14	US-10-050-902-234
12	356	58.4	115	14	US-10-050-898-234
13	356	58.4	115	14	US-10-295-074-1
14	356	58.4	115	16	US-10-658-834A-208
15	356	58.4	115	16	US-10-658-834A-574

16	356	58.4	115	16	US-10-658-834A-580	Sequence 580, App
17	356	58.4	115	16	US-10-658-834A-587	Sequence 587, App
18	356	58.4	115	16	US-10-658-834A-589	Sequence 589, App
19	356	58.4	115	16	US-10-658-834A-595	Sequence 595, App
20	356	58.4	123	14	US-10-289-454-337	Sequence 337, App
21	356	58.4	123	14	US-10-050-902-337	Sequence 337, App
22	356	58.4	123	14	US-10-050-898-337	Sequence 337, App
23	356	58.4	134	14	US-10-289-454-233	Sequence 233, App
24	356	58.4	134	14	US-10-400-377-12	Sequence 12, Appl
25	356	58.4	134	14	US-10-400-708-12	Sequence 12, Appl
26	356	58.4	134	14	US-10-298-148-12	Sequence 12, Appl
27	356	58.4	134	14	US-10-050-902-233	Sequence 233, App
28	356	58.4	134	14	US-10-050-898-233	Sequence 233, App
29	356	58.4	136	14	US-10-289-454-336	Sequence 336, App
30	356	58.4	136	14	US-10-050-902-336	Sequence 336, App
31	356	58.4	136	14	US-10-050-898-336	Sequence 336, App
32	356	58.4	138	14	US-10-289-454-335	Sequence 335, App
33	356	58.4	138	14	US-10-050-902-335	Sequence 335, App
34	356	58.4	138	14	US-10-050-898-335	Sequence 335, App
35	356	58.4	285	14	US-10-295-074-9	Sequence 9, Appl
36	356	58.4	285	14	US-10-295-074-11	Sequence 11, Appl
37	356	58.4	287	14	US-10-295-074-15	Sequence 15, Appl
38	355	58.2	115	16	US-10-658-834A-568	Sequence 568, App
39	355	58.2	115	16	US-10-658-834A-575	Sequence 575, App
40	355	58.2	115	16	US-10-658-834A-581	Sequence 581, App
41	355	58.2	115	16	US-10-658-834A-585	Sequence 585, App
42	355	58.2	115	16	US-10-658-834A-596	Sequence 596, App
43	355	58.2	115	16	US-10-658-834A-597	Sequence 597, App
44	354	58.0	115	16	US-10-658-834A-576	Sequence 576, App
45	354	58.0	115	16	US-10-658-834A-582	Sequence 582, App

ALIGNMENTS

RESULT 1

US-09-755-633-10
; Sequence 10, Application US/09755633
; Patent No. US2002012700A1
; GENERAL INFORMATION:
; APPLICANT: Yang, Shumin
; APPLICANT: McCall, Catherine A.
; APPLICANT: Weber, Eric R.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF
; FILE REFERENCE: IM-2-Cl-Cl
; CURRENT FILING DATE: 2001-01-05
; CURRENT FILING NUMBER: US/09/755,633
; PRIOR FILING DATE: 1999-05-28
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/087,306
; PRIOR FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 10
; LENGTH: 115
; TYPE: PRT
; ORGANISM: Canis familiaris
US-09-755-633-10

Query Match 100.0%; Score 610; DB 9; Length 115;
Best Local Similarity 100.0%; Pred. No. 1.9e-64;
Matches 115; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FAVENPMNRLVAETLLSTRTWLIGDGNLMIPPEKNHQLCIKEVFGIDTLKNQTA 60
DB 1 FAVENPMNRLVAETLLSTRTWLIGDGNLMIPPEKNHQLCIKEVFGIDTLKNQTA 60
QY 61 HGEAVDKLFQNLISLKEHIERQKRCAGERWRVTKFDLYQLVFLGVINTEWTPSS 115
DB 61 HGEAVDKLFQNLISLKEHIERQKRCAGERWRVTKFDLYQLVFLGVINTEWTPSS 115

RESULT 2
US-10-218-654-86
; Sequence 86, Application US/10218654
; Publication No. US20030099609A1
; GENERAL INFORMATION:
; APPLICANT: Sim, Gek-Kee
; APPLICANT: Yang, Shumin
; APPLICANT: Dreitz, Matthew J.
; APPLICANT: Wonderling, Ramani S.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF
; FILE REFERENCE: IM-2-C1
; CURRENT APPLICATION NUMBER: US/10/218,654
; PRIOR FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: US/09/322,409
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/087,306
; PRIOR FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 154
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 86
; LENGTH: 115
; TYPE: PRT
; ORGANISM: Canis familiaris
US-10-218-654-86
Query Match 100.0%; Score 610; DB 14; Length 115;
Best Local Similarity 100.0%; Pred. No. 1.9e-64;
Matches 115; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 FAVENPNRLVAETLLTLLSTHRTWLIGDGNLMPTPENKQHLCIKEVFGIDTLKNQTA 60
DB 1 FAVENPNRLVAETLLTLLSTHRTWLIGDGNLMPTPENKQHLCIKEVFGIDTLKNQTA 60
QY 61 HGEAVDKLFQNLSLIKEHIERQKRCACGERWRVTKFLDYQLQVFLGVNINTEWTPES 115
DB 61 HGEAVDKLFQNLSLIKEHIERQKRCACGERWRVTKFLDYQLQVFLGVNINTEWTPES 115
RESULT 3
US-10-262-439-86
; Sequence 86, Application US/10262439
; Publication No. US20030143196A1
; GENERAL INFORMATION:
; APPLICANT: Sim, Gek-Kee
; APPLICANT: Yang, Shumin
; APPLICANT: Dreitz, Matthew J.
; APPLICANT: Wonderling, Ramani S.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF
; FILE REFERENCE: IM-2-C2
; CURRENT APPLICATION NUMBER: US/10/262,439
; CURRENT FILING DATE: 2002-09-30
; PRIOR APPLICATION NUMBER: US/09/451,527
; PRIOR FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: 09/322,409
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/087,306
; PRIOR FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 86
; LENGTH: 115
; TYPE: PRT
; ORGANISM: Canis familiaris
US-10-262-439-86
Query Match 100.0%; Score 610; DB 14; Length 115;
Best Local Similarity 100.0%; Pred. No. 1.9e-64;
Matches 115; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 FAVENPNRLVAETLLTLLSTHRTWLIGDGNLMPTPENKQHLCIKEVFGIDTLKNQTA 60

DB 1 FAVENPNRLVAETLLTLLSTHRTWLIGDGNLMPTPENKQHLCIKEVFGIDTLKNQTA 60
QY 61 HGEAVDKLFQNLSLIKEHIERQKRCACGERWRVTKFLDYQLQVFLGVNINTEWTPES 115
DB 61 HGEAVDKLFQNLSLIKEHIERQKRCACGERWRVTKFLDYQLQVFLGVNINTEWTPES 115
RESULT 4
US-09-755-633-5
; Sequence 5, Application US/09755633
; Patent No. US20020127200A1
; GENERAL INFORMATION:
; APPLICANT: Yang, Shumin
; APPLICANT: McCall, Catherine A.
; APPLICANT: Weber, Eric R.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF
; FILE REFERENCE: IM-2-C1-C1
; CURRENT APPLICATION NUMBER: US/09/755,633
; CURRENT FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: 09/322,409
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/087,306
; PRIOR FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 134
; TYPE: PRT
; ORGANISM: Canis familiaris
US-09-755-633-5
Query Match 100.0%; Score 610; DB 9; Length 134;
Best Local Similarity 100.0%; Pred. No. 2.3e-64;
Matches 115; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 FAVENPNRLVAETLLTLLSTHRTWLIGDGNLMPTPENKQHLCIKEVFGIDTLKNQTA 60
DB 20 FAVENPNRLVAETLLTLLSTHRTWLIGDGNLMPTPENKQHLCIKEVFGIDTLKNQTA 79
QY 61 HGEAVDKLFQNLSLIKEHIERQKRCACGERWRVTKFLDYQLQVFLGVNINTEWTPES 115
DB 80 HGEAVDKLFQNLSLIKEHIERQKRCACGERWRVTKFLDYQLQVFLGVNINTEWTPES 134
RESULT 5
US-10-218-654-81
; Sequence 81, Application US/10218654
; Publication No. US20030099609A1
; GENERAL INFORMATION:
; APPLICANT: Sim, Gek-Kee
; APPLICANT: Yang, Shumin
; APPLICANT: Dreitz, Matthew J.
; APPLICANT: Wonderling, Ramani S.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF
; FILE REFERENCE: IM-2-C1
; CURRENT APPLICATION NUMBER: US/10/218,654
; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: US/09/322,409
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/087,306
; PRIOR FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 154
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 81
; LENGTH: 134
; TYPE: PRT
; ORGANISM: Canis familiaris
US-10-218-654-81
Query Match 100.0%; Score 610; DB 14; Length 134;
Best Local Similarity 100.0%; Pred. No. 2.3e-64;

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; SEQ ID NO 588
; LENGTH: 115
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-658-834A-588

Query Match 58.7%; Score 358; DB 16; Length 115;
Best Local Similarity 62.5%; Pred. No. 1.9e-34;
Matches 70; Conservative 16; Mismatches 26; Indels 0; Gaps 0;

QY 4 ENPNRLVAETLLTLLSHTRTWLIGDGNLMIPPEKNHOLCIKEVFOGIDTLKQTAHGE 63
DB 4 EIPTSALVKETALLSTHRTLLIANETLPIPVFKNHQLCETEIFOGIGTLESQTVQGG 63
QY 64 AVDKLFQNLSLIKHIERQKRCAGERRWRTKFLDYLVQFLGVINTEWTPES 115
DB 64 TVERLFKNLSLIKXIDGKKCKGERRRNVQFLDYLVQFLGVNTEWIES 115

RESULT 8
US-10-658-834A-569
; Sequence 569, Application US/10658834A
; Publication No. US20040132977A1
; GENERAL INFORMATION:
; APPLICANT: Gantier, Rene
; APPLICANT: Guyon, Thierry
; APPLICANT: Drittanti, Lilla
; APPLICANT: Vega, Manuel
; TITLE OF INVENTION: Rational Evolution of Cytokines for Higher Stability, En
; TITLE OF INVENTION: Acid
; TITLE OF INVENTION: Molecules and Related Applications
; FILE REFERENCE: 38751-922
; CURRENT APPLICATION NUMBER: US/10/658,834A
; CURRENT FILING DATE: 2003-09-08
; PRIOR APPLICATION NUMBER: 60/457,135
; PRIOR FILING DATE: 2003-03-21
; PRIOR APPLICATION NUMBER: 60/409,898
; PRIOR FILING DATE: 2002-09-09
; NUMBER OF SEQ ID NOS: 1306
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 569
; LENGTH: 115
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-658-834A-569

Query Match 58.5%; Score 357; DB 16; Length 115;
Best Local Similarity 62.5%; Pred. No. 2.5e-34;
Matches 70; Conservative 16; Mismatches 26; Indels 0; Gaps 0;

QY 4 ENPNRLVAETLLTLLSHTRTWLIGDGNLMIPPEKNHOLCIKEVFOGIDTLKQTAHGE 63
DB 4 EIPTSALVKETALLSTHRTLLIANETLPIPVFKNHQLCETEIFOGIGTLESQTVQGG 63
QY 64 AVDKLFQNLSLIKHIERQKRCAGERRWRTKFLDYLVQFLGVINTEWTPES 115
DB 64 TVERLFKNLSLIKXIDGKKCKGERRRNVQFLDYLVQFLGVNTEWIES 115

RESULT 9
US-10-295-074-13
; Sequence 13, Application US/10295074
; Publication No. US20030185845A1
; GENERAL INFORMATION:
; APPLICANT: Pharmexa A/S
; TITLE OF INVENTION: NOVEL IMMUNOGENIC MIMETICS OF MULTIMER PROTEINS
; FILE REFERENCE: P1013DK00
; CURRENT APPLICATION NUMBER: US/10/295,074
; CURRENT FILING DATE: 2002-11-15
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 287

```

; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Two human IL5 monomers joined by diglycine linker and including P30 and P2 epitopes
US-10-295-074-13

Query Match 58.4%; Score 357; DB 14; Length 287;
Best Local Similarity 61.9%; Pred. No. 8.2e-34;
Matches 70; Conservative 17; Mismatches 26; Indels 0; Gaps 0;
Qy 3 VENPMRLVAETLLSTHRTWLIGDGNLMPTPENKKNHQLCIKEVFGQIDTLKNOTAHG 62
Db 43 LEIPTSALVKETALLSTHRTLLIANETLRIPVPVHKHQLCTEEIFQGIQTLESQTVQGG 102
Qy 63 BAVDKLFQNLISLKEHIERQKRCAGRWRTKFLDYQLQVFLGVINTWTPES 115
Db 103 GTVERLFKNLSLIKKYIDGQKKCGEERRRVNQFLDYQLQVFLGVNTWIIIES 155

RESULT 10
US-10-289-454-234
; Sequence 234, Application US/10289454
; Publication No. US20030157479A1
; GENERAL INFORMATION:
; APPLICANT: Bachmann, Martin
; APPLICANT: Jennings, Gary
; APPLICANT: Sonderegger, Ivo
; TITLE OF INVENTION: Antigen Arrays for Treatments of Allergic Eosinophilic Diseases
; FILE REFERENCE: 1700.0360001
; CURRENT APPLICATION NUMBER: US/10/289,454
; CURRENT FILING DATE: 2003-02-10
; PRIOR APPLICATION NUMBER: US 60/396,636
; PRIOR FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: PCT/IB02/00166
; PRIOR FILING DATE: 2002-01-21
; PRIOR APPLICATION NUMBER: US 10/050,902
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: US 60/331,045
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 386
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 234
; LENGTH: 115
; TYPE: PRT
; ORGANISM: processed human IL-5
US-10-289-454-234

Query Match 58.4%; Score 356; DB 14; Length 115;
Best Local Similarity 62.5%; Pred. No. 3.2e-34;
Matches 70; Conservative 16; Mismatches 26; Indels 0; Gaps 0;
Qy 4 ENPMRLVAETLLSTHRTWLIGDGNLMPTPENKKNHQLCIKEVFGQIDTLKNOTAHG 63
Db 4 EIPTSALVKETALLSTHRTLLIANETLRIPVPVHKHQLCTEEIFQGIQTLESQTVQGG 63
Qy 64 AVDKLFQNLISLKEHIERQKRCAGRWRTKFLDYQLQVFLGVINTWTPES 115
Db 64 TVERLFKNLSLIKKYIDGQKKCGEERRRVNQFLDYQLQVFLGVNTWIIIES 115

RESULT 11
US-10-050-902-234
; Sequence 234, Application US/10050902
; Publication No. US20030175290A1
; GENERAL INFORMATION:
; APPLICANT: Renner, Wolfgang A.
; APPLICANT: Bachmann, Martin
; APPLICANT: Tissot, Alain
; APPLICANT: Maurer, Patrick
; APPLICANT: Lechner, Franziska
; APPLICANT: Sebbel, Peter
; APPLICANT: Piossek, Christine

; TITLE OF INVENTION: Molecular Antigen Array
; FILE REFERENCE: 1700.0190004
; CURRENT APPLICATION NUMBER: US/10/050,902
; CURRENT FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: US 60/262,379
; PRIOR FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: US 60/288,549
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: US 60/326,998
; PRIOR FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: US 60/331,045
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 350
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 234
; LENGTH: 115
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-050-902-234

Query Match 58.4%; Score 356; DB 14; Length 115;
Best Local Similarity 62.5%; Pred. No. 3.2e-34;
Matches 70; Conservative 16; Mismatches 26; Indels 0; Gaps 0;
Qy 4 ENPMRLVAETLLSTHRTWLIGDGNLMPTPENKKNHQLCIKEVFGQIDTLKNOTAHG 63
Db 4 EIPTSALVKETALLSTHRTLLIANETLRIPVPVHKHQLCTEEIFQGIQTLESQTVQGG 63
Qy 64 AVDKLFQNLISLKEHIERQKRCAGRWRTKFLDYQLQVFLGVINTWTPES 115
Db 64 TVERLFKNLSLIKKYIDGQKKCGEERRRVNQFLDYQLQVFLGVNTWIIIES 115

RESULT 12
US-10-050-898-234
; Sequence 234, Application US/10050898
; Publication No. US20030175711A1
; GENERAL INFORMATION:
; APPLICANT: Renner, Wolfgang A.
; APPLICANT: Bachmann, Martin
; APPLICANT: Tissot, Alain
; APPLICANT: Maurer, Patrick
; APPLICANT: Lechner, Franziska
; APPLICANT: Sebbel, Peter
; APPLICANT: Piossek, Christine
; APPLICANT: Orlmann, Rainer
; APPLICANT: Luond, Rainer
; APPLICANT: Staufenbiel, Matthias
; APPLICANT: Frey, Peter
; TITLE OF INVENTION: Molecular Antigen Array
; FILE REFERENCE: 1700.0190005
; CURRENT APPLICATION NUMBER: US/10/050,898
; CURRENT FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: US 60/262,379
; PRIOR FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: US 60/288,549
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: US 60/326,998
; PRIOR FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: US 60/331,045
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 350
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 234
; LENGTH: 115
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-050-898-234

Query Match 58.4%; Score 356; DB 14; Length 115;
Best Local Similarity 62.5%; Pred. No. 3.2e-34;
Matches 70; Conservative 16; Mismatches 26; Indels 0; Gaps 0;

Query Match	58.4%	Score 356;	DB 16;	Length 115;
Best Local Similarity	62.5%;	Pred. NO. 3.2e-34;		
Matches 70;	Conservative 16;	Mismatches 26;	Indels 0;	Gaps 0;

Blank Sheet

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 24, 2004, 23:55:53 ; Search time 22.6305 Seconds
(without alignments)
488.810 Million cell updates/sec

Title: US-10-787-382-10
Perfect score: 610
Sequence: 1 FAVENPMRLVAETLLTLLST.....FLDYLVQLGVINTWTPES 115

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 78:.*
1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	491	80.5	134	2 JC5116	interleukin-5 prec
2	356	58.4	134	1 A28477	interleukin-5 prec
3	347	56.9	133	1 ICM55	interleukin-5 prec
4	332	54.4	132	1 A4818	interleukin-5 prec
5	78.5	12.9	258	2 T47758	hypothetical prote
6	74.5	12.2	1232	2 B39432	Arp-dependent deox
7	73.5	12.0	253	2 T47757	hypothetical prote
8	73	12.0	1199	2 G69698	RNA polymerase (be
9	72.5	11.9	451	2 S33816	kinesin light chai
10	72.5	11.9	649	2 S33813	kinesin light chai
11	72.5	11.9	677	2 S33814	kinesin light chai
12	72.5	11.9	686	2 S33815	kinesin light chai
13	72	11.8	401	2 S28653	hypothetical prote
14	71	11.6	216	2 B69498	hypothetical prote
15	71	11.6	300	2 F84594	hypothetical prote
16	71	11.6	328	2 F64187	p-aminobenzoate sy
17	71	11.6	446	2 S76228	hypothetical prote
18	71	11.6	461	2 T38698	noc1 protein - fis
19	70	11.5	933	2 A59350	myosin - Acetabula
20	69.5	11.4	253	2 C97331	araC-type DNA-bind
21	69.5	11.4	331	2 G83876	hypothetical prote
22	69.5	11.4	1188	2 JC4889	phosphatidylinosit
23	69	11.3	215	2 F45355	ORF2 protein - Aut
24	69	11.3	345	2 S66958	UPE1 protein - yea
25	69	11.3	759	2 F64662	trans-Golgi membra
26	69	11.3	1871	2 D96698	probable DNA polym
27	69	11.3	1894	2 T02155	DNA-directed DNA p
28	68.5	11.2	190	2 S23712	interferon alpha-I
29	68.5	11.2	638	2 AE2115	hypothetical prote

30 68.5 11.2 709 2 T32089
31 68.5 11.2 1102 2 S65235
32 68 11.1 215 2 B72854
33 68 11.1 414 2 G84311
34 68 11.1 529 2 S35306
35 68 11.1 767 1 COZPCD
36 68 11.1 1055 2 T10432
37 68 11.1 1621 2 A82255
38 67.5 11.1 1189 2 JC6118
39 67 11.0 215 2 T41780
40 67 11.0 356 2 S15156
41 67 11.0 570 2 AG1228
42 67 11.0 2311 2 T06161
43 66.5 10.9 274 2 T21284
44 66.5 10.9 590 2 H71977
45 66.5 10.9 767 2 T37844

ALIGNMENTS

RESULT 1

JC5116
interleukin-5 precursor - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 02-Feb-1997 #sequence_revision 27-Feb-1997 #text_change 20-Jun-2000
C:Accession: JC5116
R:Werten, B.; Gobright, E.; Seow, H.F.
Gene 176, 273-274, 1996
A:Title: The nucleotide sequence of the bovine interleukin-5-encoding cDNA.
A:Reference number: JC5116; MUID:97075944; PMID:8918267
A:Accession: JC5116
A:Molecule type: mRNA
A:Residues: 1-134 <MER>
A:Cross-references: EMBL:Z67872; NID:gl113120; PIDN:CRA91779.1; PID:gl113121
A:Experimental source: lymphocytes
C:Comment: This protein plays a role in the eosinophilia associated with parasitic dise
C:Genetics:
A:Gene: IL-5
C:Superfamily: interleukin-5
C:Keywords: cytokine; glycoprotein; growth factor; homodimer; lymphokine; T-cell
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-134/Product: interleukin-5 #status predicted <MAT>
F:63/Disulfide bonds: interchain (to 105) #status predicted
F:76.90/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:105/Disulfide bonds: interchain (to 63) #status predicted

Query Match 80.5%; Score 491; DB 2; Length 134;
Best Local Similarity 81.6%; Pred. No. 9.1e-42;
Matches 93; Conservative 12; Mismatches 9; Indels 0; Gaps 0;

QY 2 AVENPMRLVAETLLTLLSTHRTWLGDNLMIPPEKNHOLCTKEVFQGIIDTLKNQTAH 61

DB 21 AVESTMRLVAETLLTLLSSHRTLLIGDGNLMIPPTQHTNHOLCTKEEVEFQGIIDTLKNQTAQ 80

QY 62 GEANDKLFLNLSLKEHETEROKEKACAGRWVTKFDLYLVQLGVINTWTPES 115

DB 81 GDAVKIFQNLSLKEIYIDLQKRGGERMRVKQFLDYLVQLGVINTWTPES 134

RESULT 2

A28477
interleukin-5 precursor - human
N:Alternate names: B-cell growth factor II; cytotoxic T lymphocyte inducer; eosinophil
C:Species: Homo sapiens (man)
C:Date: 01-Dec-1989 #sequence_revision 07-Jul-1995 #text_change 22-Jun-1999
C:Accession: A28477; A33883; A26112; A39881; JX0106; S15775
R:Tanabe, T.; Konishi, M.; Mizuta, T.; Noma, T.; Honjo, T.
J. Biol. Chem. 262: 16580-16584, 1987
A:Title: Molecular cloning and structure of the human interleukin-5 gene.
A:Reference number: A28477; MUID:86059042; PMID:2824500
A:Accession: A28477
A:Molecule type: DNA

A;Title: Isolation, structure and expression of cDNA and genomic clones for murine eosin n-5.
A;Reference number: S00807; MUID:88254802; PMID:3133208
A;Accession: S00807
A:Molecule type: DNA
A;Residues: 1-133 <CAM>
A;Cross-references: EMBL:X06271; NID:g52695; PIDN:CXA29607.1; PID:g52686
A;Accession: A38758
A:Molecule type: mRNA
A;Residues: 1-133 <CAZ>
A;Cross-references: EMBL:X06270; NID:g52687; PIDN:CAA29606.1; PID:g52688
R;Kinashi, T.; Harada, N.; Severinson, E.; Tanabe, T.; Sideras, P.; Konishi, M.; Azuma, R.; Mizuta, T.R.; Tanabe, T.; Nakakubo, H.; Noma, T.; Honjo, T.
Nature 324, 70-73, 1986
A;Title: Cloning of complementary DNA encoding T-cell replacing factor and identity with growth factors 1, 5i-57, 1986
A;Molecule type: protein
A;Reference number: JS0077; MUID:90180853; PMID:3078564
A;Accession: JS0077
A:Molecule type: DNA
A;Residues: 1-133 <MI2>
R;Takahashi, T.; Yamaguchi, N.; Mita, S.; Yamaguchi, Y.; Suda, T.; Tomimaga, A.; Kikuchi Mol. Immunol. 27, 911-920, 1990
A;Title: Structural comparison of murine T-cell (BLSIKI2)-derived T-cell-replacing factor A;Reference number: PH0102; MUID:91015093; PMID:2215480
A;Accession: PH0102
A:Molecule type: protein
A;Residues: 21-45,'X','47 <TA>
R;Yokota, T.; Coffman, R.L.; Hagiwara, H.; Rennick, D.M.; Takebe, Y.; Yokota, K.; Gemmel Proc. Natl. Acad. Sci. U.S.A. 84, 7388-7392, 1987
A;Title: Isolation and characterization of lymphokine cDNA clones encoding mouse and hum A;Reference number: A39881; MUID:88041112; PMID:2823259
A;Accession: B39881
A>Status: Preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A;Residues: 1-14,'AA',15-133 <YOK>
C;Genetics:
A;Introns: 47/3; 58/3; 101/3
C;Superfamily: interleukin-5
C;Keywords: cytokine; glycoprotein; growth factor; homodimer; lymphokine; T-cell F.1-18/Domain: signal sequence #status predicted <SIG>
F.19-133/Product: Interleukin-5 #status predicted <MAT>
F.46/Binding site: carbohydrate (Asn) (covalent) #status experimental
F.62/Disulfide bonds: interchain (to 104) #status predicted
F.75,89/Binding site: carbohydrate (Asn) (covalent) #status predicted
F.104/Disulfide bonds: interchain (to 62) #status predicted

Query Match 56.9%; Score 347; DB 1; Length 133;
Best Local Similarity 58.4%; Pred. No. 2e-27; 29; Indels 0; Gaps 0;
Matches 66; Conservative 18; Mismatches

QY 2 AVENPMRLVAETLLSTHRTWLIGDNLNMIPTEPNKHQLCIKEVFGQIDTLKNQTAAH 61
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 20 AMEIPMSVTVKKETLTQLSARRALLTSNETMLPVPTKHNHQLCIGEIQGLDLKNQTVR 79

QY 62 GEAVDKLFQNLSLIKEHTEROKKCAGRWTKFDLYQLGVINTWTFPE 114
| = | = | = | = | = | : | : | : | : | : | : | : | : | : | : |
DB 80 GTVEMLPFQNLSLIKXYIDROKKGEEERRTRDFLDYLQBFLGVMSTEWAWNE 132

RESULT 4
A48418
interleukin-5 precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
A;Accession: A48418; S37641
R;Uberla, K.; Li, W.Q.; Qin, Z.H.; Richter, G.; Raabe, T.; Diamantstein, T.; Blankenstein

Cytokine 3, 72-81, 1991
A>Title: The rat interleukin-5 gene: characterization and expression by retroviral gene
A/Reference number: A48418; MUID:91355638; PMID:1653053
A/Accession: A48418
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-132 <UBE>
A/Cross-references: EMBL:X54419; NID:g313254; PIDN:CAA38283.1; PID:g313255
A/Experimental source: cell line TR5-1
A/Note: sequence extracted from NCBI backbone (NCBI:63651, NCBI:63652)
C/Superfamily: interleukin-5
C/Keywords: cytokine; glycoprotein; growth factor; homodimer; lymphokine; T-cell
F/1-17/Domain: signal sequence #status predicted <SIG>
F/45-74/88/Product: interleukin-5 #status predicted <MAT>
F/61/Dsulfide bonds: interchain (to 103) #status predicted
F/103/Dsulfide bonds: interchain (to 61) #status predicted

Query Match 54.4%; Score 332; DB 1; Length 132;
Best Local Similarity 56.6%; Pred. No. 6.2e-26;
Matches 64; Conservative 19; Mismatches 31; Indels 0; Gaps 0;

QY 2 AVENPMNLVAETLLSTHRTWLGDNLMPTPNKHQLCIKVFGIDTLKNQTAH 61
DB 19 AMBIPMSTVVKETLIQLSTHALLTNETNRLPVPVTHKHQLCIGIFQGLDILKNQTVR 78
QY 62 GEAVDFLQNLSLIKKHIERKRCACGERWRVTKFLDYQLQVFLGVINTEWTP 114
DB 79 GGVTEILFQNLSLIKKYIDQKCKGEEKRKTHTFDYLOEFLGVNTEWAME 131

RESULT 5
T47758
hypothetical protein F2413.60 - Arabidopsis thaliana
C/Species: Arabidopsis thaliana (mouse-ear cress)
C/Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 28-Jul-2000
C/Accession: T47758
R/Nyakatura, G.; Partmann, B.; Dauner, D.; Sterr, W.; Holland, R.; Weichselgartner, M.;
submitted to the Protein Sequence Database, February 2000
A/Reference number: Z24475
A/Accession: T47758
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-258 <NYA>
A/Cross-references: EMBL:AL138655
A/Experimental source: cultivar Columbia; BAC clone F2413
C/Genetics:
A/Map position: 3
A/Introns: 109/3
A/Note: F2413.60
C/Superfamily: Arabidopsis thaliana hypothetical protein F2413.60

Query Match 12.9%; Score 78.5; DB 2; Length 258;
Best Local Similarity 26.8%; Pred. No. 2.5;
Matches 22; Conservative 15; Mismatches 38; Indels 7; Gaps 2;

QY 9 RLVAEITLLSTHRTWLGDNLMPTPNKHQLCIKVFGIDTLKNQTAHGA 64
DB 161 KAVANYISTVSATR---LGDNEYVWQISGSKHNFISNVLGLEDRFVLVDMSSRSQ 217
QY 65 VDKLFQNLSLIKKHIERKRC 86
DB 218 GERIFYTLHLQVEKIENYKLNLC 239

RESULT 6
B39432
ATP-dependent deoxyribonuclease chain A adda - Bacillus subtilis
N/Alternate names: ATP-dependent exonuclease synthesis protein Adda
C/Species: Bacillus subtilis
C/Date: 21-Feb-1992 #sequence_revision 21-Feb-1992 #text_change 02-Feb-2001
C/Accession: B39432; H69582
R/Kooistra, J.; Venema, G.

J. Bacteriol. 173, 3644-3655, 1991
A>Title: Cloning, sequencing, and expression of Bacillus subtilis genes involved in ATP-
A/Reference number: A39432; MUID:91267926; PMID:1646786
A/Accession: B39432
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-1232 <KOO>
A/Cross-references: GB:M63489; NID:g142438; PIDN:AAA22201.1; PID:g142440
A/Experimental source: K. Crogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,
Krogh, P.; Konigstein, G.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetell
Rieger, M.; Rivolta, C.; Roche, B.; Rose, M.; Sadale, Y.; Sato, T.; Scanlon
Fiegler, M.; Rivoita, C.; Rocha, E.; Schroeter, R.; Scoffone, P.; Sekiguchi, J.; Sekowska, A.; Seroi
Akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama,
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yoshikawa, H.; Danchin, A.
A/Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A/Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A/Reference number: A69580; MUID:98044033; PMID:9384377
A/Accession: H69582
A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-1232 <KUN>
A/Cross-references: GB:Z99109; GB:AL009126; NID:G2633260; PIDN:CAB12903.1; PID:e1183065
A/Experimental source: strain 168
C/Genetics:
A/Gene: addA
C/Keywords: nucleotide binding; P-loop
F/30-37/Region: nucleotide-binding motif A (P-loop)

Query Match 12.2%; Score 74.5; DB 2; Length 1232;
Best Local Similarity 22.2%; Pred. No. 38;
Matches 24; Conservative 24; Mismatches 37; Indels 23; Gaps 4;

QY 3 VENPMNLVAETLLSTHRTWLG--DGNLMPTPNKHQLCIKVFGIDTLKNQTA 60
DB 633 IDNPY----QDPLASVLRSPVIGADENLSLRLENKKAPY-----YEAMKDYLA 679
QY 61 HGEAVDFLQNLSLIKKHIERQK-----KRCACGERWRVTKFLDYL 100
DB 680 AGDRSDELYQKLTIFYGHLQKWRFAFSKNHVSSELIWEVYRDTKMYDV 727

RESULT 7
T47757
hypothetical protein F2413.50 - Arabidopsis thaliana
C/Species: Arabidopsis thaliana (mouse-ear cress)
C/Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 28-Jul-2000
C/Accession: T47757
R/Nyakatura, G.; Partmann, B.; Dauner, D.; Sterr, W.; Holland, R.; Weichselgartner, M.;
submitted to the Protein Sequence Database, February 2000
A/Reference number: Z24475
A/Accession: T47757
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-253 <NYA>
A/Cross-references: EMBL:AL138655
A/Experimental source: cultivar Columbia; BAC clone F2413
C/Genetics:
A/Map position: 3
A/Introns: 104/3
A/Note: F2413.50
C/Superfamily: Arabidopsis thaliana hypothetical protein F2413.60

Query Match 12.0%; Score 73.5; DB 2; Length 253;
Best Local Similarity 27.1%; Pred. No. 7.6;
Matches 23; Conservative 15; Mismatches 34; Indels 13; Gaps 3;

QY 9 RLVAETLLTSLTHTWLTGNGNLMPTPENKNHOLCIKEVFGID-----TLKNQTAH 61
 Db 156 KAVASYLSTVATR---LGNENVRVQSSSKIHNFISNVLGIEEDGDFVLVDVSSRSQ 212
 QY 62 GEAVDKLFQNLISLKEHIERQKRC 86
 Db 213 GE---RLFYTLHLQVENMDYKINC 234

RESULT 8

G69698
 RNA polymerase (beta' subunit) rpoC - Bacillus subtilis
 C:Species: Bacillus subtilis
 C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 02-Sep-2000
 C:Accession: G69698
 R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berth
 C.; Bron, S.; Brouillette, S.; Bruschini, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Ch
 A.; Ehrlich, S.D.; Emerson, P.T.; Ehtian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
 Nature 390, 249-256, 1997
 A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gall
 iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.
 Koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,
 A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mausel
 Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle
 Rieger, M.; Rivolta, C.; Roche, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon,
 A:Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seron
 akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama,
 T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K
 A:Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
 A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
 A:Reference number: A69580; MUID:9804033; PMID:9384377
 A:Accession: G69698
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-1199 <KUN>
 A:Cross-references: GB:299104; GB:AL009126; NID:92632267; PID:G69698.1; PID:e1182041;
 A:Experimental source: strain 168
 C:Genetics:
 A:Gene: rpoC
 C:Superfamily: Escherichia coli DNA-directed RNA polymerase beta' chain

Query Match 12.0%; Score 73; DB 2; Length 1199;
 Best Local Similarity 34.7%; Pred. No. 51;
 Matches 26; Conservative 12; Mismatches 31; Indels 6; Gaps 4;

QY 35 TPENKHOLCIKEVFGIDTLKN--QTAHG-EAVDKLFQNLISLKE--HIERQKRCAGE 89
 Db 142 TPLEKKQLLSEKEVAYLDYGNKFGQASMGAEAIHKLQDIDLVKEVDMLKEELKTSQ 201

QY 90 -RWRTKFLDYLOVF 103
 Db 202 RRTAIRKRLVLEAF 216

RESULT 9

S33816
 Kinesin light chain isoform 4 - sea urchin (Strongylocentrotus purpuratus)
 C:Species: Strongylocentrotus purpuratus (purple urchin)
 C:Date: 08-Dec-1993 #sequence_revision 01-Dec-1995 #text_change 09-Sep-1997
 C:Accession: S33816
 R:Wedaman, K.P.; Knight, A.E.; Kendrick-Jones, J.; Scholley, J.M.
 J. Mol. Biol. 231, 155-158, 1993
 A:Title: Sequences of sea urchin kinesin light chain isoforms.
 A:Reference number: S33813; MUID:93267648; PMID:8496962
 A:Accession: S33816
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-451 <WED>
 A:Cross-references: EMBL:L08259; NID:g161531; PID:g161532

Query Match 11.9%; Score 72.5; DB 2; Length 451;
 Best Local Similarity 25.9%; Pred. No. 19;
 Matches 21; Conservative 19; Mismatches 30; Indels 11; Gaps 3;

QY 27 GDGNLMPTPENKNHOLC--IKEVFGIDTLKNQTAHGEAVDKLFQNLISLKEHIERQKK 84
 Db 15 GQGNL-----SQEITGTREVIGLEQLKNE--HNDILNSLYQSLKMLKKDTPGDSN 65
 QY 85 RCAGERWRVTKFLDYLOVFLG 105
 Db 66 LVEEKTDIIEKSLSLGLG 86

RESULT 10

S33813
 Kinesin light chain - sea urchin (Strongylocentrotus purpuratus)
 C:Species: Strongylocentrotus purpuratus (purple urchin)
 C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Sep-1997
 C:Accession: S33813
 R:Wedaman, K.P.; Knight, A.E.; Kendrick-Jones, J.; Scholley, J.M.
 J. Mol. Biol. 231, 155-158, 1993
 A:Title: Sequences of sea urchin kinesin light chain isoforms.
 A:Reference number: S33813; MUID:93267648; PMID:8496962
 A:Accession: S33813
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-649 <WED>
 A:Cross-references: EMBL:L10233; NID:g161525; PID:g161526

Query Match 11.9%; Score 72.5; DB 2; Length 649;
 Best Local Similarity 25.9%; Pred. No. 28;
 Matches 21; Conservative 19; Mismatches 30; Indels 11; Gaps 3;

QY 27 GDGNLMPTPENKNHOLC--IKEVFGIDTLKNQTAHGEAVDKLFQNLISLKEHIERQKK 84
 Db 15 GQGNL-----SQEITGTREVIGLEQLKNE--HNDILNSLYQSLKMLKKDTPGDSN 65

QY 85 RCAGERWRVTKFLDYLOVFLG 105
 Db 66 LVEEKTDIIEKSLSLGLG 86

RESULT 11

S33814
 Kinesin light chain - sea urchin (Strongylocentrotus purpuratus)
 C:Species: Strongylocentrotus purpuratus (purple urchin)
 C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Sep-1997
 C:Accession: S33814
 R:Wedaman, K.P.; Knight, A.E.; Kendrick-Jones, J.; Scholley, J.M.
 J. Mol. Biol. 231, 155-158, 1993
 A:Title: Sequences of sea urchin kinesin light chain isoforms.
 A:Reference number: S33813; MUID:93267648; PMID:8496962
 A:Accession: S33814
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-677 <WED>
 A:Cross-references: EMBL:L10234; NID:g161527; PID:g161528

Query Match 11.9%; Score 72.5; DB 2; Length 677;
 Best Local Similarity 25.9%; Pred. No. 30;
 Matches 21; Conservative 19; Mismatches 30; Indels 11; Gaps 3;

QY 27 GDGNLMPTPENKNHOLC--IKEVFGIDTLKNQTAHGEAVDKLFQNLISLKEHIERQKK 84
 Db 15 GQGNL-----SQEITGTREVIGLEQLKNE--HNDILNSLYQSLKMLKKDTPGDSN 65

QY 85 RCAGERWRVTKFLDYLOVFLG 105
 Db 66 LVEEKTDIIEKSLSLGLG 86

RESULT 12

S33815
 Kinesin light chain isoform 3 - sea urchin (Strongylocentrotus purpuratus)
 C:Species: Strongylocentrotus purpuratus (purple urchin)
 C:Date: 08-Dec-1993 #sequence_revision 01-Dec-1995 #text_change 01-Dec-2000

Search completed: August 25, 2004, 00:06:25
Job time : 23.6305 secs

Blank sheet

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 24, 2004, 23:41:12 ; Search time 12.9317 Seconds
(without alignments)
463.052 Million cell updates/sec

Title: US-10-787-382-10

Perfect score: 610

Sequence: 1 FAVENPMNLVAETLLST.....FLDYQLVFLGVINTWTPES 115

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	610	100.0	134	1 IL5_CANFA	Q95176 canis fami
2	510	83.6	134	1 IL5_FELCA	O77515 felis silve
3	494	81.0	134	1 IL5_HORSE	Q02899 equus cabal
4	491	80.5	134	1 IL5_BOVIN	P52173 bos tauris
5	487	79.8	132	1 IL5_SHEEP	Q28586 ovis aries
6	372	61.0	135	1 IL5_CAVPO	O08997 cavia porce
7	361	59.2	134	1 IL5_CERTO	P46685 cercocobus
8	358	58.7	132	1 IL5_MERUN	O62575 meriones un
9	356	58.4	134	1 IL5_HUMAN	P05113 homo sapien
10	354	58.0	132	1 IL5_SIGHI	Q98819 sigmodon hi
11	352	57.7	134	1 IL5_MACMU	P48093 macaca mula
12	347	56.9	133	1 IL5_MOUSE	P04401 mus musculu
13	346	56.7	139	1 IL5_MACEU	O9xt91 macropus eu
14	332	54.4	132	1 IL5_RAT	Q08125 rattus norv
15	94.5	15.5	590	1 MP41_MXVVL	Q9801 myxoma viru
16	74.5	12.2	1232	1 ADDA_BACSU	P23478 bacillus eu
17	73	12.0	1199	1 RPOC_BACSU	P37871 bacillus eu
18	72.5	11.9	686	1 KLC_STRPU	Q05090 strongyloce
19	72	11.8	401	1 Y148_METSM	P22344 methanobrev
20	71.5	11.7	437	1 SECY_STRGB	Q59912 streptomyce
21	71	11.6	216	1 YJ87_ARCFU	Q28292 archaeoglob
22	71	11.6	328	1 YB70_HARIN	Q57537 haemophilus
23	71	11.6	461	1 TIPI1_SCHPO	P79055 schizosacch
24	69	11.3	346	1 UFE1_YEAST	P41834 saccharomyc
25	68.5	11.2	349	1 EGC2_VIBUO	Q8d4q0 vibrio vuln
26	68	11.1	169	1 HSCB_BUCBP	Q89a17 buchnera ap
27	68	11.1	215	1 Y034_NPVAC	P21287 autographa
28	68	11.1	529	1 CRT1_MYXAX	Q02861 myxococcus
29	68	11.1	767	1 CC10_SCHPO	P01129 schizosacch
30	68	11.1	1055	1 RPOC_PEDAC	P77917 pediococcus
31	67.5	11.1	439	1 ARKY_THETN	Q8r7c3 thermoanaer
32	66.5	10.9	767	1 CUL1_SCHPO	P51790 schizosacch
33	66	10.8	119	1 RPOZ_CAUCR	P58056 caulobacter

34 66 10.8 864 1 SYL_WIGBR Q8d333 wiggleswort
35 65.5 10.7 248 1 NAG1_CANAL Q04802 candida alb
36 85.5 10.7 889 1 SEC3_DROME Q9vq4 drosophila
37 65 10.7 163 1 CYPH_UROFA Q0060 uromyces fa
38 65 10.7 295 1 SYGA_BACSU P54380 bacillus su
39 65 10.7 664 1 DHSA_HUMAN P31040 homo sapien
40 65 10.7 738 1 ST11_YEAST P23561 saccharomyc
41 64.5 10.6 225 1 YP93_MYCPN P75197 mycoplasma
42 64 10.5 295 1 EPTS_BACAA Q81wk9 bacillus an
43 64 10.5 366 1 YP59_STAM Q99tt7 staphylococ
44 64 10.5 429 1 ARKY_PYRAE Q8zu55 pyrobaculum
45 64 10.5 430 1 TEK2_MOUSE Q92297 mus musculu

ALIGNMENTS

RESULT 1
IL5_CANFA

ID IL5_CANFA STANDARD; PRT; 134 AA.
AC Q95J76;
DT 15-MAR-2004 (Rel. 43, Created)
DT 15-MAR-2004 (Rel. 43, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Interleukin-5 precursor (Il-5) (T-cell replacing factor) (TRF)
DE (Eosinophil differentiation factor).
GN IL5.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21334408; PubMed=1140633;
RA Yang S., Sellins K.S., Weber E., McCall C.;
RT "Canine interleukin-5: molecular characterization of the gene and
RT expression of biologically active recombinant protein.";
RL J. Interferon Cytokine Res. 21:361-367(2001).
CC -!- FUNCTION: Factor that induces terminal differentiation of late-
CC developing B-cells to immunoglobulin secreting cells (By
CC similarity).
CC -!- SUBUNIT: Homodimer; disulfide-linked (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the IL-5 family.
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AF331920; AAL10716.1; -.
CC EMBL; AF331919; AAL10715.1; -.
CC InterPro; IPR009079; 4.helix_cytokine.
CC InterPro; IPR000186; Interleukin_5.
CC Pfam; PF02025; IL5; 1.
CC PRINTS; PR00432; INTERLEUKIN5.
CC ProDom; PD006721; Interleukin_5; 1.
CC Cytokine; Growth factor; Glycoprotein; Signal.
CC SIGNAL 21
CC CHAIN 22 134 INTERLEUKIN-5.
CC DISULFID 63 63 INTERCHAIN (WITH C-105) (BY SIMILARITY).
CC DISULFID 105 105 INTERCHAIN (WITH C-63) (BY SIMILARITY).
CC CARBOHYD 76 76 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 90 90 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC SEQUENCE 134 AA; 15307 MW; 003C86D94D6FF4C6 CRC64;

Query Match 100.0%; Score 610; DB 1; Length 134;

Best Local Similarity 100.0%; Pred. No. 2.le-55;

Matches 115; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 FAVENPNRLVAETLLSTHRTWLTGDNLMIPPTPENKNHOLCIKEVFOGIDTLKNQTA 60
Db 20 FAVENPNRLVAETLLSTHRTWLTGDNLMIPPTPENKNHOLCIKEVFOGIDTLKNQTA 79
QY 61 HGEAVDKLFQNLSLIKEHIEROKKRCAGRWRTKFLDYLVQVFLGVINTEWTPES 115
Db 80 HGEAVDKLFQNLSLIKEHIEROKKRCAGRWRTKFLDYLVQVFLGVINTEWTPES 134

RESULT 2
IL5_FELCA
ID IL5_FELCA STANDARD; PRT; 134 AA.
AC 077515; 062740;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Interleukin-5 precursor (IL-5) (T-cell replacing factor) (TRF)
DE (Eosinophil differentiation factor).
GN IL5.
OS Felis silvestris catus (Cat).
OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_TaxID=9685;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98452719; PubMed=9781459;
RA Padraig P.A., Qin Y., Wells T.N.C., Solway J., Camoretti-Mercado B.;
RT "Sequence and structural analysis of feline interleukin-5 cDNA.";
RL Am. J. Vet. Res. 59:1263-1269(1998).
RN [2]
RP SEQUENCE OF 12-128 FROM N.A.
RA Harley R., Day M.J., Gruffydd-Jones T.J., Harbour D.A., Helps C.R.;
RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Factor that induces terminal differentiation of late-
CC developing B-cells to immunoglobulin secreting cells (By
CC similarity).
CC -!- SUBUNIT: Homodimer; disulfide-linked (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the IL-5 family.
CC
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CC
CC EMBL; AF025436; AAC64505.1; -.
CC EMBL; AF051372; AAC05752.1; -.
CC HSP; P05113; IHL.
CC InterPro; IPR000186; Interleukin_5.
CC Pfam; PF02025; IL5; 1.
CC PRINTS; PR00432; INTERLEUKIN_5.
CC ProDom; PD06721; Interleukin_5; 1.
CC Cytokine; Growth factor; Glycoprotein; Signal.
CC SIGNAL 1 19
CC CHAIN 20 134
CC INTERLEUKIN-5.
CC DISULFID 63 63
CC INTERCHAIN (WITH C-105) (BY SIMILARITY).
CC FT DISULFID 105 105
CC INTERCHAIN (WITH C-63) (BY SIMILARITY).
CC FT CARBOHYD 76 76
CC N-LINKED (GLCNAC. .) (POTENTIAL).
CC FT CARBOHYD 90 90
CC N-LINKED (GLCNAC. .) (POTENTIAL).
CC FT CARBOHYD 104 105
CC KC -> NF (IN REF. 2).
CC FT CONFLICT 108 111
CC ERWR -> KWK (IN REF. 2).
CC FT CONFLICT 114 114
CC K -> N (IN REF. 2).
CC FT CONFLICT 117 117
CC D -> N (IN REF. 2).
CC FT CONFLICT 121 121
CC V -> F (IN REF. 2).
CC FT CONFLICT 125 126
CC VI -> LL (IN REF. 2).
CC SQ SEQUENCE 134 AA; 87D18DB8F8C8920 CRC64;

Query Match 83.68; Score 510; DB 1; Length 134;
Best Local Similarity 84.28; Pred. No. 3.4e-45;
Matches 96; Conservative 10; Mismatches 8; Indels 0; Gaps 0;

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QY 2 AVENPMNLVAETLLSTHRTWLTGDNLMIPPTPENKNHOLCIKEVFOGIDTLKNQTAH 61
Db 21 AVQSPMNLVAETLLSTHRTWLTGDNLMIPPTPENKNHOLCIKEVFOGIDTLKNQTV 80
QY 62 GEAVDKLFQNLSLIKEHIEROKKRCAGRWRTKFLDYLVQVFLGVINTEWTPES 115
Db 81 GDAVKLFQNLSLIKEHIEROKKRCAGRWRTKFLDYLVQVFLGVINTEWTPES 134

RESULT 3
IL5_HORSE
ID IL5_HORSE STANDARD; PRT; 134 AA.
AC 002659;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Interleukin-5 precursor (IL-5) (T-cell replacing factor) (TRF)
DE (Eosinophil differentiation factor).
GN IL5.
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP SEQUENCE FROM N.A.
RX Vandergriff E.V., Horohov D.W.;
RA Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Factor that induces terminal differentiation of late-
CC developing B-cells to immunoglobulin secreting cells (By
CC similarity).
CC -!- SUBUNIT: Homodimer; disulfide-linked (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the IL-5 family.
CC
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CC
CC EMBL; U91947; AAB51382.1; -.
CC HSP; P05113; IHL.
CC InterPro; IPR000186; Interleukin_5.
CC Pfam; PF02025; IL5; 1.
CC PRINTS; PR00432; INTERLEUKIN_5.
CC ProDom; PD06721; Interleukin_5; 1.
CC Cytokine; Growth factor; Glycoprotein; Signal.
CC SIGNAL 1 19
CC CHAIN 20 134
CC INTERLEUKIN-5.
CC DISULFID 63 63
CC INTERCHAIN (WITH C-105) (BY SIMILARITY).
CC FT DISULFID 105 105
CC INTERCHAIN (WITH C-63) (BY SIMILARITY).
CC FT CARBOHYD 76 76
CC N-LINKED (GLCNAC. .) (POTENTIAL).
CC FT CARBOHYD 90 90
CC N-LINKED (GLCNAC. .) (POTENTIAL).
CC SQ SEQUENCE 134 AA; 2914840E3E7A006D CRC64;

Query Match 81.08; Score 494; DB 1; Length 134;
Best Local Similarity 84.18; Pred. No. 1.5e-43;
Matches 95; Conservative 8; Mismatches 10; Indels 0; Gaps 0;

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RESULT 4
IL5_BOVIN

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ID IL5_BOVIN STANDARD; PRT; 134 AA.
AC F52173;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Interleukin-5 precursor (IL-5) (T-cell replacing factor) (TRF)
DE (Eosinophil differentiation factor).
GN IL5.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]_TaxID=9913;
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RX MEDLINE=97075944; PubMed=8918267;
RA Vertens B., Gobright E., Sew H.F.;
RT "The nucleotide sequence of the bovine interleukin-5-encoding cDNA.";
RL Gene 176:273-274(1996).
CC -!- FUNCTION: Factor that induces terminal differentiation of late-
CC developing B-cells to immunoglobulin secreting cells (By
CC similarity).
CC -!- SUBUNIT: Homodimer; disulfide-linked.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the IL-5 family.
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CC -----
DR EMBL; Z67872; CA91779.1; -.
DR F1R; JCS116; JCS116.
DR HSSP; P05113; 1HUL.
DR InterPro; IPR000186; Interleukin_5.
DR Pfam; PF02025; IL5; 1.
DR PRINTS; PR00432; INTERLEUKIN5.
DR ProDom; PD006721; Interleukin_5.
DR Cytokine; Growth factor; Glycoprotein; Signal.
KW SIGNAL
FT CHAIN 1 21
FT INTERLEUKIN-5.
FT DISULFID 63 63 INTERCHAIN (WITH C-105) (BY SIMILARITY).
FT DISULFID 105 105 INTERCHAIN (WITH C-63) (BY SIMILARITY).
FT CARBOHYD 76 76 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 90 90 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 134 AA; 15229 MW; 0B3A2328EE7431F4 CRC64;

Query Match 80.5%; Score 491; DB 1; Length 134;
Best Local Similarity 81.6%; Pred. No. 3e-43;
Matches 93; Conservative 12; Mismatches 9; Indels 0; Gaps 0;

QY 2 AVENPMNLVAETLTLLSTHRTWLTGDNLMIPENKNHOLCIKEVFGIDTLKNQTAH 61
DB 21 AVESTMNLVAETLTLLSSHRTLLIGDGNLMITPQTHNOLCIEEVFGIDTLKNQTAQ 80
QY 62 GEAVDKLFQNLSLIKEHIEROKRCACGERWRVTKFLDYLVQVFLGVINTWTPES 115
DB 81 GDAVKKIFQNLSLIKEYIDLQKRKCGGERWRVKQFLDYLVQVFLGVINTWTPES 134

RESULT 5
IL5_SHEEP
ID IL5_SHEEP STANDARD; PRT; 132 AA.
AC Q28586;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Interleukin-5 precursor (IL-5) (T-cell replacing factor) (TRF)
DE (Eosinophil differentiation factor).

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GN IL5.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]_TaxID=9940;
RP SEQUENCE FROM N.A.
RA Bryson C.E., Viney E., Brandon M., Boyd A.W.;
RL Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.
RN [2]_TaxID=9940;
RP SEQUENCE FROM N.A.
RA Seco H.-F., David M.-J., McWaters P.G., Hurst L., Wood P.R.;
RT "Cloning of ovine interleukin-5 cDNA.";
RL submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Factor that induces terminal differentiation of late-
CC developing B-cells to immunoglobulin secreting cells (By
CC similarity).
CC -!- SUBUNIT: Homodimer; disulfide-linked (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the IL-5 family.
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CC -----
DR EMBL; U17053; AAB60629.1; -.
DR EMBL; U17052; AAB60629.1; JOINED.
DR EMBL; U35038; AAC99991.1; -.
DR HSSP; P05113; 1HUL.
DR InterPro; IPR000186; Interleukin_5.
DR Pfam; PF02025; IL5; 1.
DR PRINTS; PR00432; INTERLEUKIN5.
DR ProDom; PD006721; Interleukin_5.
DR Cytokine; Growth factor; Glycoprotein; Signal.
KW SIGNAL
FT CHAIN 1 19
FT INTERLEUKIN-5.
FT DISULFID 61 61 INTERCHAIN (WITH C-103) (BY SIMILARITY).
FT DISULFID 103 103 INTERCHAIN (WITH C-61) (BY SIMILARITY).
FT CARBOHYD 74 74 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 88 88 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 132 AA; 14974 MW; D783F2B720E249D9 CRC64;

Query Match 79.8%; Score 487; DB 1; Length 132;
Best Local Similarity 80.7%; Pred. No. 7.5e-43;
Matches 92; Conservative 13; Mismatches 9; Indels 0; Gaps 0;

QY 2 AVENPMNLVAETLTLLSTHRTWLTGDNLMIPENKNHOLCIKEVFGIDTLKNQTAH 61
DB 19 AVESTMNLVAETLTLLSTHRTWLTGDNLMIPQTHNOLCIEEVFGIDTLKNQTAQ 78
QY 62 GEAVDKLFQNLSLIKEHIEROKRCACGERWRVTKFLDYLVQVFLGVINTWTPES 115
DB 79 GDAVKKIFQNLSLIKEYIDLQKRKCGGERWRVKQFLDYLVQVFLGVINTWTPES 132

RESULT 6
IL5_CAVPO
ID IL5_CAVPO STANDARD; PRT; 135 AA.
AC Q08587;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Interleukin-5 precursor (IL-5) (T-cell replacing factor) (TRF)
DE (Eosinophil differentiation factor).
GN IL5.
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.

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```

NCBI_TaxID=10141;
[1]
SEQUENCE FROM N.A.
MEDLINE=96289181; PubMed=8764226;
RA Mansour M., Karmilowicz M., Hawrylik S.J., Nalcerio B., Angilly J.,
RA Conklyn M.J., Lilly C.M., Drzen J.M., Lee S.E., Auperin D.D.,
RA de Wet J.R., Cohan V.L., Showell H.J., Danley D.E.;
RA "Production and characterization of guinea pig IL-5 in baculovirus-
RT infected insect cells";
RL Am. J. Physiol. 270:L1002-L1007(1996).
CC -!- FUNCTION: Factor that induces terminal differentiation of late-
CC developing B-cells to immunoglobulin secreting cells (By
CC similarity).
CC -!- SUBUNIT: Homodimer; disulfide-linked (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the IL-5 family.
CC
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CC
CC EMBL; U34588; AAB61357.1; -
CC HSSP; P05113; 1HUL
CC InterPro; IPR000186; Interleukin_5.
CC Pfam; PF02025; IL5; 1
CC PRINTS; PR00432; INTERLEUKIN5.
CC ProDom; PD006721; Interleukin_5; 1.
CC Cytokine; Growth factor; Glycoprotein; Signal.
CC SIGNAL 1 19 BY SIMILARITY.
CC CHAIN 20 135 INTERLEUKIN-5.
CC DISULFID 64 64 INTERCHAIN (WITH C-106) (BY SIMILARITY).
CC FT DISULFID 106 106 INTERCHAIN (WITH C-64) (BY SIMILARITY).
CC FT CARBOHYD 48 48 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 77 77 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 91 91 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC SQ SEQUENCE 135 AA; 15291 MW; B885252132F52731 CRC64;
Query Match 61.0%; Score 372; DB 1; Length 135;
Best Local Similarity 68.5%; Pred. No. 4.3e-31;
Matches 74; Conservative 11; Mismatches 23; Indels 0; Gaps 0;
QY 7 MRLVATLTLLSTHRTWLTGDNLMIPPTENKQHLCIKVEFGQIDTLKNTAHEAVD 66
DB 27 LRALVRETLLSTHRTWLTGDNLMIPPTENKQHLCIKVEFGQIDTLKNTAHEAVD 86
QY 67 KLFQNLSLIKHEIEROKRCAGRWRTKFLDYQLVFLGVINTEWTEPE 114
DB 87 TLFQNLSLIKKHLDLQKCGERRRVKFLDYQLVFLGVINTEWTEPE 134
RESULT 7
IL5_CERTO
ID IL5_CERTO STANDARD; PRT; 134 AA.
AC P46685;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Interleukin-5 precursor (IL-5) (T-cell replacing factor) (TRF)
DE (Eosinophil differentiation factor).
GN IL5.
OS Cercopithecus torquatus atys (Red-crowned mangabey) (Sooty mangabey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Cercopithecus.
OX NCBI_TaxID=9531;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Fuji;
RX MEDLINE=96003435; PubMed=7561102;

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RA Villinger F.J., Brar S.S., Mayne A.E., Chikkala N., Ansari A.A.;
RT "Comparative sequence analysis of cytokine genes from human and
RT nonhuman primates.";
RL J. Immunol. 155:3946-3954(1995).
CC -!- FUNCTION: Factor that induces terminal differentiation of late-
CC developing B-cells to immunoglobulin secreting cells (By
CC similarity).
CC -!- SUBUNIT: Homodimer; disulfide-linked (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the IL-5 family.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; L26033; AAA99971.1; -
CC HSSP; P05113; 1HUL
CC InterPro; IPR000186; Interleukin_5.
CC Pfam; PF02025; IL5; 1
CC PRINTS; PR00432; INTERLEUKIN5.
CC ProDom; PD006721; Interleukin_5; 1.
CC Cytokine; Growth factor; Glycoprotein; Signal.
CC SIGNAL 1 19 BY SIMILARITY.
CC CHAIN 20 134 INTERLEUKIN-5.
CC DISULFID 63 63 INTERCHAIN (WITH C-105) (BY SIMILARITY).
CC FT DISULFID 105 105 INTERCHAIN (WITH C-63) (BY SIMILARITY).
CC FT CARBOHYD 22 22 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 47 47 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 90 90 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC SQ SEQUENCE 134 AA; 15339 MW; 7BDD491C437981ED CRC64;
Query Match 59.2%; Score 361; DB 1; Length 134;
Best Local Similarity 63.4%; Pred. No. 5.7e-30;
Matches 71; Conservative 17; Mismatches 24; Indels 0; Gaps 0;
QY 4 ENPMNRVLAETLTLLSTHRTWLTGDNLMIPPTENKQHLCIKVEFGQIDTLKNTAHEG 63
DB 23 EIPTSALVKETLTLLSTHRTWLTGDNLMIPPTENKQHLCIKVEFGQIDTLKNTAHEG 82
QY 64 AVDKLFQNLSLIKHEIEROKRCAGRWRTKFLDYQLVFLGVINTEWTEPE 115
DB 83 TVERLFQNLSLIKKIDGQKCGERRRVNQLDYQLVFLGVINTEWTEPE 134
RESULT 8
IL5_MERUN
ID IL5_MERUN STANDARD; PRT; 132 AA.
AC Q62575;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Interleukin-5 precursor (IL-5) (T-cell replacing factor) (TRF)
DE (Eosinophil differentiation factor).
GN IL5.
OS Meriones unguiculatus (Mongolian jird) (Mongolian gerbil).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Gerbillinae;
OC Meriones.
OX NCBI_TaxID=10047;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Mai Z., Klei T.R.;
RL Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Factor that induces terminal differentiation of late-
CC developing B-cells to immunoglobulin secreting cells (By
CC similarity).
CC -!- SUBUNIT: Homodimer; disulfide-linked (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted.

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CC -1- SIMILARITY: Belongs to the IL-5 family.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; L37780; AAA65675.1; -.
CC DR HSP; P05113; 1HUL.
CC DR InterPro; IPR000186; Interleukin_5.
CC DR Pfam; PF020235; IL5_1.
CC DR PRINTS; PR00432; INTERLEUKINS.
CC DR ProDom; PD006721; Interleukin_5; 1.
CC KW Cytokine; Growth factor; Glycoprotein; Signal.
CC FT SIGNAL 1 17 POTENTIAL.
CC FT CHAIN 18 132 INTERLEUKIN-5.
CC FT DISULFID 61 61 INTERCHAIN (WITH C-103) (BY SIMILARITY).
CC FT DISULFID 103 103 INTERCHAIN (WITH C-61) (BY SIMILARITY).
CC FT CARBOHYD 45 45 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 74 74 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 88 88 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC SQ SEQUENCE 132 AA; 15164 MW; 60CE3852F9F84261 CRC64;
CC
CC Query Match 58.7%; Score 358; DB 1; Length 132;
CC Best Local Similarity 61.1%; Pred. No. 1.1e-29;
CC Matches 69; Conservative 18; Mismatches 26; Indels 0; Gaps 0;
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CC QY 2 AVENPMNLVAETLLSTRTWLIGDNLMIPTPKNKHQKICVFQIDTLKNQTAH 61
CC DB 19 ALSIPMSAVKETLIQLSTHRLTLSTNETVRLPVPTHKNEHQLCIGIFQGLDILKNQTAH 78
CC
CC QY 62 GEAVDKLFQNLISLKHIEROKRCAGERRVTKFDLYQVFLGVNTWETPE 114
CC DB 79 GGAVETLFQNLISLKHIEROKRCAGERRRARRQFLDYQSFGLGVNWTWETME 131
CC
CC RESULT 9
CC IL5_HUMAN
CC ID IL5_HUMAN STANDARD; PRT; 134 AA.
CC AC P05113; Q13840;
CC DT 13-AUG-1987 (Rel. 05, Created)
CC DT 13-AUG-1987 (Rel. 05, Last sequence update)
CC DT 10-OCT-2003 (Rel. 42, Last annotation update)
CC DE Interleukin-5 precursor (IL-5) (T-cell replacing factor) (TRF)
CC DE (Eosinophil differentiation factor) (B cell differentiation factor 1).
CC GN IL5.
CC OS Homo sapiens (Human).
CC OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
CC OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
CC OX NCBI_TaxID=9606;
CC RN [1]
CC RP SEQUENCE FROM N.A.
CC RX MEDLINE=87066782; PubMed=3024129;
CC RA Azuma C., Tanabe T., Konishi M., Kinashi T., Noma T., Matsuda F.,
CC RA Yabuta Y., Takatsu K., Hammarstrom L., Smith C.I.E., Severinson E.,
CC RA Honjo T.;
CC RT "Cloning of cDNA for human T-cell replacing factor (interleukin-5)
CC RT and comparison with the murine homologue."
CC RL Nucleic Acids Res. 14:9149-9158(1986).
CC RN [2]
CC RP SEQUENCE FROM N.A.
CC RX MEDLINE=88059042; PubMed=2824500;
CC RA Tanabe T., Konishi M., Mizuta T., Noma T., Honjo T.;
CC RT "Molecular cloning and structure of the human interleukin-5 gene."
CC RL J. Biol. Chem. 262:16580-16584(1987).
CC RN [3]
CC RP SEQUENCE FROM N.A.
CC RX MEDLINE=88016145; PubMed=3498940;
CC RA Campbell H.D., Tucker W.Q.J., Hort Y., Martinson M.E., Mayo G.,
CC RA Clutterbuck E.J., Sanderson C.J., Young I.G.;

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RT "Molecular cloning, nucleotide sequence, and expression of the gene
RT encoding human eosinophil differentiation factor (interleukin 5).";
RT Proc. Natl. Acad. Sci. U.S.A. 84:6629-6633(1987).
RN [4]
CC RP SEQUENCE FROM N.A.
CC RX MEDLINE=88041112; PubMed=2823259;
CC RA Yokota T., Coffman R.L., Hagiwara H., Rennick D.M., Takebe Y.,
CC RA Yokota K., Gemmell L., Shrader B., Yang G., Meyerson P., Luh J.,
CC RA Hoy P., Pene J., Briere F., Spits H., Banchereau J., de Vries J.,
CC RA Lee F.D., Arai N., Arai K.;
CC RT "Isolation and characterization of lymphokine cDNA clones encoding
CC mouse and human IGA-enhancing factor and eosinophil
CC colony-stimulating factor activities: relationship to interleukin
CC 5.";
CC Proc. Natl. Acad. Sci. U.S.A. 84:7388-7392(1987).
RN [5]
CC RP SEQUENCE FROM N.A.
CC RA Honjo T., Takatsu K., Severinson E.;
CC RT Submitted (FEB-1992) to the EMBL/GenBank/DBJ databases.
RN [6]
CC RP SEQUENCE FROM N.A.
CC RA Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Yi Q.,
CC RA Nickerson D.A.;
CC RT Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
RN [7]
CC RP SEQUENCE OF 20-134, AND DISULFIDE BONDS.
CC RX MEDLINE=90299868; PubMed=2361960;
CC RA Minamitake Y., Kodama S., Katayama T., Adachi H., Tanaka S.,
CC RA Tsujimoto M.;
CC RT "Structure of recombinant human interleukin 5 produced by Chinese
CC hamster ovary cells.";
CC J. Biochem. 107:292-297(1990).
RN [8]
CC RP DISULFIDE BONDS.
CC RX MEDLINE=91243878; PubMed=2037074;
CC RA Proudfoot A.E.I., Davies J.G., Turcatti G., Wingfield P.T.;
CC RT "Human interleukin-5 expressed in Escherichia coli: assignment of the
CC disulfide bridges of the purified unglycosylated protein.";
CC FEBS Lett. 283:61-64(1991).
RN [9]
CC RP X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS).
CC RX MEDLINE=93247642; PubMed=8483502;
CC RA Milburn M.V., Hassell A.M., Lambert M.H., Jordan S.R.,
CC RA Proudfoot A.E.I., Graber P., Wells T.N.C.;
CC RT "A novel dimer configuration revealed by the crystal structure at
CC 2.4-A resolution of human interleukin-5.";
CC Nature 363:172-176(1993).
CC CC -1- FUNCTION: Factor that induces terminal differentiation of late-
CC developing B-cells to immunoglobulin secreting cells.
CC CC -1- SUBUNIT: Homodimer; disulfide-linked.
CC CC -1- SUBCELLULAR LOCATION: Secreted.
CC CC -1- SIMILARITY: Belongs to the IL-5 family.
CC CC -1- DATABASE: NAME=R&D Systems' cytokine mini-reviews; IL5;
CC WWW="http://www.rndsystems.com/asp/g_sitebuilder.asp?bodyId=207".
CC -----
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CC -----
CC EMBL; X04688; CAA28390.1; -.
CC DR EMBL; J03478; AAA74469.1; -.
CC DR EMBL; J02971; AAA98620.1; -.
CC DR EMBL; X12705; CAA31210.1; -.
CC DR EMBL; X12706; CAA31211.1; -.
CC DR EMBL; AF353265; AAK19759.1; -.
CC DR PIR; A28477; A28477.
CC DR PDB; 1HUL; 07-DEC-95.
CC DR Genew; HGNC:6016; IL5.
CC DR MIM; 147850; -.

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DR GO: 0005576; C:extracellular; TAS.
 DR GO: 0005137; F:interleukin-5 receptor binding; TAS.
 DR GO: 0009626; P:hypersensitive response; TAS.
 DR GO: 0006954; P:inflammatory response; TAS.
 DR InterPro: IPR000186; Interleukin_5.
 DR Pfam: PF02025; IL5; 1.
 DR PRINTS: PR00432; INTERLEUKIN5.
 DR ProDom: PD06721; Interleukin_5; 1.
 KW Cytokine; Growth factor; Glycoprotein; Signal; 3D-structure.
 FT SIGNAL 1 19
 FT CHAIN 20 134 INTERLEUKIN-5.
 FT DISULFID 63 63 INTERCHAIN (WITH C-105).
 FT DISULFID 105 105 INTERCHAIN (WITH C-63).
 FT CARBOHYD 22 22 O-LINKED.
 FT CARBOHYD 47 47 N-LINKED (GLCNAC. . .).
 FT CARBOHYD 88 88 F -> L (IN REF. 5; CAA31210).
 FT HELIX 26 38
 FT TURN 39 40
 FT TURN 41 45
 FT TURN 46 46
 FT STRAND 51 54
 FT HELIX 60 62
 FT HELIX 64 77
 FT TURN 82 82
 FT HELIX 83 103
 FT TURN 104 105
 FT STRAND 108 111
 FT HELIX 112 128
 FT TURN 129 129
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 Query Match 58.4%; Score 356; DB 1; Length 134;
 Best Local Similarity 62.5%; Pred. No. 1.8e-29;
 Matches 70; Conservative 16; Mismatches 26; Indels 0; Gaps 0;
 QY 4 ENPMRLVAETLTLLSTHRTWLIGDGNLMTPTENKKNHQLCKEYFQGIIDTLKNQTAHGE 63
 Db 23 EIPTSALVKTLLSTHRTWLIGDGNLMTPTENKKNHQLCKEYFQGIIDTLKNQTAHGE 82
 QY 64 AVDKLFQNLSLIKHEIRQKRCAGRWRTKFLDYQLQVFLGVINTWTPES 115
 Db 83 TVERLFNLSLIKKYIDQKKCKGERRRVNQFLDYQLQVFLGVNTWTEIES 134
 RESULT 10
 IL5_SIGHI STANDARD; PRT; 132 AA.
 AC Q9ESI9;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Interleukin-5 precursor (IL-5) (T-cell replacing factor) (TRF)
 DE (Eosinophil differentiation factor).
 GN IL5.
 OS Sigmodon hispidus (Hispid cotton rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;
 OC Sigmodon.
 OX NCBI_TaxID=42415;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Spleen;
 RX MEDLINE=20510033; PubMed=11054577;
 RA Howard S., Jacquet A., Haumont M., Daminet V., Milican F., Glineur F.,
 RT "cloning, expression and purification of recombinant cotton rat
 interleukin-5";
 RL Gene 257:149-155 (2000).
 CC -!- FUNCTION: Factor that induces terminal differentiation of late-
 developing B-cells to immunoglobulin secreting cells.
 CC -!- SUBUNIT: Homodimer; disulfide-linked.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the IL-5 family.

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 or send an email to license@ebi.ac.uk).
 CC EMBL: AF148211; AAC16722.1; --
 DR HSP: P05113; IHUL.
 DR InterPro: IPR000186; Interleukin_5.
 DR Pfam: PF02025; IL5; 1.
 DR PRINTS: PR00432; INTERLEUKIN5.
 DR ProDom: PD06721; Interleukin_5; 1.
 KW Cytokine; Growth factor; Glycoprotein; Signal.
 FT SIGNAL 1 19
 FT CHAIN 20 132 INTERLEUKIN-5.
 FT DISULFID 61 61 INTERCHAIN (WITH C-103) (BY SIMILARITY).
 FT DISULFID 103 103 INTERCHAIN (WITH C-61) (BY SIMILARITY).
 FT CARBOHYD 45 45 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 74 74 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 88 88 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 132 AA; 15434 MW; B328B81B2371FEB9 CRC64;
 Query Match 58.0%; Score 354; DB 1; Length 132;
 Best Local Similarity 59.6%; Pred. No. 2.9e-29;
 Matches 68; Conservative 17; Mismatches 29; Indels 0; Gaps 0;
 QY 1 FAVENPMRLVAETLTLLSTHRTWLIGDGNLMTPTENKKNHQLCKEYFQGIIDTLKNQTA 60
 Db 18 FAVEPMHTVVKETLIQLSTHRTWLIGDGNLMTPTENKKNHQLCKEYFQGIIDTLKNQTV 77
 QY 61 HGEAVDKLFQNLSLIKHEIRQKRCAGRWRTKFLDYQLQVFLGVINTWTPTE 114
 Db 78 RGGTVETLFQNLSLIKKYIDQKKCKGERRRVNQFLDYQLQVFLGVNTWTE 131
 RESULT 11
 IL5_MACMU STANDARD; PRT; 134 AA.
 AC P48093;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Interleukin-5 precursor (IL-5) (T-cell replacing factor) (TRF)
 DE (Eosinophil differentiation factor).
 GN IL5.
 OS Macaca mulatta (Rhesus macaque).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
 OC Cercopitheidae; Macaca.
 OX NCBI_TaxID=9544;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Blood;
 RX MEDLINE=96003435; PubMed=7561102;
 RA Villinger F.J., Brar S.S., Mayne A.E., Chikkala N., Ansari A.A.;
 RT "Comparative sequence analysis of cytokine genes from human and
 nonhuman primates";
 RL J. Immunol. 155:3946-3954 (1995).
 CC -!- FUNCTION: Factor that induces terminal differentiation of late-
 developing B-cells to immunoglobulin secreting cells (By
 similarity).
 CC -!- SUBUNIT: Homodimer; disulfide-linked (By similarity).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the IL-5 family.
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 CC -----
 DR EMBL; U19848; AAA86710.1; -
 DR HSP; P05113; 1HUL
 DR InterPro; IPR000186; Interleukin_5.
 DR Pfam; PF02025; IL5; 1.
 DR PRINTS; PR00432; INTERLEUKINS.
 DR ProDom; PD06721; Interleukin_5; 1.
 KW Cytokine; Growth factor; Glycoprotein; Signal.
 FT SIGNAL 1 19 BY SIMILARITY.
 FT CHAIN 20 134 INTERLEUKIN-5.
 FT DISULFID 63 63 INTERCHAIN (WITH C-105) (BY SIMILARITY).
 FT DISULFID 105 105 INTERCHAIN (WITH C-63) (BY SIMILARITY).
 FT CARBOHYD 22 22 O-LINKED (BY SIMILARITY).
 FT CARBOHYD 47 47 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 90 90 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 134 AA; 15150 MW; DC985ECF4BAB86A3 CRC64;
 Query Match 57.7%; Score 352; DB 1; Length 134;
 Best Local Similarity 62.5%; Pred. No. 4.7e-29;
 Matches 70; Conservative 15; Mismatches 27; Indels 0; Gaps 0;
 QY 4 ENPMRLVAETLLSTHRTWLTGDNLMIPENKNHOLCIKEVFGQIDTLKNQTAHGE 63
 Db 23 EIPASALVKETALLSTHRTLLANETLRIPVPHKHQLCTEIEIFQIGITLESQIVQGG 82
 QY 64 AVDKLFQNLKHEHIEROKKRCAGRWRTKFLDYQLVFLGVINTEWTPES 115
 Db 83 TVBERLFKNLSLIRKYGQKKGCEERRVNOFLDYQLVFLGVINTEWTPES 134
 RESULT 12
 IL5_MOUSE STANDARD; PRT; 133 AA.
 AC P04401;
 DT 20-MAR-1987 (Rel. 04, Created)
 DT 01-NOV-1988 (Rel. 09, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Interleukin-5 precursor (IL-5) (T-cell replacing factor) (TRF) (B-cell
 DE growth factor II) (BCGF-II) (Eosinophil differentiation factor)
 DE (Cytotoxic T lymphocyte inducer).
 GN IL5 OR IL-5.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 CX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=88254802; PubMed=3133208;
 RA Campbell H.D., Sanderson C.J., Wang Y., Hort Y., Martinson M.E.,
 RA Tucker W.D., Stellanwagen A., Strath M., Young I.G.;
 RT "Isolation, structure and expression of cDNA and genomic clones for
 RT murine eosinophil differentiation factor: Comparison with other
 RT eosinophilopoietic lymphokines and identity with interleukin-5";
 RL Eur. J. Biochem. 174:345-352(1988).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/c;
 RX MEDLINE=87065032; PubMed=3024009;
 RA Kinashi T., Harada N., Severinson E., Tanabe T., Sideras P.,
 RA Konishi M., Azuma C., Tomimaga A., Bergstedt-Lindqvist S.,
 RA Takahashi M., Matsuda F., Yaita Y., Takatsu K., Honjo T.;
 RT "Cloning of complementary DNA encoding T-cell replacing factor and
 RT identity with B-cell growth factor II";
 RL Nature 324:70-73(1986).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90180853; PubMed=3078564;
 RA Mizuta T.R., Tanabe T., Nakakubo H., Noma T., Honjo T.;
 RA "Molecular cloning and structure of the mouse interleukin-5 gene";
 RL Growth Factors 1:51-57(1988).
 CC -!- FUNCTION: Factor that induces terminal differentiation of late-

CC developing B-cells to immunoglobulin secreting cells.
 CC -!- SUBUNIT: Homodimer; disulfide-linked.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the IL-5 family.
 CC -----
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 CC -----
 CC EMBL; X06270; CAA29606.1; -
 CC EMBL; X06271; CAA29607.1; -
 CC EMBL; X04601; CAA28266.1; -
 CC PIR; S00807; ICMS5.
 CC HSP; P05113; 1HUL.
 CC MGD; MGI:96557; IL5.
 DR InterPro; IPR000186; Interleukin_5.
 DR Pfam; PF02025; IL5; 1.
 DR PRINTS; PR00432; INTERLEUKINS.
 DR ProDom; PD06721; Interleukin_5; 1.
 KW Cytokine; Growth factor; Glycoprotein; Signal.
 FT SIGNAL 1 20
 FT CHAIN 21 133 INTERLEUKIN-5.
 FT DISULFID 62 62 INTERCHAIN (WITH C-104) (BY SIMILARITY).
 FT DISULFID 104 104 INTERCHAIN (WITH C-62) (BY SIMILARITY).
 FT CARBOHYD 46 46 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 75 75 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 89 89 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 133 AA; 15410 MW; C6DC091682452AF4 CRC64;
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 Best Local Similarity 58.4%; Pred. No. 1.5e-28;
 Matches 66; Conservative 18; Mismatches 29; Indels 0; Gaps 0;
 QY 2 AVENPMRLVAETLLSTHRTWLTGDNLMIPENKNHOLCIKEVFGQIDTLKNQTAH 61
 Db 20 AVEIPMSVVKETLLTQLSAHRALLTSNETMELPVTNKHQLCIGEIFQGLDILKNQTVR 79
 QY 62 GEAVDKLFQNLKHEHIEROKKRCAGRWRTKFLDYQLVFLGVINTEWTPES 114
 Db 80 GGTVELFQNLKLINKYIDROKGBERRETROFLDYQLVFLGVINTEWTPES 132
 RESULT 13
 IL5_MOUSE STANDARD; PRT; 139 AA.
 AC Q9XT91;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Interleukin-5 precursor (IL-5) (T-cell replacing factor) (TRF)
 DE (Eosinophil differentiation factor).
 GN IL5.
 OS Macropus eugenii (Tamar wallaby).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Metatheria; Diprotodontia; Macropodidae; Macropus.
 CX NCBI_TaxID=9315;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99432005; PubMed=10501836;
 RA Hawken R.J., Maccarone P., Toder R., Marshall Graves J.A.,
 RA Maddox J.F.;
 RT "Isolation and characterization of marsupial IL5 genes";
 RL Immunogenetics 49:942-948(1999).
 CC -!- FUNCTION: Factor that induces terminal differentiation of late-
 CC developing B-cells to immunoglobulin secreting cells (By
 CC similarity).
 CC -!- SUBUNIT: Homodimer; disulfide-linked (By similarity).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the IL-5 family.

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 CC -----
 DR EMBL; AF064209; AAD37462.1; -
 DR HSSP; P05113; 1HUL.
 DR InterPro; IPR000186; Interleukin_5.
 DR Pfam; PF02025; IL5; 1.
 DR PRINTS; PR00432; INTERLEUKIN5.
 DR ProDom; PD006721; Interleukin_5; 1.
 KW Cytokine; Growth factor; Glycoprotein; Signal.
 FT SIGNAL 1 19 BY SIMILARITY.
 FT CHAIN 20 139 INTERLEUKIN-5.
 FT DISULFID 64 64 INTERCHAIN (WITH C-106) (BY SIMILARITY).
 FT DISULFID 106 106 INTERCHAIN (WITH C-64) (BY SIMILARITY).
 FT CARBOHYD 48 48 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 77 77 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 91 91 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 139 AA; 15784 MW; CE16342A68F10622 CRC64;

 Query Match 56.78; Score 346; DB 1; Length 139;
 Best Local Similarity 57.68; Pred. No. 2e-28;
 Matches 68; Conservative 20; Mismatches 26; Indels 4; Gaps 1;

 QY 2 AVENPMRLVAETLLTSLTHTLIGDGNLMIPPTPNKHQLCIKEVFGQIDTLKNOTAH 61
 DB 22 ATGNPVSRLVTETLSLTARTLLIGNTLRLISIPDQNHPLCIEBIFQIETLKNQTA 81

 QY 62 GEAVDKLFQNLISLKEHIERQKRCAGRWRTKFLDYQLQVFLGVINTWTPES 115
 DB 82 ENVVEKIFQNLSSLGKVIYATKCKGERRRVEQFLDYLEEFRLTINIEWNTWTVES 139

 RESULT 14
 IL5_RAT
 ID IL5_RAT STANDARD; PRT; 132 AA.
 AC Q08125;
 DT 01-OCT-1994 (Rel. 30, Created)
 DT 01-OCT-1994 (Rel. 30, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Interleukin-5 precursor (IL-5) (T-cell replacing factor) (TRF) (B-cell
 DE growth factor II) (SCGF-II) (Eosinophil differentiation factor)
 DE (Cytotoxic T lymphocyte inducer).
 GN IL5 OR IL-5.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=101116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Lewis;
 RX MEDLINE=91355638; PubMed=1653053;
 RA Ueberli K.T., Li W., Guin Z., Richter G., Raabe T.,
 RA Diamantstein T., Blanckenstein T.;
 RT "The rat interleukin-5 gene: characterization and expression by
 RT retroviral gene transfer and polymerase chain reaction.";
 RL Cytokine 3:72-81(1991).
 CC -!- FUNCTION: Factor that induces terminal differentiation of late-
 CC developing B-cells to immunoglobulin secreting cells.
 CC -!- SUBUNIT: Homodimer; disulfide-linked.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the IL-5 family.
 CC -----
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 CC -----
 DR EMBL; X54419; CAA38283.1; -
 DR PIR; A48418; A48418.
 DR HSSP; P05113; 1HUL.
 DR InterPro; IPR000186; Interleukin_5.
 DR Pfam; PF02025; IL5; 1.
 DR PRINTS; PR00432; INTERLEUKIN5.
 DR ProDom; PD006721; Interleukin_5; 1.
 KW Cytokine; Growth factor; Glycoprotein; Signal.
 FT SIGNAL 1 19 BY SIMILARITY.
 FT CHAIN 20 132 INTERLEUKIN-5.
 FT DISULFID 61 61 INTERCHAIN (WITH C-103) (BY SIMILARITY).
 FT DISULFID 103 103 INTERCHAIN (WITH C-61) (BY SIMILARITY).
 FT CARBOHYD 45 45 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 74 74 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 88 88 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 132 AA; 15207 MW; 214A928B4C047031 CRC64;

 Query Match 54.48; Score 332; DB 1; Length 132;
 Best Local Similarity 56.68; Pred. No. 5.1e-27;
 Matches 64; Conservative 18; Mismatches 31; Indels 0; Gaps 0;

 QY 2 AVENPMRLVAETLLTSLTHTLIGDGNLMIPPTPNKHQLCIKEVFGQIDTLKNOTAH 61
 DB 19 AWEIPMTVVKETLIQLSTHRLTSTNRLPVTNKHQLCIKEVFGQIDTLKNOTVR 78

 QY 62 GEAVDKLFQNLISLKEHIERQKRCAGRWRTKFLDYQLQVFLGVINTWTP 114
 DB 79 GGTVEILLFQNLISLKKYIDGKCKGERRRTRHFLDYQLQVFLGVINTWAME 131

 RESULT 15
 MP44_MYXVL
 ID MP44_MYXVL STANDARD; PRT; 590 AA.
 AC Q080Q1;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Probable metalloendopeptidase Gl-type (EC 3.4.24.-).
 GN M045L.
 OS Myxoma virus (strain Lausanne).
 OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
 OC Leporipoxvirus.
 OX NCBI_TaxID=31530;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20032073; PubMed=10562494;
 RA Cameron C., Hota-Mitchell S., Chen L., Barrett J., Cao J.X.,
 RA Macaulay C., Willer D., Evans D., McFadden G.;
 RT "The complete DNA sequence of myxoma virus.";
 RL Virology 264:298-318(1999).
 CC -!- FUNCTION: Seems to be involved in viral proteins maturation by
 CC cleavage at Ala-Gly--Xaa motifs (By similarity).
 CC -!- COFACTOR: Binds 1 zinc ion (potential).
 CC -!- SIMILARITY: Belongs to peptidase family M44.
 CC -----
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 CC -----
 DR EMBL; AF170726; AAF14933.1; -
 DR MEROPS; M44_001;
 DR InterPro; IPR005072; Peptidase_M44.
 DR Pfam; PF03410; Peptidase_M44; 1.
 KW Hydrolase; Metalloprotease; Zinc.
 FT METAL 41 41
 FT ACT_SITE 44 44 POTENTIAL.

FT METAL 45 ZINC (CATALYTIC) (POTENTIAL).
SQ SEQUENCE 590 AA; 68224 MW; 1DEE178930C75984 CRC64;
Query Match 15.5%; Score 94.5; DB 1; Length 590;
Best/Local Similarity 25.7%; Pred. No. 0.054;
Matches 36; Conservative 23; Mismatches 38; Indels 43; Gaps 7;
QY 5 NPMNRLVAETLLSLTHRTWLIGDGNLMPTP-----ENKNHQ-----LCIKEVFOGI 52
Db 185 NTEGRLPACPLATPCTVRT-IIGKTIWVSPFYVMVRVPEPSLHNLISILCLYEIYHLV 243
QY 53 DTLKNQTAHGEAYD-KLFQNLSLIKEH-----IEROKKFCAGERWRVTKF 96
Db 244 DY-----ETVDNKLVTFTFSFIHEHDYERFLQSSGRNLNTIYKKIRLCYGGDFLMNVY 295
QY 97 LDYLQV-----FLGVINTE 110
Db 296 LSPFCIRHDFDYLTIVNTD 315

Search completed: August 25, 2004, 00:02:58
Job time : 13.9317 secs

Blank

Sheet

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 24, 2004, 23:54:03 ; Search time 66.9679 Seconds
(without alignments)
541.821 Million cell updates/sec

Title: US-10-787-382-10

Perfect score: 610

Sequence: 1 FAVENPMNRLVAETLLTLLST.....FLDYQLQVFLGVINTWTPES 115

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- 1: SP_archea.*
- 2: SP_bacteria.*
- 3: SP_fungi.*
- 4: SP_human.*
- 5: SP_invertebrate.*
- 6: SP_mammal.*
- 7: SP_mhc.*
- 8: SP_organelle.*
- 9: SP_phage.*
- 10: SP_plant.*
- 11: SP_rodent.*
- 12: SP_virus.*
- 13: SP_vertebrate.*
- 14: SP_unclassified.*
- 15: SP_virus.*
- 16: SP_bacteriap.*
- 17: SP_archeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	610	100.0	134	Q95J76	Q95J76 canis famil
2	563	92.3	118	Q9TV10	Q9TV10 canis famil
3	505	82.8	134	Q9TSD7	Q9TSD7 felis silve
4	501	82.1	134	Q9MYN5	Q9MYN5 sus scrofa
5	382	62.6	134	Q8MKH1	Q8MKH1 salmairi sci
6	325	53.3	132	Q9X2C9	Q9X2C9 rattus norv
7	109.5	18.0	40	Q9XT92	Q9XT92 smnthopsis
8	78.5	12.9	258	Q9M1K0	Q9M1K0 arabidopsis
9	76.5	12.5	158	Q96575	Q96575 leucophaea
10	75	12.3	292	Q8PUD3	Q8PUD3 mechanosarc
11	73.5	12.0	253	Q9M1K1	Q9M1K1 arabidopsis
12	73	12.0	248	Q8RVK0	Q8RVK0 helianthus
13	73	12.0	623	Q7XRA0	Q7XRA0 oryza sativ
14	73	12.0	661	Q921P5	Q921P5 mus musculu
15	73	12.0	664	Q8K2B3	Q8K2B3 mus musculu
16	72.5	11.9	229	Q9CLF5	Q9CLF5 pasteurella

ALIGNMENTS

RESULT 1

Q95J76

ID Q95J76 PRELIMINARY; PRT; 134 AA.

AC Q95J76;
DT 01-DEC-2001 (TRENBLrel. 19, Created)
DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Interleukin-5.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21334408; PubMed=11440633;
RA Yang S., Sellins K.S., Weber E., McCall C.;
RT "Canine interleukin-5: molecular characterization of the gene and
expression of biologically active recombinant protein.";
RL J. Interferon Cytokine Res. 21:361-367(2001).
DR EMBL; AF331920; AAL10716.1; -;
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005137; F:interleukin-5 receptor binding; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR000186; Interleukin_5.
DR Pfam; PF02025; IL5; 1
DR PRINTS; PR00432; INTERLEUKIN_5.
DR ProDom; PD006721; Interleukin_5; 1.
SQ SEQUENCE 134 AA; 15307 MW; 003C86D94D6FF4C6 CRC64;

Query Match 100.0%; Score 610; DB 6; Length 134;
Best Local Similarity 100.0%; Pred. No. 3.3e-56;
Matches 115; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FAVENPMNRLVAETLLTLLSTRTWLIGGNLMIPPENKHNQLCIKKEVFOQIDILKNQTA 60
DB 20 FAVENPMNRLVAETLLTLLSTRTWLIGGNLMIPPENKHNQLCIKKEVFOQIDILKNQTA 79
QY 61 HGEAVDKLFQNLISLIKEHIERKQKRCACERWEVTKFLDYQLQVFLGVINTWTPES 115

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Db 80 HGEAVDKLFQNLSEKHEIERQKRCAGRWRTKFLDYQLQVFLGVINTEWTPES 134
|||||
RESULT 2
Q9TV10 ID Q9TV10 PRELIMINARY; PRT; 118 AA.
AC Q9TV10;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Interleukin-5 (Fragment).
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RA German A.J., Helps C.R., Harley R., Hall E.J., Day M.J.;
RT "Cloning and sequencing of canine interleukin-5";
PL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF091133; AAC46991.1; -.
DR HSSP; P05113; IHUL.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005137; F:interleukin-5 receptor binding; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR000186; Interleukin_5.
DR Pfam; PF02025; IL5; 1.
DR PRINTS; PR00432; INTERLEUKINS.
DR ProDom; PD006721; Interleukin_5; 1.
FT NON TER 1
FT NON TER 118
SQ SEQUENCE 118 AA; 13507 MW; 36A5563DD67C968C CRC64;

Query Match 92.38; Score 563; DB 6; Length 118;
Best Local Similarity 93.78; Pred. No. 2.4e-51;
Matches 104; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FAVENPNRLVAETLTLLSHRTWLTGDNLMIPTEPNKHQLCIKEVFGQIDTLKNQTA 60
|||||
Db 8 FAVENPNRLVAETLTLLSHRTWLTGDNLMIPTEPNKHQLCIKEVFGQIDTLKNQTA 67
|||||
Qy 61 HGEAVDKLFQNLSEKHEIERQKRCAGRWRTKFLDYQLQVFLGVINTEW 111
|||||
Db 68 HGEAVDKLFQNLSEKHEIERQKRCAGRWRTKFLDYQLQVFLGVINTEW 118
|||||

RESULT 3
Q9TSD7 ID Q9TSD7 PRELIMINARY; PRT; 134 AA.
AC Q9TSD7;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Interleukin 5
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_TaxID=9685;
RN [1]
RP SEQUENCE FROM N.A.
RA Vandegrift E., Hughes K.J., O'Reilly K.L.;
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF068770; AAC27616.1; -.
DR HSSP; P05113; IHUL.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005137; F:interleukin-5 receptor binding; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR000186; Interleukin_5.
DR Pfam; PF02025; IL5; 1.
DR PRINTS; PR00432; INTERLEUKINS.
DR ProDom; PD006721; Interleukin_5; 1.
SQ SEQUENCE 134 AA; 15176 MW; 9A118B78F8C820 CRC64;

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Query Match 82.88; Score 505; DB 6; Length 134;
Best Local Similarity 84.18; Pred. No. 3.5e-45;
Matches 95; Conservative 10; Mismatches 8; Indels 0; Gaps 0;

Qy 2 AVENPNRLVAETLTLLSHRTWLTGDNLMIPTEPNKHQLCIKEVFGQIDTLKNQTAH 61
|||||
Db 21 AVQSPNRLVAETLTLLSHRTWLTGDNLMIPTEPNKHQLCIKEVFGQIDTLKNRTVP 80
|||||
Qy 62 GEAVDKLFQNLSEKHEIERQKRCAGRWRTKFLDYQLQVFLGVINTEWTP 114
|||||
Db 81 GDAVEKLFQNLSEKHEIERQKRCAGRWRTKFLDYQLQVFLGVINTEW 133
|||||

RESULT 4
Q9MYM5 ID Q9MYM5 PRELIMINARY; PRT; 134 AA.
AC Q9MYM5;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Interleukin-5.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20130134; PubMed=1063563;
RA Sylvain H., Matvienko O., Leonchiks A., Alving K., van der Ploeg I.;
RT "Molecular cloning, expression, and purification of pig interleukin-5";
RL Immunogenetics 51:59-64(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Johnsen C.K., Grondahl-Hansen J., Johansen R., Jørgensen G.,
RA Høeggaard P.M.H.;
RT "Sus scrofa mRNA for interleukin-5";
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ010088; CAB70611.2; -.
DR HSSP; P05113; IHUL.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005137; F:interleukin-5 receptor binding; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR000186; Interleukin_5.
DR Pfam; PF02025; IL5; 1.
DR PRINTS; PR00432; INTERLEUKINS.
DR ProDom; PD006721; Interleukin_5; 1.
SQ SEQUENCE 134 AA; 15191 MW; B485D562A028A899 CRC64;

Query Match 82.18; Score 501; DB 6; Length 134;
Best Local Similarity 85.18; Pred. No. 9.1e-45;
Matches 97; Conservative 7; Mismatches 10; Indels 0; Gaps 0;

Qy 2 AVENPNRLVAETLTLLSHRTWLTGDNLMIPTEPNKHQLCIKEVFGQIDTLKNQTAH 61
|||||
Db 21 AVENPNRLVAETLTLLSHRTWLTGDNLMIPTEPNKHQLCIKEVFGQIDTLKNQTA 80
|||||
Qy 62 GEAVDKLFQNLSEKHEIERQKRCAGRWRTKFLDYQLQVFLGVINTEWTPES 115
|||||
Db 81 GDAVEKLFQNLSEKHEIERQKRCAGRWRTKFLDYQLQVFLGVINTEW 134
|||||

RESULT 5
Q8MKH1 ID Q8MKH1 PRELIMINARY; PRT; 134 AA.
AC Q8MKH1;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

```

DE Interleukin-5.
OS Saimiri sciureus (Common squirrel monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Saimiri.
OX NCBI_TaxID=9521;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21972723; PubMed=11976788;
RA Hazaud J.M., Laverne A., Kazanji M.;
RT "Molecular cloning, characterization, and quantification of squirrel
RT monkey (Saimiri sciureus) Th1 and Th2 cytokines";
RJ Immunogenetics 54:20-29(2002).
DR EMBL; AF294756; AAK92043.1; -.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005137; F:interleukin-5 receptor binding; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR000186; Interleukin_5.
DR Pfam; PF02025; IL5; 1.
DR PRINTS; PR00432; INTERLEUKIN5.
DR PRODOM; PD06721; Interleukin_5; 1.
SQ SEQUENCE 134 AA; 15210 MW; EAFACCA5DB48767C CRC64;

Query Match 62.6%; Score 382; DB 6; Length 134;
Best Local Similarity 68.2%; Pred. No. 2.9e-32;
Matches 75; Conservative 11; Mismatches 24; Indels 0; Gaps 0;

Qy 6 PMRLVAETLTLSTHRTWIGDGNLMPTPENKNHOLCIKEVFGQIDTLKNQTAH 65
Db 25 PTGALVKETLALLSTHRTWIGDGNLMPTPENKNHOLCIKEVFGQIDTLKNQTAH 65
Qy 66 DKLFQNLSLKEHIEROKKACGERWVTKFLDYQLVFLGVINTWTPES 115
Db 85 EKLFQNLSLKEHIEROKKACGERWVTKFLDYQLVFLGVINTWTPES 115

RESULT 6
Q9R2C9 PRELIMINARY; PRT; 132 AA.
AC Q9R2C9;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Interleukin-5 precursor.
GN IL-5.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=Lou M;
RA Pierrot C.;
RT "Cloning, expression of rat IL-5 and production of neutralizing
RT antiserum: comparative study of IL-5 activity expressed in E.coli and
RT baculovirus system";
RJ Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ011299; CA09587.1; -.
DR HSSP; P05113; 1HUL.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005137; F:interleukin-5 receptor binding; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR00186; Interleukin_5.
DR Pfam; PF02025; IL5; 1.
DR PRINTS; PR00432; INTERLEUKIN5.
DR PRODOM; PD06721; Interleukin_5; 1.
KW Signal.
FT SIGNAL.
FT CHAIN.
SQ SEQUENCE 132 AA; 15191 MW; 814A87CB4C04702B CRC64;

Query Match 53.3%; Score 325; DB 11; Length 132;
Best Local Similarity 55.8%; Pred. No. 2.7e-26;
Matches 63; Conservative 18; Mismatches 32; Indels 0; Gaps 0;

Qy 2 AVENPMRLVAETLTLSTHRTWIGDGNLMPTPENKNHOLCIKEVFGQIDTLKNQTAH 61
Db 19 AVEIPMSTVAVETLTLSTHRTWIGDGNLMPTPENKNHOLCIKEVFGQIDTLKNQTVR 78
Qy 62 GEAVDKLFQNLSLKEHIEROKKACGERWVTKFLDYQLVFLGVINTWTPES 114
Db 79 GGTVEIPFQNLSLKYYIDGKRGERRRTRHFLDYQLVFLGVINTWTPES 131

RESULT 7
Q9XT92 PRELIMINARY; PRT; 40 AA.
AC Q9XT92;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Interleukin-5 (Fragment).
GN IL5.
OS Smithopsis macroura (Stripe-faced dunnart).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Metatheria; Dasyuromorphia; Dasyuridae; Sminthopsis.
OX NCBI_TaxID=9302;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99432005; PubMed=10501836;
RA Hawken R.C.; Maccarone P., Toder R., Marshall Graves J.A.,
RA Maddox J.F.;
RT "Isolation and characterization of marsupial IL5 genes";
RJ Immunogenetics 49:942-948(1999).
DR EMBL; AF064208; AAD37461.1; -.
DR HSSP; P05113; 1HUL.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005137; F:interleukin-5 receptor binding; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR00186; Interleukin_5.
DR Pfam; PF02025; IL5; 1.
DR PRINTS; PR00432; INTERLEUKIN5.
DR PRODOM; PD06721; Interleukin_5; 1.
FT NON_TER 1
FT NON_TER 40
SQ SEQUENCE 40 AA; 4695 MW; 54B93064203EA70B CRC64;

Query Match 18.0%; Score 109.5; DB 6; Length 40;
Best Local Similarity 53.8%; Pred. No. 0.00029;
Matches 21; Conservative 9; Mismatches 8; Indels 1; Gaps 1;

Qy 52 IDTLKNQTAHGEAVDKLFQNLSLKEHIEROKKACGER 90
Db 1 IETLKNQTAEDNVVERIFQNFPSLKEHITTKQC-GEK 38

RESULT 8
Q9MIK0 PRELIMINARY; PRT; 258 AA.
AC Q9MIK0;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein (Putative bHLH transcription factor).
GN F2413.60.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurooids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Nyakatura G., Fartmann B., Dauner D., Steir W., Holland R.,
RA Weichselgartner M., Mewes H.W., Lemcke K., Mayer K.F.X., Quetier F.,
RA Salanoubat M.;
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
RN [2]

Search completed: August 25, 2004, 00:05:33
Job time : 68.9679 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 30, 2004, 15:56:41 ; Search time 290.939 Seconds
(without alignments)
8907.036 Million cell updates/sec

Title: US-10-787-382-4
Perfect score: 610
Sequence: 1 caaggcaaacactgaacatt.....acagatgaatatatttgag 610

Scoring table: IDENTITY NUC
Gapop 10.0 , Capext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_29Jan04:*
1: Geneseqn1980s:*
2: Geneseqn1990s:*
3: Geneseqn2000s:*
4: Geneseqn2001as:*
5: Geneseqn2001bs:*
6: Geneseqn2002s:*
7: Geneseqn2003as:*
8: Geneseqn2003bs:*
9: Geneseqn2003cs:*
10: Geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	610	100.0	610	3	Aaz55546 Canine in
2	610	100.0	610	3	Aaz55547 Canine in
3	405.8	66.5	838	3	Aaz44265 Porcine I
4	402	65.9	402	3	Aaz55548 Canine in
5	402	65.9	402	3	Aaz55549 Canine in
6	401.8	65.9	405	4	Aaf74300 Canine in
7	379	62.1	816	3	Aaa34857 Human ade
8	379	62.1	816	3	Aaa13338 Human int
9	379	62.1	816	3	Aaf20979 Human low
10	379	62.1	816	7	Abz96673 Human nuc
11	379	62.1	816	7	Acf63368 Human int
12	379	62.1	4057	3	Aaa34858 Human ade
13	379	62.1	4057	3	Aaf20980 Human nuc
14	379	62.1	4057	7	Abz96674 Human low
15	364.4	59.7	520	2	Aat50755 Ovine IL-
16	345	56.6	345	3	Aaz55550 Canine ma
17	345	56.6	345	3	Aaz55551 Canine ma
18	344.2	51.5	393	2	Aat50756 Ovine IL-
19	293.8	48.2	393	4	Aaf74306 Canine in
20	276.6	45.3	858	8	Aal61293 hIL5-P2-P
21	275.6	45.2	402	1	Aan81380 A human B
22	275.6	45.2	858	8	Aal61294 hIL5-P30-
23	252	41.3	252	4	Aaf74305 Canine in

24	249.4	40.9	385	3	AAA43842	Aaa43842 Human sec
25	232.4	38.1	864	8	AAL61296	Aal61296 hIL5.37 v
26	232	38.0	370	1	AAN91647	Aan91647 Synthetic
27	231.4	37.9	864	8	AAL61295	Aal61295 hIL5.36 v
28	221	36.2	1945	9	ADB53890	ADB53890 Primary r
29	217.6	35.7	1533	1	AAN82431	Aan82431 B cell di
30	217.6	35.7	1534	2	AAT88013	Aat88013 Murine In
31	217.6	35.7	1623	2	AAT14925	Aat14925 T cell re
32	217.6	35.7	1623	2	AAV64062	AAV64062 Plasmid p
33	209.6	34.4	481	1	AAN80461	Aan80461 Clone 115
34	207.4	34.0	377	2	AAV01595	AAV01595 Human int
35	206.4	33.8	399	2	AAV64061	AAV64061 T cell re
36	206.4	33.8	402	2	AAT14921	Aat14921 T cell re
37	196.4	32.2	348	2	AAT14922	Aat14922 T cell re
38	194.6	31.9	342	2	AAT14923	Aat14923 T cell re
39	194.2	31.8	339	2	AAT14924	Aat14924 T cell re
40	181.4	29.7	375	3	AAC68870	Aac68870 Modified
41	178.6	29.3	357	3	AAC68871	Aac68871 Modified
42	172.2	28.2	381	3	AAC68867	Aac68867 Modified
43	168.6	27.6	375	3	AAC68872	Aac68872 Modified
44	166.4	27.3	399	3	AAC68873	Aac68873 Modified
45	166	27.2	444	3	AAC68875	Aac68875 Modified

ALIGNMENTS

RESULT 1
AAZ55546
ID AAZ55546 standard; cDNA; 610 BP.
XX
AC AAZ55546;
XX
DT 14-MAR-2000 (first entry)
XX
DE Canine interleukin-5 (IL-5) cDNA.
XX
KW Interleukin-5; IL-5; antibody; canine; inhibitor; immune response;
KW immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.
XX
OS Canis familiaris.
XX
FH Key Location/Qualifiers
FT CDS 29..433
FT /*tag= a
FT /product= "Canine IL-5"
XX
PN WO9961618-A2.
XX
PD 02-DEC-1999.
XX
PF 28-MAY-1999; 99WO-US011942.
XX
PR 29-MAY-1998; 98US-0087306P.
XX
FA (HESK-) HESKA CORP.
XX
PI Sim G, Yang S, Dreitz MJ, Wonderling RS;
DR WPI: 2000-072623/06.
DR P-PSDB; AAY58219.
XX
PT Nucleic acids encoding immunoregulatory proteins from cats or dogs,
PT useful for treating or preventing e.g. tumors or autoimmune disease.
PS Claim 1h; Page 223-224; 264pp; English.
XX
CC Sequences AAZ55546-255551 represent cDNA sequences encoding canine
CC interleukin-5 (IL-5). The invention relates to canine IL-4, canine or
CC ligand Flt-3 ligand, canine or feline CD40, canine or feline CD154 (CD40
CC ligand), canine IL-5, canine IL-13, feline interferon-alpha (IFN-alpha)
CC and feline granulocyte macrophage colony-stimulating factor (GM-CSF), and
CC nucleotides which encode these immunoregulatory proteins. The proteins,

CC their associated nucleic acids, specific antibodies and inhibitors may be
 CC used as vaccines for therapeutic or prophylactic regulation of an immune
 CC response in animals (particularly cats, dogs, horses and humans). They
 CC may be used to treat autoimmune or infectious diseases including
 CC allergies, tumours, inflammation and graft rejection, and to increase the
 CC response from a co-administered antigen. The nucleotide sequences can
 CC also be used for the recombinant production of a protein, while
 CC nucleotide fragments are useful as probes, as amplification primers and
 CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).
 CC The proteins may be used to raise antibodies and to screen for modulators
 CC of activity, while the antibodies may be used in detection, and in drug
 CC targeting

XX Sequence 610 BP; 202 A; 114 C; 139 G; 155 T; 0 U; 0 Other;

Query Match 100.0%; Score 610; DB 3; Length 610;

Best Local Similarity 100.0%; Pred. No. 2.9e-171; Indels 0; Gaps 0;

Matches 610; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAAGGCAAACTGAACTTTCAGAGCTATGAGAACTCTCTGAAATTTGAGTTTGTCTAGC 60

DB 1 CAAGGCAAACTGAACTTTCAGAGCTATGAGAACTCTCTGAAATTTGAGTTTGTCTAGC 60

QY 61 TCTTGGGGCTGCTTATGTTTCTGCTTTGCTGTAGAAATCCCATGAATAGCTGTGGC 120

DB 61 TCTTGGGGCTGCTTATGTTTCTGCTTTGCTGTAGAAATCCCATGAATAGCTGTGGC 120

QY 121 AGAGACCTTGACACTGCTTCCACTCATCGAATCTGGCTGATAGGCGATGGGAACCTGAT 180

DB 121 AGAGACCTTGACACTGCTTCCACTCATCGAATCTGGCTGATAGGCGATGGGAACCTGAT 180

QY 181 GATTCTTACTCTGAAATTAATAATCACTCACTGCTGATTAAGAAGTTTTCAGGGTAT 240

DB 181 GATTCTTACTCTGAAATTAATAATCACTCACTGCTGATTAAGAAGTTTTCAGGGTAT 240

QY 241 AGACACATTTGAAGAACCAAACTGCCACCGGGAGGCTGTGGATAAACTATTCCAAAACCTT 300

DB 241 AGACACATTTGAAGAACCAAACTGCCACCGGGAGGCTGTGGATAAACTATTCCAAAACCTT 300

QY 301 GTCTTTTAAAGAACACATAGAGCCCAAAAAAGSTGTGAGGAGAAAGATGGAG 360

DB 301 GTCTTTTAAAGAACACATAGAGCCCAAAAAAGSTGTGAGGAGAAAGATGGAG 360

QY 361 AGTGACAAAGTTCCTAGACTACCTGCAAGTATTTCTTGGTGTATTAACACCGAGTGGAC 420

DB 361 AGTGACAAAGTTCCTAGACTACCTGCAAGTATTTCTTGGTGTATTAACACCGAGTGGAC 420

QY 421 ACCGGAAGTTGAGAACAAACCGGCTTATTTGATGGAAGATTTTGGAGAAAGTGGTTT 480

DB 421 ACCGGAAGTTGAGAACAAACCGGCTTATTTGATGGAAGATTTTGGAGAAAGTGGTTT 480

QY 481 TTGCGGATGAGATGAGGCGCAACCAAGTAGTGGGACTTAAATGGCCAGTATAACTAAGC 540

DB 481 TTGCGGATGAGATGAGGCGCAACCAAGTAGTGGGACTTAAATGGCCAGTATAACTAAGC 540

QY 541 TTCAGACAAAGTAAATATTTTTCAGGCATCTACTACTTATCATTTCACACAGATGAAA 600

DB 541 TTCAGACAAAGTAAATATTTTTCAGGCATCTACTACTTATCATTTCACACAGATGAAA 600

QY 601 TATATTTGAG 610

DB 601 TATATTTGAG 610

RESULT 2

AAZ55547/c

ID AAZ55547 standard; cDNA; 610 BP.

XX AAZ55547;

AC AAZ55547;

XX 14-MAR-2000 (first entry)

XX Canine interleukin-5 (IL-5) cDNA complement.

XX Interleukin-5; IL-5; antibody; canine; inhibitor; immune response;
 KW immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.
 XX Canis familiaris.
 XX Key Location/Qualifiers
 FT CDS complement(178..582)
 FT /*tag= a
 FT /product= "Canine IL-5"
 XX WO9961618-A2.
 XX 02-DEC-1999.
 XX 28-MAY-1999; 99WO-US011942.
 XX 29-MAY-1999; 98US-0087306P.
 XX (HESK-) HESKA CORP.
 XX Sim G, Yang S, Dreitz MJ, Wonderling RS;
 XX WPI: 2000-072623/06.
 XX P-PSDB; AAY58219.
 XX Nucleic acids encoding immunoregulatory proteins from cats or dogs,
 PT useful for treating or preventing e.g. tumors or autoimmune disease.
 PT Claim 1h; Page 224-225; 264pp; English.
 CC Sequences AAZ55546-255551 represent cDNA sequences encoding canine
 CC interleukin-5 (IL-5). The invention relates to canine IL-4, canine or
 CC feline Flt-3 ligand, canine or feline CD40, canine or feline CD154 (CD40
 CC ligand), canine IL-5, canine IL-13, feline interferon-alpha (IFN-alpha)
 CC and feline granulocyte macrophage colony-stimulating factor (GM-CSF), and
 CC nucleotides which encode these immunoregulatory proteins. The proteins,
 CC their associated nucleic acids, specific antibodies and inhibitors may be
 CC used as vaccines for therapeutic or prophylactic regulation of an immune
 CC response in animals (particularly cats, dogs, horses and humans). They
 CC may be used to treat autoimmune or infectious diseases including
 CC allergies, tumours, inflammation and graft rejection, and to increase the
 CC response from a co-administered antigen. The nucleotide sequences can
 CC also be used for the recombinant production of a protein, while
 CC nucleotide fragments are useful as probes, as amplification primers and
 CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).
 CC The proteins may be used to raise antibodies and to screen for modulators
 CC of activity, while the antibodies may be used in detection, and in drug
 CC targeting

XX Query Match 100.0%; Score 610; DB 3; Length 610;

Best Local Similarity 100.0%; Pred. No. 2.9e-171; Indels 0; Gaps 0;

Matches 610; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAAGGCAAACTGAACTTTCAGAGCTATGAGAACTCTCTGAAATTTGAGTTTGTCTAGC 60

DB 610 CAAGGCAAACTGAACTTTCAGAGCTATGAGAACTCTCTGAAATTTGAGTTTGTCTAGC 551

QY 61 TCTTGGGGCTGCTTATGTTTCTGCTTTGCTGTAGAAATCCCATGAATAGCTGTGGC 120

DB 550 TCTTGGGGCTGCTTATGTTTCTGCTTTGCTGTAGAAATCCCATGAATAGCTGTGGC 491

QY 121 AGAGACCTTGACACTGCTCTCCACTCATCGAATCTGGCTGATAGGCGATGGGAACCTGAT 180

DB 490 AGAGACCTTGACACTGCTCTCCACTCATCGAATCTGGCTGATAGGCGATGGGAACCTGAT 431

QY 181 GATTCTTACTCTGAAATTAATAATCACTCACTGCTGATTAAGAAGTTTTCAGGGTAT 240

DB 430 GATTCTTACTCTGAAATTAATAATCACTCACTGCTGATTAAGAAGTTTTCAGGGTAT 371

QY 241 AGACACATTTGAAGAACCAAACTGCCACCGGGAGGCTGTGGATAAACTATTCCAAAACCTT 300

Db 370 AGACACATTGAAGAACCAACATGCGCCACGGGAGGCTGGGATAACATATTCCTCAAAACTT 311
QY 301 GTCTTTTATAAAGAAACACATAGAGCGCCCAAAAAAGGTGTGAGGAGAAAGATGGAG 360
Db 310 GTCTTTTATAAAGAAACACATAGAGCGCCCAAAAAAGGTGTGAGGAGAAAGATGGAG 251
QY 361 AGTGACAAAGTTCCTAGACTACCTGCAAGTATTTCTTGCTGTAAATAAACACCGAGTGGAC 420
Db 250 AGTGACAAAGTTCCTAGACTACCTGCAAGTATTTCTTGCTGTAAATAAACACCGAGTGGAC 191
QY 421 ACCGGAAAGTTGAGAACAAACCGGCTTATTTAGTGGAAAGATTTTGGAGAAAGATGGTTT 480
Db 190 ACCGGAAAGTTGAGAACAAACCGGCTTATTTAGTGGAAAGATTTTGGAGAAAGATGGTTT 131
QY 481 TTTGGCGATGAGAAATGAGGCGCAACCAACAGTAGGACCTTAATGGCCAGTATACTAAGC 540
Db 130 TTTGGCGATGAGAAATGAGGCGCAACCAACAGTAGGACCTTAATGGCCAGTATACTAAGC 71
QY 541 TTCAGAGACAAAGTAAATATTTTCAGGCATCCTACTACTTTTATCAGTTTACACAGATGAAA 600
Db 70 TTCAGAGACAAAGTAAATATTTTCAGGCATCCTACTACTTTTATCAGTTTACACAGATGAAA 11
QY 601 TATATTGGAG 610
Db 10 TATATTGGAG 1

RESULT 3

AAZ44265
ID AAZ44265 standard; DNA; 838 BP.
AC AAZ44265;
XX
XX
DT 31-MAR-2000 (first entry)
XX
XX Porcine IL-5 DNA.
XX Pig; vaccine; cysticercosis; protective antigen; cC1; cC3; cC4;
KW tenial cysticercosis; gamma interferon; IFN-gamma; interleukin 5; IL-5; ss.
XX
XX
OS Sus scrofa.
XX
XX CN1231339-A.
XX
XX 13-OCT-1999.
XX
XX 29-JAN-1999; 99CN-00113447.
XX
XX 29-JAN-1999; 99CN-00113447.
XX
XX (UYTW-) UNIV NO 2 MILITARY MEDICAL PLA.
XX
XX Sun S, Dai J;
XX
XX WPI; 2000-087904/08.
XX
XX Nucleic acid vaccine for cysticercosis co-contracted by human and pig.
XX
XX Claim 3; Page 9; 21pp; Chinese.

CC This invention describes a novel nucleic acid vaccine for preventing and
CC curing human and pork cysticercosis. The invention involves the formation
CC of a eukaryotic expression plasmid from fusion transcript expression unit
CC consisting of three protective antigen genes (cC1, cC3 and cC4) of pig
CC tenial cysticercosis and coexpression unit of related cell factor gamma
CC interferon (IFN-gamma) and pork interleukin 5 (IL-5) genes. The
CC production and purification process of said nucleic acid vaccine is
CC simple and convenient, the physical and chemical properties of the
CC vaccine are stable, and the vaccine is easy to store and transport, and
CC possesses effective immunological protective function for human and pig
CC cysticercosis. This sequence represents the pig IL-5 gene used in the
CC method of the invention

XX Sequence 838 BP; 280 A; 148 C; 171 G; 239 T; 0 U; 0 Other;
SQ
Query Match 66.5%; Score 405.8; DB 3; Length 838;
Best Local Similarity 84.8%; Pred. No. 2.2e-110;
Matches 498; Conservative 0; Mismatches 67; Indels 22; Gaps 3;
QY 1 CAAGCGCAACACCTGAACATTTTCAGAGCTATGAGAAATGCTTCTGAAATTTGAGTTTGTCTAGC 60
Db 17 CAAGCGCAACACCTGAACATTTTCAGAGCTATGAGAAATGCTTCTGAAATTTGAGTTTGTCTAGC 76
QY 61 TCTTGGGCTGCTCTATGTTTCTGCTTTGCTGTAGAAAAATCCCATGAAATAGATGCTGTGGC 120
Db 77 TCTTGGGCTGCTCTATGTTTCTGCTTTGCTGTAGAAAAATCCCATGAAATAGATGCTGTGGC 136
QY 121 AGAGACCTTGACACTGCTCTCCACTCATCGAACTTGCTGATAGCCGATGGAACCTGAT 180
Db 137 AGAGACCTTGACACTGCTCTCCACTCATCGAACTTGCTGATAGCCGATGGAACCTGAT 196
QY 181 GATTCCTACTCTCTGAAATATAAATCAACCACTGTGCATTAAGAAAGTTTTCAGGCTAT 240
Db 197 GATTCCTACTCTCTGAAATATAAATCAACCACTGTGCATTAAGAAAGTTTTCAGGCTAT 256
QY 241 AGACACATTGAAGAAACCAACTGCCAGGGGGAGCTGTGGATAAACTATTCCCAAACTT 300
Db 257 AGACACATTGAAGAAACCAACTGCCAGGGGGAGCTGTGGATAAACTATTCCCAAACTT 316
QY 301 GTCTTTTATAAAGAAACACATAGAGCGCCAAAAAAGGTGTGAGGAGAAAGATGGAG 360
Db 317 GTCTTTTATAAAGAAACACATAGAGCGCCAAAAAAGGTGTGAGGAGAAAGATGGAG 376
QY 361 AGTGACAAAGTTCCTAGACTACCTGCAAGTATTTCTTGCTGTAAATAAACACCGAGTGGAC 420
Db 377 AGTAAAAAAGTTCCTAGACTACCTGCAAGTATTTCTTGCTGTAAATAAACACCTGAGTGGAC 436
QY 421 ACCGGAAGTTGAGAACCAACCGGCTTATTTAGTGGAAAGATTTTGGAGAAAGAA----- 474
Db 437 AATGAAAGTTGAGATGAATGAATGAATGAATGAATGAATGAATGAATGAATGAATGAATGAATGA 496
QY 475 -TGGTTTTTTGGCCATGAGAAATGAGGCGCAACCAACAGTAGGACTTAATGGCAGTATA 533
Db 497 TGTATTATTTTGAATGAGATGAGGCGCAACCAACCAACCAACCAACCAACCAACCAACCAACCA 542
QY 534 ACTAAGCTTCAGACACAAAGTAAATATTTTCAGGCATCCTACTACTTTT 580
Db 543 ATTAAGCTTCAGATGCAAAAG-CAATTTTTCAGGCATCCTACTACTTTT 588

RESULT 4

AAZ55548
ID AAZ55548 standard; cDNA; 402 BP.
XX
XX AC AAZ55548;
XX
XX 14-MAR-2000 (first entry)
XX
XX Canine interleukin-5 (IL-5) cDNA coding region.
XX
XX Interleukin-5; IL-5; antibody; canine; inhibitor; immune response;
KW immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.
XX
XX Canis familiaris.
OS
XX WO9961618-A2.
XX
XX 02-DEC-1999.
XX
XX 28-MAY-1999; 99WO-US011942.
XX
XX 29-MAY-1998; 98US-0087306P.
XX
XX (HESK-) HESKA CORP.

PI Sim G, Yang S, Dreitz MJ, Wonderling RS;
 XX WPI: 2000-072623/06.
 DR P-PSDB; AAY58219.
 XX
 XX Nucleic acids encoding immunoregulatory proteins from cats or dogs,
 PT useful for treating or preventing e.g. tumors or autoimmune disease.
 XX
 XX Claim 1h; Page 225; 264pp; English.
 XX
 CC Sequences AA255546-255551 represent cDNA sequences encoding canine
 CC interleukin-5 (IL-5). The invention relates to canine IL-4, canine or
 CC feline Flt-3 ligand, canine or feline CD40, canine or feline CD154 (CD40
 CC ligand), canine IL-5, canine IL-13, feline interferon-alpha (IFN-alpha)
 CC and feline granulocyte macrophage colony-stimulating factor (GM-CSF), and
 CC nucleotides which encode these immunoregulatory proteins. The proteins,
 CC their associated nucleic acids, specific antibodies and inhibitors may be
 CC used as vaccines for therapeutic or prophylactic regulation of an immune
 CC response in animals (particularly cats, dogs, horses and humans). They
 CC may be used to treat autoimmune or infectious diseases including
 CC allergies, tumours, inflammation and graft rejection, and to increase the
 CC response from a co-administered antigen. The nucleotide sequences can
 CC also be used for the recombinant production of a protein, while
 CC nucleotide fragments are useful as probes, as amplification primers and
 CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).
 CC The proteins may be used to raise antibodies and to screen for modulators
 CC of activity, while the antibodies may be used in detection, and in drug
 CC targeting
 XX
 SQ Sequence 402 BP; 129 A; 79 C; 93 G; 101 T; 0 U; 0 Other;
 Query Match 65.9%; Score 402; DB 3; Length 402;
 Best Local Similarity 100.0%; Pred. No. 2.2e-109;
 Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 29 ATGAGATGCTTCTGAATTTGAGTTTGCTAGCTCTGGGCTGCCCTATGTTCTGCTTT 88
 DB 1 ATGAGATGCTTCTGAATTTGAGTTTGCTAGCTCTGGGCTGCCCTATGTTCTGCTTT 60
 QY 89 GCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACTCAT 148
 DB 61 GCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACTCAT 120
 QY 149 CGAATCTGGCTGATAGCGGATGGAACTGATGATCTTCTGAAATATAAATATCAT 208
 DB 121 CGAATCTGGCTGATAGCGGATGGAACTGATGATCTTCTGAAATATAAATATCAT 180
 QY 209 CAATGTGCAATTAAGAAGTTTTTCAGGGTATAGACACATTGAAGAACCAAACTGCCAC 268
 DB 181 CAATGTGCAATTAAGAAGTTTTTCAGGGTATAGACACATTGAAGAACCAAACTGCCAC 240
 QY 269 GGGAGGCTGTGATAAATCTTCCAACTTCTTTTAAATAAGAACACATAGAGCG 328
 DB 241 GGGAGGCTGTGATAAATCTTCCAACTTCTTTTAAATAAGAACACATAGAGCG 300
 QY 329 CAAAAAATAAGGTGTGAGGAGAAAGATGGAGAGTGCACAAAGTTCCTAGACTACCTGCAA 388
 DB 301 CAAAAAATAAGGTGTGAGGAGAAAGATGGAGAGTGCACAAAGTTCCTAGACTACCTGCAA 360
 QY 389 GTATTCTTGGTGTATTAACACCCGATGACACCGGAAAGT 430
 DB 361 GTATTCTTGGTGTATTAACACCCGATGACACCGGAAAGT 402
 RESULT 5
 AA255549/c
 ID AA255549 standard; cDNA; 402 BP.
 XX
 AC AA255549;
 XX
 DT 14-MAR-2000 (first entry)
 XX
 XX Canine interleukin-5 (IL-5) cDNA coding region complement.

XX
 KW Interleukin-5; IL-5; antibody; canine; inhibitor; immune response;
 KW immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.
 XX
 OS Canis familiaris.
 XX
 PN WO9961618-A2.
 XX
 PD '02-DEC-1999.
 XX
 PF 28-MAY-1999; 99WO-US011942.
 XX
 PR 29-MAY-1998; 98US-0087306P.
 XX
 PA (HESK-) HESKA CORP.
 XX
 PI Sim G, Yang S, Dreitz MJ, Wonderling RS;
 XX WPI: 2000-072623/06.
 DR P-PSDB; AAY58219.
 XX
 CC Nucleic acids encoding immunoregulatory proteins from cats or dogs,
 CC useful for treating or preventing e.g. tumors or autoimmune disease.
 XX
 CC Claim 1h; Page 226; 264pp; English.
 CC
 CC Sequences AA255546-255551 represent cDNA sequences encoding canine
 CC interleukin-5 (IL-5). The invention relates to canine IL-4, canine or
 CC feline Flt-3 ligand, canine or feline CD40, canine or feline CD154 (CD40
 CC ligand), canine IL-5, canine IL-13, feline interferon-alpha (IFN-alpha)
 CC and feline granulocyte macrophage colony-stimulating factor (GM-CSF), and
 CC nucleotides which encode these immunoregulatory proteins. The proteins,
 CC their associated nucleic acids, specific antibodies and inhibitors may be
 CC used as vaccines for therapeutic or prophylactic regulation of an immune
 CC response in animals (particularly cats, dogs, horses and humans). They
 CC may be used to treat autoimmune or infectious diseases including
 CC allergies, tumours, inflammation and graft rejection, and to increase the
 CC response from a co-administered antigen. The nucleotide sequences can
 CC also be used for the recombinant production of a protein, while
 CC nucleotide fragments are useful as probes, as amplification primers and
 CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).
 CC The proteins may be used to raise antibodies and to screen for modulators
 CC of activity, while the antibodies may be used in detection, and in drug
 CC targeting
 XX
 SQ Sequence 402 BP; 101 A; 93 C; 79 G; 129 T; 0 U; 0 Other;
 Query Match 65.9%; Score 402; DB 3; Length 402;
 Best Local Similarity 100.0%; Pred. No. 2.2e-109;
 Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 29 ATGAGATGCTTCTGAATTTGAGTTTGCTAGCTCTGGGCTGCCCTATGTTCTGCTTT 88
 DB 402 ATGAGATGCTTCTGAATTTGAGTTTGCTAGCTCTGGGCTGCCCTATGTTCTGCTTT 343
 QY 89 GCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACTCAT 148
 DB 342 GCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACTCAT 283
 QY 149 CGAATCTGGCTGATAGCGGATGGAACTGATGATCTTCTGAAATATAAATATCAT 208
 DB 282 CGAATCTGGCTGATAGCGGATGGAACTGATGATCTTCTGAAATATAAATATCAT 223
 QY 209 CAATGTGCAATTAAGAAGTTTTTCAGGGTATAGACACATTGAAGAACCAAACTGCCAC 268
 DB 222 CAATGTGCAATTAAGAAGTTTTTCAGGGTATAGACACATTGAAGAACCAAACTGCCAC 163
 QY 269 GGGAGGCTGTGATAAATCTTCCAACTTCTTTTAAATAAGAACACATAGAGCG 328
 DB 162 GGGAGGCTGTGATAAATCTTCCAACTTCTTTTAAATAAGAACACATAGAGCG 103
 QY 329 CAAAAAATAAGGTGTGAGGAGAAAGATGGAGAGTGCACAAAGTTCCTAGACTACCTGCAA 388

Db 102 CAAAAAAGGTTGTGAGGAGAAAGATGGAGAGTGACAAAGTTCTAGACTACTGCAA 43
Qy 389 GTATTTCTTGGTGTATATAACACCGAGTGGACACCGGAAAGT 430
Db 42 GTATTTCTTGGTGTATATAACACCGAGTGGACACCGGAAAGT 1

RESULT 6
AAF74300
ID AAF74300 standard; DNA; 405 BP.
XX AAF74300;
AC AAF74300;
DT 04-MAY-2001 (first entry)
DE Canine interleukin-5 coding sequence #1.
KW Dog; interleukin-5; IL-5; allergy; cancer; gene therapy;
KW inflammatory reaction; ds.
XX
XX Canis sp.
XX
XX WO200111049-A2.
PN
XX
PD 15-FEB-2001.
XX
XX 09-AUG-2000; 2000WO-US021651.
PF
XX
XX 10-AUG-1999; 99US-00371615.
PR
XX
XX (IDEX-) IDEXX LAB INC.
PA
XX
XX Guo H, Lawton R, Mermer B, Aliyappa AP;
PI
XX
XX WPI; 2001-191542/19.
DR
XX
DR P-PSDB; AAB72615.
XX
XX Novel canine interleukin 5 polynucleotide and polypeptides are used for
PT generating antibodies which are useful in treating allergies in dogs.
XX
XX Claim 31; Page 46; 48pp; English.
PS
XX
XX The present invention provides the protein and coding sequences of the
CC canine interleukin-5 (IL-5) protein. This can be used to treat allergies,
CC cancer and inflammatory reactions in dogs. The present sequence is one
CC version of the IL-5 coding sequence shown in the specification
XX
SQ Sequence 405 BP; 131 A; 77 C; 94 G; 103 T; 0 U; 0 Other;

Query Match 65.9%; Score 401.8; DB 4; Length 405;
Best Local Similarity 99.5%; Pred No. 2.6e-109;
Matches 403; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 29 ATGAGATGCTTCTGAATTTGAGTTTCTAGCTTCTGGGCTGCTATGTTTCTGCTTT 88
Db 1 ATGAGATGCTTCTGAATTTGAGTTTCTAGCTTCTGGGCTGCTATGTTTCTGCTTT 60
Qy 89 GCTCTAGAAATCCCATGATAGTGGTGGGAGACCTTGACCTGCTCTCCACTCAT 148
Db 61 GCTCTAGAAATCCCATGATAGTGGTGGGAGACCTTGACCTGCTCTCCACTCAT 120
Qy 149 CGAACTGGCTGATAGGCGATGGAACTGATGATTTCTACTCTGAAATAAAATCAC 208
Db 121 CGAACTGGCTGATAGGCGATGGAACTGATGATTTCTACTCTGAAATAAAATCAC 180
Qy 209 CAACCTGTCATTAAGAAGTTTTCAGGTTATAGACATTAAGACCAACTGCCAC 268
Db 181 CAACCTGTCATTAAGAAGTTTTCAGGTTATAGACATTAAGACCAACTGCCAC 240
Qy 269 GGGGAGGCTGGGTAACCTATTCCTGCTTTTAAATAAAGAACACATAGAGCGC 328
Db 241 GGGGAGGCTGGGTAACCTATTCCTGCTTTTAAATAAAGAACACATAGAGCGC 300

Qy 329 CAAAAAAGGTTGTGAGGAGAAAGATGGAGAGTGACAAAGTTCTAGACTACTGCAA 388
Db 301 CAAAAAAGGTTGTGAGGAGAAAGATGGAGAGTGACAAAGTTCTAGACTACTGCAA 360
Qy 389 GTATTTCTTGGTGTATATAACACCGAGTGGACACCGGAAAGT 433
Db 361 GTATTTCTTGGTGTATATAACACCGAGTGGACACCGGAAAGT 405

RESULT 7
AAA34857
ID AAA34857 standard; DNA; 816 BP.
XX
XX AAA34857;
AC
DT 28-JUL-2000 (first entry)
XX
DE Human adenosine receptor related polynucleotide SEQ ID NO:2546.
KW
KW Human; adenosine receptor; low adenosine antisense oligonucleotide;
KW phosphorothioate; impaired respiration; inflammation; allergy;
KW allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
KW antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway;
KW lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;
KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
KW cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.
XX
XX Homo sapiens.
OS
XX WO200009525-A2.
PN
XX
PD 24-FEB-2000.
XX
XX 03-AUG-1999; 99WO-US017712.
PF
XX
XX 03-AUG-1998; 98US-0095212P.
PR
XX
XX (UYEC-) UNIV EAST CAROLINA.
PA
XX
XX Nyce JW;
PI
XX
XX WPI; 2000-205371/18.
DR
XX
XX New antisense oligonucleotides useful for treating e.g. pulmonary
PT vasoconstriction, inflammation, allergies, asthma, hypertension,
PT bronchitis, emphysema, respiratory distress syndrome, ischemia or
PT cancers.
XX
XX Disclosure; Page 716; 1343pp; English.
PS
XX
XX The present invention describes a new composition comprising an antisense
CC oligonucleotide (ON) with low adenosine (up to 15%), which targets
CC nucleic acids involved in bronchoconstriction, allergies, and/or
CC inflammation. The ON can have antiinflammatory, antiallergic,
CC antiasthmatic, cytostatic and analgesic activities. The compositions are
CC useful for the treatment of diseases associated with inflammation,
CC impaired airways, including lung disease and diseases whose secondary
CC effects afflict the lungs of a subject. They can be used for treating
CC e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma,
CC impaired respiration, respiratory distress syndrome, pain, cystic
CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive
CC pulmonary disease (COPD), and cancers such as leukaemias, lymphomas,
CC carcinomas, and cancers which may metastasise to the lungs, including
CC breast and prostate cancer. The reduction of the adenosine content of the
CC ONs reduces side effects. The A-containing ONs break down with the
CC release of deoxyadenosine which activates adenosine receptors causing
CC bronchoconstriction and inflammation. AAA32313 to AAA35312 represent the
CC nucleotide sequences given in the sequence listing from the present
CC invention, which correspond to SEQ ID NO:1 to 2815, and then the last 185
CC sequences are also called SEQ ID NO:1 to 185, but the sequences differ
CC from the previously named sequences. SEQ ID NO:11 to 1680 (AAA32323 to
CC AAA33992) are specifically claimed ONs from the present invention. N.B.

CC Sequences given in the disclosure of the present invention do not match
 CC up with their corresponding SEQ ID NO: sequences given in the sequence
 CC listing
 XX
 SQ Sequence 816 BP; 277 A; 137 C; 164 G; 238 T; 0 U; 0 Other;
 Query Match 62.1%; Score 379; DB 3; Length 816;
 Best Local Similarity 79.1%; Pred. No. 2.1e-102;
 Matches 463; Conservative 0; Mismatches 120; Indels 2; Gaps 1;
 QY 2 AAGCAACACCTGACATTTTCAGAGCTATGAGATGCTTCTGAAATTTGAGTTGCTAGCT 61
 DB 18 AAGCAACACCTGACATTTTCAGAGCTATGAGATGCTTCTGAAATTTGAGTTGCTAGCT 77
 QY 62 CTTGGGGTGCCTATGTTTCTGCTTTGCTGTGAAATCCCATGATAGTGGTGGCA 121
 DB 78 CTTGGAGTGCCTACGTGTATGCCATCCACAGAAATTCCTGATGCTATTTGGTGA 137
 QY 122 GAGACCTTGACATGCTTCCACTCATCGAATTTGGCTGATAGCGATGGAACTGATG 181
 DB 138 GAGACCTTGACATGCTTCCACTCATCGAATTTGGCTGATAGCGATGGAACTGATG 197
 QY 182 ATTCCTACTCTGAAATATAAATACCAACTGTGCACTGAAGAAATCTTTCAGGGA 241
 DB 198 ATTCCTGTCTGTACATAAATACCAACTGTGCACTGAAGAAATCTTTCAGGGA 257
 QY 242 GACACATTTGAAGAACCAAACTGCCACCGGAGGCTGTGGATTAATCCAAACTTG 301
 DB 258 GGCACATTTGAGACTAACTGTTTGTTCAGCCAAAGATTTTGGAGGAGGACAT 317
 QY 302 TCTTTAATAAAGAACACATAGACGCGCAAAAAAGGTGTGAGGAGAAAGATGGAGA 361
 DB 318 TCTTTAATAAAGAACACATTTGAGCGGCAAAAAAGGTGTGAGGAGAAAGACGAGA 377
 QY 362 GTGCAAAAGTTCTAGACTACCTGCAAGTATTTCTGGTGTAAATAACACCGAGTGA 421
 DB 378 GTAAACCAATTCCTAGACTACCTGCAAGAGTTTCTGGTGTAAATAACACCGAGTGA 437
 QY 422 CCGAAAGTTGAGAACAAACCGCTTATTTAGTGGAGAGATTTTGGAGAGAGATG--GTT 479
 DB 438 ATAGAAAGTTGAGACTAACTGTTTGTTCAGCCAAAGATTTTGGAGGAGAGGACAT 497
 QY 480 TTTTGGCGATGAGAAATGAGGCGCAACCAACAGTAGGCACTTAATGGCCAGTATACTAAG 539
 DB 498 TTACTGCAGTGAGAAATGAGGCGCAACCAACAGTAGGCACTTAATTTTCAATATAATTA 557
 QY 540 CTTTCAGAGACAAAGTAAATATTTTCAGGCATCTTACTACTTATCA 584
 DB 558 CTTTCAGAGGAAAGTAAATATTTTCAGGCATCTTACTACTTATCA 602

RESULT 8

AAA13338
 ID AAA13338 standard; cDNA; 816 BP.
 XX
 AC AAA13338;
 XX
 DT 25-JUL-2000 (first entry)
 XX
 DE Human interleukin-5 (IL-5) nucleotide sequence.
 XX
 KW Human; interleukin-5; IL-5; inflammatory disease; asthma; eczema;
 KW antisense oligonucleotide; allergic rhinitis; inflammatory skin disease;
 KW allergic conjunctivitis; inhibitor; ss.
 XX
 OS Homo sapiens.
 XX
 PN US6048726-A.
 XX
 PD 11-APR-2000.
 XX
 PF 15-MAY-1998; 98US-00079839.
 XX

PR 15-MAY-1998; 98US-00079839.
 XX (WELT/) WELTMAN J K.
 PA (KARI/) KARIM A S.
 XX
 PI Weltman JK, Karim AS;
 XX
 DR WPI; 2000-302784/26.
 XX
 PT Oligonucleotide comprising non-natural internucleoside linkage, useful
 PT for inhibiting interleukin-5 expression and treating inflammatory
 PT diseases, asthma, allergic rhinitis, allergic conjunctivitis.
 XX
 PS Disclosure; Col 3-4; 11pp; English.
 XX
 CC This sequence represents the human interleukin-5 (IL-5) encoding
 CC nucleotide sequence. Interleukin-5 is involved in eosinophilic
 CC inflammation and inflammatory disorders. The present invention relates to
 CC an IL-5 antisense oligonucleotide (see AAI3337) which inhibits the
 CC expression of IL-5. The antisense oligonucleotide has at least one non-
 CC natural internucleoside linkage. The oligonucleotide is able to inhibit
 CC IL-5 secretion in a dose dependent manner, and is useful for inhibiting
 CC IL-5 expression and therefore treating inflammatory diseases, asthma,
 CC allergic rhinitis, allergic conjunctivitis and inflammatory skin diseases
 CC such as eczema
 XX
 SQ Sequence 816 BP; 277 A; 137 C; 164 G; 238 T; 0 U; 0 Other;
 Query Match 62.1%; Score 379; DB 3; Length 816;
 Best Local Similarity 79.1%; Pred. No. 2.1e-102;
 Matches 463; Conservative 0; Mismatches 120; Indels 2; Gaps 1;
 QY 2 AAGCAACACCTGACATTTTCAGAGCTATGAGATGCTTCTGAAATTTGAGTTGCTAGCT 61
 DB 18 AAGCAACACCTGACATTTTCAGAGCTATGAGATGCTTCTGAAATTTGAGTTGCTAGCT 77
 QY 62 CTTGGGGTGCCTATGTTTCTGCTTTGCTGTGAAATCCCATGATAGTGGTGGCA 121
 DB 78 CTTGGAGTGCCTACGTGTATGCCATCCACAGAAATTCCTGATGCTATTTGGTGA 137
 QY 122 GAGACCTTGACATGCTTCCACTCATCGAATTTGGCTGATAGCGATGGAACTGATG 181
 DB 138 GAGACCTTGACATGCTTCCACTCATCGAATTTGGCTGATAGCGATGGAACTGATG 197
 QY 182 ATTCCTACTCTGAAATATAAATACCAACTGTGCACTGAAGAAATCTTTCAGGGA 241
 DB 198 ATTCCTGTCTGTACATAAATACCAACTGTGCACTGAAGAAATCTTTCAGGGA 257
 QY 242 GACACATTTGAAGAACCAAACTGCCACCGGAGGCTGTGGATTAATCCAAACTTG 301
 DB 258 GGCACATTTGAGACTAACTGTTTGTTCAGCCAAAGATTTTGGAGGAGGACAT 317
 QY 302 TCTTTAATAAAGAACACATAGACGCGCAAAAAAGGTGTGAGGAGAAAGATGGAGA 361
 DB 318 TCTTTAATAAAGAACACATTTGAGCGGCAAAAAAGGTGTGAGGAGAAAGACGAGA 377
 QY 362 GTGCAAAAGTTCTAGACTACCTGCAAGTATTTCTGGTGTAAATAACACCGAGTGA 421
 DB 378 GTAAACCAATTCCTAGACTACCTGCAAGAGTTTCTGGTGTAAATAACACCGAGTGA 437
 QY 422 CCGAAAGTTGAGAACAAACCGCTTATTTAGTGGAGAGATTTTGGAGAGAGATG--GTT 479
 DB 438 ATAGAAAGTTGAGACTAACTGTTTGTTCAGCCAAAGATTTTGGAGGAGAGGACAT 497
 QY 480 TTTTGGCGATGAGAAATGAGGCGCAACCAACAGTAGGCACTTAATGGCCAGTATACTAAG 539
 DB 498 TTACTGCAGTGAGAAATGAGGCGCAACCAACAGTAGGCACTTAATTTTCAATATAATTA 557
 QY 540 CTTTCAGAGACAAAGTAAATATTTTCAGGCATCTTACTACTTATCA 584
 DB 558 CTTTCAGAGGAAAGTAAATATTTTCAGGCATCTTACTACTTATCA 602

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RESULT 9
AAF20979
ID AAF20979 standard; DNA; 816 BP.
XX
AC AAF20979;
XX
DT 14-MAR-2001 (first entry)
XX
DE Human low adenosine antisense oligonucleotide related sequence #2546.
XX
KW Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
KW human; airway disorder; bronchoconstriction; lung inflammation;
KW surfactant depletion; respiratory; bronchodilator; antiinflammatory;
KW immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic;
KW respiratory obstruction; pulmonary obstruction; impeded respiration;
KW surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
KW respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
KW pulmonary hypertension; emphysema; pulmonary transplantation rejection;
KW chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
KW cancer; ss.
XX
OS Homo sapiens.
XX
PN W0200062736-A2.
XX
PD 26-OCT-2000.
XX
PF 24-MAR-2000; 2000WO-US008020.
XX
PR 06-APR-1999; 99US-0127958P.
XX
PA (UVEC-) UNIV EAST CAROLINA.
XX
PA (NYCE/) NYCE J W.
XX
PI Nyce JW;
XX
XX WPI; 2000-679539/66.
XX
FT Low adenosine (A) content antisense oligonucleotides which do not trigger
FT adenosine receptors during metabolism, useful e.g. for treating cancers
FT and respiratory obstructions.
XX
PS Disclosure; Page 788; 1592pp; English.
XX
CC The present invention describes low adenosine (A) content antisense
CC oligonucleotides and compositions (I) comprising them. In the antisense
CC oligonucleotides the A is replaced by a 'Universal' or alternative base.
CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
CC immunosuppressive, antiasthmatic, hypotensive and cytostatic activities.
CC The antisense oligonucleotides and (I) can be used to down-regulate the
CC expression and or activity of target polypeptides associated with
CC lung/respiratory disorders and malignancies, such as stimulating and
CC activating peptide factors and transmitters, transcription factors,
CC immunoglobulins and antibodies, antibody receptors, cytokines and
CC chemokines, endogenously produced specific and non-specific enzymes,
CC binding proteins, adhesion molecules and their receptors, cytokine and
CC chemokine receptors, adenosine receptors, bradykinin receptors, central
CC nervous system (CNS) and peripheral nervous and non-nervous system
CC receptors, CNS and peripheral nervous and non-nervous system peptide
CC transmitters, defensins, growth factors, vasoactive peptides and
CC receptors, binding proteins and malignancy associated proteins. The
CC antisense oligonucleotides may be used in this way to treat disorders
CC including respiratory obstruction (especially pulmonary obstruction
CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies) and/or
CC surfactant hypoproduction which are associated with a disease or
CC condition selected from pulmonary vasoconstriction, inflammation,
CC allergies, asthma, impeded respiration, respiratory distress syndrome
CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
CC pulmonary transplantation rejection, pulmonary infections, bronchitis,
CC and/or cancer. AAF18434 to AAF21543 represent human polynucleotide
CC fragments and antisense oligonucleotides used in the exemplification of
CC the present invention
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XX SQ Sequence 816 BP; 277 A; 137 C; 164 G; 238 T; 0 U; 0 Other;
XX
XX Query Match 62.1%; Score 379; DB 3; Length 816;
XX Best Local Similarity 79.1%; Pred. No. 2.1e-102; Indels 1;
XX Matches 463; Conservative 0; Mismatches 120;
XX
QY 2 AAGCGAAACACTGAAACATTTTCAGAGCTATGAGAAATGCTTCTGAATTTGAGTTTGTAGCT 61
DB 18 AAGGCAACAGCGAAGCTTTTCAGAGCCATGAGGATGCTTCTGCAATTTGAGTTTGTAGCT 77
QY 62 CTTGGGGCTGCTATGTTTCTGCTTTCCTAGTAAATCCCATGAATAGACTGGTGACA 121
DB 78 CTTGGAGTGGCTAGCTGCTATGCCATCCCAAGAAATTTCCCAAGTGCATTTGGTGAAA 137
QY 122 GAGACCTTGACACTCTCTCCACTCATCGAACTTGGCTGATAGGCGATGGGAACCTGATG 181
DB 138 GAGACCTTGGCACTGCTTCTACTCATCGAACTCTGCTGATAGCAATGAGACTCTGAGG 197
QY 182 ATTCTACTCTCGAAATAAATAACCAACTGTCATTAAGAAAGTTTTTTCAGGGTATA 241
DB 198 ATTCTGTCTCTGTACATAAAAAATCACCACACTGTGCACTGAAGAAATCTTTTCAGGGA 257
QY 242 GACACATTGAAGAACCAAACTGCCACGGGAGGCTGTGGATAAACTATTCCAAAACCTTG 301
DB 258 GGCACACTGGAGAGTCAAACTGTGCAAGGGGTACTGTGGAAAGACTATTCAAAAACCTTG 317
QY 302 TCTTTAAATAAAGAACACATAGAGCGCCAAAAAAGGTGTGCAAGGAAGATGGAGA 361
DB 318 TCTTTAAATAAAGAAATACATTGACGGCCAAAAAAGGTGTGGGAAGAACGCGAGA 377
QY 362 GTGACAAAGTTCTAGACTACTCTGCAAGTATTTCTTGGTGTATATAAACCAGAGTGGACA 421
DB 378 GTAAACCAATTCCTAGACTACTCTGCAAGAGTTTCTTGGTGTATATAAACCAGAGTGGATA 437
QY 422 CCGGAAAGTTGAGAAACAAACCGGCTTATTGTAGTGGAAAGATTTTGGGAAGAAGATG -GTT 479
DB 438 ATAGAAAGTTGAGACTAAACTGGTTTGTGAGCCAAAGATTTTGGAGGAGAAAGCACATT 497
QY 480 TTTTGGCGATGAGATGAGGGCCAAACACAGTAGGAGCTTAATGGCCAGTATACTAAG 539
DB 498 TTACTGCACTGAGAAATGAGGGCCAAAGAGAGTCAAGGCTTAAATTTTCAATATATATTTAA 557
QY 540 CTTTCAGAGACAAAGTAAATATTTTCAGGCATCTCTACTCTTTATCA 584
DB 558 CTTTCAGAGGAAAGTAAATATTTTCAGGCATCTCTACTCTTTGCCA 602
XX
RESULT 10
ABZ96673
ID ABZ96673 standard; DNA; 816 BP.
XX
XX ABZ96673;
XX
XX 17-OCT-2003 (first entry)
XX
XX Human nucleic acid sequence.
XX
XX Human; antisense; lung dysfunction; nasal airway dysfunction;
XX antiinflammatory steroid; ubiquinone; antiinflammatory; anti-allergic;
XX antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
XX antisense gene therapy; respiratory; lung; adenosine sensitivity;
XX adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
XX lung inflammation; respiratory disease; ds.
XX
XX Homo sapiens.
XX
XX W0200285308-A2.
XX
XX 31-OCT-2002.
XX
XX 23-APR-2002; 2002WO-US013135.
XX
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PR 24-APR-2001; 2001US-0286137P.
 XX (EPIG-) EPIGENESIS PHARM INC.
 XX Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
 XX Miller S, Tang L, Shahabuddin S;
 XX WPI; 2003-229219/22.
 DR
 XX
 PT Pharmaceutical composition for treating ailments associated with impaired
 PT respiration, has oligo(s) antisense to specific gene(s) or its
 PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
 PT ubiquinone.
 XX
 PS Disclosure; SEQ ID NO 11915; 872pp; English.
 XX
 CC The invention relates to a novel pharmaceutical composition, which has a
 CC first active agent comprising an oligonucleotide antisense to the
 CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
 CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
 CC junctions of genes encoding a polypeptide associated with lung and/or
 CC nasal airway dysfunction and a second active agent comprising an
 CC antiinflammatory steroid and ubiquinone. A composition of the invention
 CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
 CC immunosuppressive, and cytostatic activity. The composition may have a
 CC use in antisense gene therapy. The composition is useful for treating or
 CC preventing a respiratory, lung or malignant disease or condition, also
 CC for enhancing the prophylactic or therapeutic respiratory effect of an
 CC antiinflammatory steroid in a subject, for reducing or depleting levels
 CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
 CC receptor, producing bronchodilation, increasing levels of ubiquinone or
 CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
 CC lung inflammation, lung allergies, or a respiratory disease or condition.
 CC Note: The sequence data for this patent is not represented in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences

Sequence 816 BP; 277 A; 137 C; 164 G; 238 T; 0 U; 0 Other;

Query Match 62.1%; Score 379; DB 7; Length 816;
 Best Local Similarity 79.1%; Pred. No. 2.1e-102;
 Matches 463; Conservative 0; Mismatches 120; Indels 2; Gaps 1;

Qy 2 AAGCAACACTGACATTTTCAGAGCTATGAGATGCTTCTGAATTTGAGTTTGTAGCT 61
 Db 18 AAGCAACACGAGAAACGTTTCAGAGCCATGAGGATGCTTCTGCAATTTGAGTTTGTAGCT 77
 Qy 62 CTTGGGCTGCTATGTTCTGCTTTGCTGTAGAAATCCCATGATGAGCTGTGGCA 121
 Db 78 CTTGGAGCTGCTACGTGTATGCAATCCCAAGAAATCCCAAGTGCATTTGGTGA 137
 Qy 122 GAGACCTTGACCTGCTCTCCACTCATCGAACTTGGCTGATAGCGGACCTGATG 181
 Db 138 GAGACCTTGACCTGCTCTCTCTACTCATCGAACTTGGCTGATAGCGGACCTGATG 197
 Qy 182 ATTCCTACTCTGTAATAAATACCAACTGCTGCAATTAAGAAAGTTTTCAGGTA 241
 Db 198 ATTCCTGTTCTGTACATAAATATCACTGCTGCAATTAAGAAAGTTTTCAGGTA 257
 Qy 242 GACACATTAAGAACCAACTGCGGAGGCTGTGATAAATTTCCAAACCTG 301
 Db 258 GGCACATTAAGAACCAACTGCGGAGGCTGTGATAAATTTCCAAACCTG 317
 Qy 302 TCTTTAATAAGAACCAACTGCGGAGGCTGTGATAAATTTCCAAACCTG 361
 Db 318 TCTTTAATAAGAACCAACTGCGGAGGCTGTGATAAATTTCCAAACCTG 377
 Qy 362 GTGACAAAGTTCTAGACTACCTGCAAGTATTTCTTGGTGTATAAACCAGGTCG 421
 Db 378 GTAAACCAATCTAGACTACCTGCAAGTATTTCTTGGTGTATAAACCAGGTCG 437
 Qy 422 CCGGAAAGTTGAGAACCAACCGGCTTATTTAGTGAAGATTTTGGAGGAATG--GTT 479

Db 438 ATAGAAAGTTGAGACTAAACTGGTTTGTTCAGCAAAAGATTTTGGAGGAGGACATT 497
 Qy 480 TTTTGGCGATGAGATGAGGCGCCCAACCAAGTAGTAGGACTTTAATGGCCAGTATAACTAAG 539
 Db 498 TTACTGCGAGTGAATGAGGCGCCCAAGAAAGAGTCCAGGCTTAAATTTCAATATAATTAA 557
 Qy 540 CTTGAGAGACAAAGTAAATATTTTTCAGGCATCTCTACTTATCA 584
 Db 558 CTTGAGAGGAAAGTAAATATTTTCAGGCATCTCTACTTATCA 602

RESULT 11

ACF63368
 ID ACF63368 standard; DNA; 816 BP.

XX
 AC ACF63368;

XX
 DT 09-OCT-2003 (first entry)

XX
 DE Human interleukin 5 gene SEQ ID NO:90.

XX Human; pharmacological; hypotensive; antilipemic; vasotropic; laxative;
 KW dermatological; antidepressant; tranquiliser; antiinflammatory; eczema;
 KW antitumor; antimigraine; neuroprotective; antiparkinsonian; analgesic;
 KW gynaecological; virucide; vulnery; antithritic; antipsoriatic; cold;
 KW antimicrobial; cytostatic; litholytic; pathological disorder; depression;
 KW abnormal appetite; hypertension; hypercholesterolaemia; hyperlipidaemia;
 KW erectile dysfunction; anxiety; stress; inflammatory bowel syndrome;
 KW ulcerative colitis; Crohn's disease; renal stone; gall stone; migraine;
 KW constipation; headache; seizure; multiple sclerosis; polymyositis;
 KW fibromyalgia; Parkinson's disease; amyotrophic lateral sclerosis; trauma;
 KW chronic pain; pre-menstrual syndrome; sinusitis; carpal tunnel syndrome;
 KW chronic fatigue syndrome; rosacea; arthritis; psoriasis; prostatitis;
 KW inflammation; heart burn; infection; colon cancer; malignant melanoma;
 KW skin disorder; gene; ds.

XX Homo sapiens.

XX WO2003006478-A1.

XX 23-JAN-2003.

XX 10-JUL-2002; 2002WO-US021664.

XX 10-JUL-2001; 2001US-0303820P.

XX (OLIG-) OLIGOS ETC INC.

XX Dale RMK, Arrow A, Thompson T;

XX WPI; 2003-221709/21.

XX Composition with a modified oligonucleotide useful for treating a patient
 PT with a pathological disorder such as abnormal appetite, hypertension,
 PT eczema, anxiety, stress, and cancer.

XX Claim 6; Page 90; 173pp; English.

XX The present invention describes a composition (I) suitable for
 CC administration in a mammal, which comprises a modified oligonucleotide
 CC (II) of 7-75 nucleotides containing 7 or more contiguous ribose groups
 CC linked by achiral 5'-3' internucleoside phosphate linkages, where the
 CC modified oligonucleotide is complementary to a region of a gene
 CC associated with a pathological disorder. Also described: (1) a
 CC nutritional supplement comprising (II); and (2) a cosmetic composition
 CC comprising (II), where the modified oligonucleotide is complementary to a
 CC region of a gene associated with a skin disorder. (I) and (II) can have
 CC hypotensive, antilipemic, vasotropic, dermatological, antidepressant,
 CC tranquiliser, antiinflammatory, antitumor, laxative, antimigraine,
 CC neuroprotective, antiparkinsonian, analgesic, gynaecological, virucide,
 CC vulnery, antithritic, antipsoriatic, antimicrobial, cycostatic and
 CC litholytic activities. (I) can be used for treating a patient with a
 CC pathological disorder selected from abnormal appetite, hypertension,

Qy 182 ATTCCTACTCTGTAATAAATAATCAACAACTGTGCAATTAAGAAAGTTTTCAGGGTATA 241
Dy 3439 ATTCCTGTCTGTACATAAATAATCAACAACTGTGCACTGAAGAAATCTTTTCAGGAATA 3498
Qy 242 GACACATTGAAGACCAACCTGCCACGGGAGGCTGTGATATAAATATTCCAAAACCTTG 301
Dy 3499 GGCACTGTGAGAGTCAACTGTGCAAGGGGTACTGTGGAAGACTATTCAAAACCTTG 3558
Qy 302 TCTTTAATAAAGAACACATAGAGCGCCAAAAAAGGTGTGCAGAGAAAGATGGAGA 361
Dy 3559 TCCTTAATAAAGAAATACATTGACCGCCAAAAAAGGTGTGGAAGAAAGACGGAGA 3618
Qy 362 GTGACAAAGTCTAGACTACCTGCAAGTATTTCTTGGTGTATTAACACCGAGTGGACA 421
Dy 3619 GTAACCAATTCCTAGACTACCTGCAAGTATTTCTTGGTGTATTAACACCGAGTGGATA 3678
Qy 422 CCGGAAAGTTGAGAACCAACCGGCTTATTTAGTGAAGATTTTGGAGAGAAATGGTTTT 481
Dy 3679 ATAGAAAGTTGAGACTAACTGGTTTTCGACCAAGATTTTGGAGAGAGACATT 3738
Qy 482 TT--GGGATGAGAAATGAGGGCCCAACACAGTAGGACTTAATGGCCAGTATACTAAG 539
Dy 3739 TTACTGCAGTGAGAAATGAGGGCCCAAGAAAGATCAGGCCCTTAATTTCAATATAATTAA 3798
Qy 540 CTTGAGAGACAAAGTAAATATTTTCAGGCATCTTACTACTTTATCA 584
Dy 3799 CTTGAGGGGAAGTAAATATTTTCAGGCATCTTACTGACACTTTGGCA 3843

RESULT 13
AAF20980 ID AAF20980 standard; DNA; 4057 BP.
XX AC AAF20980;
XX DT 14-MAR-2001 (first entry)
XX DE Human low adenosine antisense oligonucleotide related sequence #2547.
XX KW Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
XX KW human; airway disorder; bronchoconstriction; lung inflammation;
XX KW surfactant depletion; respiratory; bronchodilator; antiinflammatory;
XX KW immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic;
XX KW respiratory obstruction; pulmonary vasoconstriction; impeded respiration;
XX KW surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
XX KW respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
XX KW pulmonary hypertension; emphysema; pulmonary transplantation rejection;
XX KW chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
XX KW cancer; ss.
XX OS Homo sapiens.
XX FN WO200062736-A2.
XX PD 26-OCT-2000.
XX PF 24-MAR-2000; 2000WO-US008020.
XX PR 06-APR-1999; 99US-0127958P.
XX PA (UYEC-) UNIV EAST CAROLINA.
XX PA (NYCE/) NYCE J W.
XX PI Nyce JW;
XX DR WPI; 2000-679539/66.
XX PT Low adenosine (A) content antisense oligonucleotides which do not trigger
XX PT adenosine receptors during metabolism, useful e.g. for treating cancers
XX PT and respiratory obstructions.
XX PS Disclosure; Page 788-789; 1592pp; English.

XX CC The present invention describes low adenosine (A) content antisense
CC oligonucleotides and compositions (I) comprising them. In the antisense
CC oligonucleotides the A is replaced by a 'Unifal' or alternative base.
CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
CC immunosuppressive, antiasthmatic, hypotensive and cytostatic activities.
CC The antisense oligonucleotides and (I) can be used to down-regulate the
CC expression and or activity of target polypeptides associated with
CC lung/respiratory disorders and malignancies, such as stimulating and
CC activating peptide factors and transmitters, transcription factors,
CC immunoglobulins and antibodies, antibody receptors, cytokines and
CC chemokines, endogenously produced specific and non-specific enzymes,
CC binding proteins, adhesion molecules and their receptors, cytokine and
CC chemokine receptors, adenosine receptors, bradykinin receptors, central
CC nervous system (CNS) and peripheral nervous and non-nervous system
CC receptors, CNS and peripheral nervous and non-nervous system peptide
CC transmitters, defensins, growth factors, vasoactive peptides and
CC receptors, binding proteins and malignancy associated proteins. The
CC antisense oligonucleotides may be used in this way to treat disorders
CC including respiratory obstruction (especially pulmonary obstruction
CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies) and/or
CC surfactant hypoproduction which are associated with a disease or
CC condition selected from pulmonary vasoconstriction, inflammation,
CC allergies, asthma, impeded respiration, respiratory distress syndrome
CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
CC pulmonary transplantation rejection, pulmonary infections, bronchitis,
CC and/or cancer. AAF18434 to AAF21543 represent human polynucleotide
CC fragments and antisense oligonucleotides used in the exemplification of
CC the present invention
XX CC
SQ Sequence 4057 BP; 1303 A; 683 C; 796 G; 1275 T; 0 U; 0 Other;
Query Match 62.1%; Score 379; DB 3; Length 4057;
Best Local Similarity 79.1%; Pred. No. 4.1e-102;
Matches 463; Conservative 0; Mismatches 120; Indels 2; Gaps 1;
Qy 2 AAGCAACACTGAACATTTTCAGAGCTATGAGAAATGCTTCTGAATTTGAGTTGCTAGCT 61
Dy 3259 AAGCAACACTGAACATTTTCAGAGCTATGAGAAATGCTTCTGAATTTGAGTTGCTAGCT 3318
Qy 62 CTTGGGCTGCTATGTTTCTGCCCTTTGCTGTAGAAATCCCATGATAGCTGCTGCGCA 121
Dy 3319 CTTGGAGTGTGCTACGTGTATGCCATCCCAACAGAAATTTCCCAAGTGATTTGGTGA 3378
Qy 122 GAGACCTTGACACTGCTCTCCACTCATCGAATTTGGCTGATAGCGGATGGAACTGATG 181
Dy 3379 GAGACCTTGACACTGCTCTCTCTCTCATCGAATTTGCTGTAGCAATGAGACTCTGAGG 3438
Qy 182 ATTCCTACTCTGAAATATAAATCAACAACTGTGCAATTAAGAAAGTTTTCAGGGTATA 241
Dy 3439 ATTCCTGTCTGTACATAAATAATCAACAACTGTGCAATTAAGAAAGTTTTCAGGGTATA 3498
Qy 242 GACACATTGAAGAACCAACCTGCCACGGGAGGCTGTGATATAAATATTCCAAAACCTTG 301
Dy 3499 GGCACTGTGAGAGTCAACTGTGCAAGGGGTACTGTGGAAGACTATTCAAAACCTTG 3558
Qy 302 TCTTTAATAAAGAACACATAGAGCGCCAAAAAAGGTGTGCAGAGAAAGATGGAGA 361
Dy 3559 TCCTTAATAAAGAAATACATTGACCGCCAAAAAAGGTGTGGAAGAAAGACGGAGA 3618
Qy 362 GTGACAAAGTCTAGACTACCTGCAAGTATTTCTTGGTGTATTAACACCGAGTGGACA 421
Dy 3619 GTAACCAATTCCTAGACTACCTGCAAGTATTTCTTGGTGTATTAACACCGAGTGGATA 3678
Qy 422 CCGGAAAGTTGAGAACCAACCGGCTTATTTAGTGAAGATTTTGGAGAGAAATGGTTTT 481
Dy 3679 ATAGAAAGTTGAGACTAACTGGTTTTCGACCAAGATTTTGGAGAGAGACATT 3738
Qy 482 TT--GGGATGAGAAATGAGGGCCCAACACAGTAGGACTTAATGGCCAGTATACTAAG 539
Dy 3739 TTACTGCAGTGAGAAATGAGGGCCCAAGAAAGATCAGGCCCTTAATTTCAATATAATTAA 3798
Dy 3739 TTACTGCAGTGAGAAATGAGGGCCCAAGAAAGATCAGGCCCTTAATTTCAATATAATTAA 3798

QY	540	CTTCAGAGCAAGTAATAATTTTCAGGCATCTCTACTACTATTATCA	584
DB	3799	CTTCAGAGCAAGTAATAATTTTCAGGCATCTCTACTACTATTATCA	3843
RESULT 14			
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ID	ABZ96674	standard; DNA; 4057 BP.	
XX	AC	ABZ96674;	
XX	AC	ABZ96674;	
DT	17-OCT-2003	(first entry)	
XX	DE	Human nucleic acid sequence.	
XX	XX	Human; antisense; lung dysfunction; nasal airway dysfunction;	
XX	XX	antiinflammatory steroid; ubiquinone; antiinflammatory; antiasthmatic;	
XX	XX	antiallergic; hypotensive; immunosuppressive; cytostatic; gene therapy;	
XX	XX	antisense gene therapy; respiratory; lung; adenosine sensitivity;	
XX	XX	adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;	
XX	XX	lung inflammation; respiratory disease; ds.	
OS	XX	Homo sapiens.	
XX	XX	WO200285308-A2.	
PN	XX	31-OCT-2002.	
PD	XX	23-APR-2002; 2002WO-US013135.	
XX	XX	24-APR-2001; 2001US-0286137P.	
PF	XX	(EPIC-) EPIGENESIS PHARM INC.	
PR	XX	Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;	
PA	XX	Miller S, Tang L, Shahabuddin S;	
PI	XX	WPI; 2003-229219/22.	
PT	XX	Pharmaceutical composition for treating ailments associated with impaired	
PT	XX	respiration, has oligo(s) antisense to specific gene(s) or its	
PT	XX	corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or	
PT	XX	ubiquinone.	
PS	XX	Disclosure; SEQ ID NO 11916; 872pp; English.	
CC	XX	The invention relates to a novel pharmaceutical composition, which has a	
CC	XX	first active agent comprising an oligonucleotide antisense to the	
CC	XX	initiation codon, coding region, 5' or 3' end genomic flanking regions,	
CC	XX	5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of	
CC	XX	junctions of genes encoding a polypeptide associated with lung and/or	
CC	XX	nasal airway dysfunction and a second active agent comprising an	
CC	XX	antiinflammatory steroid and ubiquinone. A composition of the invention	
CC	XX	has antiinflammatory, antiallergic, antiasthmatic, hypotensive,	
CC	XX	immunosuppressive, and cytostatic activity. The composition may have a	
CC	XX	use in antisense gene therapy. The composition is useful for treating or	
CC	XX	preventing a respiratory, lung or malignant disease or condition, also	
CC	XX	for enhancing the prophylactic or therapeutic respiratory effect of an	
CC	XX	antiinflammatory steroid in a subject, for reducing or depleting levels	
CC	XX	of, or reducing sensitivity to adenosine, reducing levels of adenosine	
CC	XX	receptor, producing bronchodilation, increasing levels of ubiquinone or	
CC	XX	lung surfactant in a subject's tissue, or treating bronchoconstriction,	
CC	XX	lung inflammation, lung allergies, or a respiratory disease or condition.	
CC	XX	Note: The sequence data for this patent is not represented in the printed	
CC	XX	specification, but was obtained in electronic format directly from WIPO	
CC	XX	at ftp.wipo.int/pub/published_pct_sequences	
XX	XX	Sequence 4057 BP; 1303 A; 683 C; 796 G; 1275 T; 0 U; 0 Other;	
Query Match			
Best Local Similarity 62.1%; Score 379; DB 7; Length 4057;			
Matches 463; Conservative 0; Mismatches 120; Indels 2; Gaps 1;			

QY	2	AAGCGAAACACTGAACATTTTCAGAGCTATGAGATGCTTCTGANTTTGAGTTTCTAGCT	61
DB	3259	AAGCGAAACCGAGAACGTTTCAGAGCCATGAGGATGTTCTGCAATTTGAGTTTCTAGCT	3318
QY	62	CTTGCGGCTGCTATGTTTCTGCTTGTAGAAAATCCCATGAAATAGACTCGTGGA	121
DB	3319	CTTGAGCTGCTACGTGATGCCATCCCGACAGAAATCCCGACAGTGCATTGTTGAAA	3378
QY	122	GAGACCTTGACACTGCTCTCCACTCATCGAACTGGCTGATAGCGGATGGAACTGATG	181
DB	3379	GAGACCTTGCGACTGCTTTTACTCATCGAACTGCTGATAGCAATGAGACTCTGAGG	3438
QY	182	ATTCTCTCTCTGAAAATAAAAAATCAGCAACTGTCATTAAGAAAGTTTTTCAGGGTATA	241
DB	3439	ATTCTCTCTCTGATATAAAAAATCAGCAACTGTCATTAAGAAAGTTTTTCAGGGTATA	3498
QY	242	GACACATTTGAAGAACCAAACTGCCCGGAGGCTGTGATATAAACTATTCCAAAACTTG	301
DB	3499	GCGACACTGGAGAGTCAAACTGTGCAAGGGGCTACTGTGGAAGACTATTCAAAACTTG	3558
QY	302	TCTTTAATAAAGAACACATAGAGCGCCAAAAAGGTTGTCAGGAGAAAGATGAGGA	361
DB	3559	TCCTTTAATAAAGAAATACATTGACGGCCAAAAAGGTTGTCAGGAGAAAGATGAGGA	3618
QY	362	GTGACAAAGTTCTCTAGACTACCTGCAAGTATTTCTTGGTGTATAAACAACCGAGTGACA	421
DB	3619	GTAAACCAATTTCTCTAGACTACCTGCAAGAGTTTCTTGGTGTATAAACAACCGAGTGACA	3678
QY	422	CCGAAAGTTGAGAACAAACCGGCTTATTGTAGTGGAGATTTTGGAGAGAAATGGTTTT	481
DB	3679	ATAGAAAGTTGAGACTAAACTGGTTTGTGAGCCAAAGATTTTGGAGGAGAAAGGACAT	3738
QY	482	TT--GGCGATGAGAAATGAGGGCCAAACCAAGTAGTAGGACTTAATGGCCAGTATTAAC	539
DB	3739	TTACTGCTAGTGAATGAGGGCCAAAGAGAGTACAGCCTTAATTTCAATATTAATTTAA	3798
QY	540	CTTCAGAGCAAGTAATAATTTTCAGGCATCTCTACTACTATTATCA	584
DB	3799	CTTCAGAGCAAGTAATAATTTTCAGGCATCTCTACTACTATTATCA	3843
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ID	AA570755	standard; DNA; 520 BP.	
XX	AC	AA570755;	
XX	XX	17-OCT-2003 (revised)	
DT	24-SEP-1997	(first entry)	
XX	DE	Ovine IL-5 gene.	
XX	XX	Cytokine; ovine; sheep; interleukin-5; interleukin-12; IL-5; IL-12;	
XX	XX	livestock; cow; stress; transport; vaccine adjuvant; veterinary; cancer;	
XX	XX	immunosuppression; allergy; reproductive system; growth; early maturity;	
XX	XX	antibody; diagnosis; immunopotentiator;	
XX	XX	early haematopoietic progenitor cell; cytotoxic cell; thymocyte;	
XX	XX	secretion; IgM; IgA; bacterial endotoxin; gamma-interferon; ss.	
OS	XX	Ovis aries.	
XX	XX	Location/Qualifiers	
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XX WO9700321-A1.
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XX 03-JAN-1997.
XX
XX 14-JUN-1996; 96WO-AU000360.
XX
XX 14-JUN-1995; 95AU-00003502.
XX
XX 27-OCT-1995; 95AU-00006244.
XX
XX (CSIR ) COMMONWEALTH SCI & IND RES ORG.
XX
XX Seow H, Wood P;
XX
XX WPI; 1997-077528/07.
XX
XX P-PSDB; AAW08479.
XX
XX Nucleic acid encoding ovine interleukin-5 or -12 - used as vaccine
XX adjuvants and to treat or prevent microbial infections in livestock.
XX
XX Claim 6; Page 39-40; 78pp; English.
XX
XX The sequences given in AAT50755-56 encode ovine interleukin-5 (IL-5).
XX Ovine IL-5 or IL-12 are used to treat and/or prevent infections in
XX livestock (esp. cows and sheep), particularly where the animals are
XX stressed, e.g. during transport. IL-5 and IL-12 can also be used as
XX adjuvants in vaccines for veterinary use (partic. weakly immunogenic
XX subunit or synthetic peptide vaccines). They may also be used to treat
XX cancer, immunosuppression and allergy, to enhance/suppress the
XX reproductive system and to promote growth or early maturity. Optionally
XX interleukin can be delivered from constructs or delivery cells and
XX antibodies are useful in enzyme immunoassays, for rapid diagnosis of
XX infection. The interleukins are immunopotentiators, especially IL-5
XX promotes growth of early haematopoietic progenitor cells and generation
XX of cytotoxic cells from thymocytes, also it stimulates production and
XX secretion of IgM and IgA (in synergism with bacterial endotoxin). IL-12
XX induces production of gamma-interferon by, and proliferation of, T and NK
XX cells and increases the (non-)specific cytolytic lymphocyte response. The
XX genetic constructs can also be used for in vitro production of IL-5 or -
XX 12. (Updated on 17-Oct-2003 to standardise OS field)
XX
XX Sequence 520 BP; 166 A; 99 C; 124 G; 131 T; 0 U; 0 Other;

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Search completed: August 30, 2004, 21:48:17
Job time : 292.939 secs

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Query Match      59.7%; Score 364.4; DB 2; Length 520;
Best Local Similarity 83.9%; Pred. No. 4e-98;
Matches 426; Conservative 0; Mismatches 76; Indels 6; Gaps 1;

QY 2 AAGCGAACAACCTGACATTTTCAGAGCTATGAGATGCTTCTGAATTTGAGTTTGTAGCT 61
Db 13 AAGCGAACAACCTGACATTTTCAGAGCTATGAGATGCTTCTGAATTTGAGTTTGTAGCT 72
QY 62 CTTGGGGCTGCCATGTTTCTGCTTTGCTGTAGAAAATCCCATGAATAGACTGGTGCA 121
Db 73 CTTGGAGCTGCCATGTTTGTGCAATGCTGTAGAAAATACCATGAATAGACTGGTGCA 132
QY 122 GAGACCTTGACATGCTCTCCACTCATCGAATTTGGCTGATAGCGGATGGGAACCTGATG 181
Db 133 GAGACCTTGACATGCTCTCCACTCATCGAATTTGGCTGATAGCGGATGGGAACCTGATG 192
QY 182 ATTCTCTACTCTGAAAATAAAATCACCACCTGTGCAATTAAGAGTTTTCAGGGTATA 241
Db 193 ATTCTCTACTCTGAGCATCAATCACCACCTGTGCAATTAAGAGTTTTCAGGGTATA 252
QY 242 GACACATTTGAGAACCAACCTGCCACGGGGAGGCTGTGGTAACTATTCAAAACCTTG 301
Db 253 GACACATTTGAGAACCAACCTGCCACGGGGAGGCTGTGGTAACTATTCAAAACCTTG 312
QY 302 TCTTTTAATAAAGAACACATAGAGCCCAAAAAAAGGTGTGCAGGAGAGATGGAGA 361

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Db 313 TCTTTTAATAAAGAAATACATAGACCTCCAAAAAGGAAGTGTGAGGAGAAAGATGGAGA 372
QY 362 GTGACAAAAGTTTCCTAGACTACCTGCAAGTATTTCTTGGTGTATAAACAACCCGAGTGGACA 421
Db 373 GTGAAACAATTCCTCGACTACCTGCAAGTATTTCTTGGTGTATAAACAACAGAGTGGACG 432
QY 422 CCGAAAAGTTGAGAACAAACCGGCTTATTGTAGTGGAAATTTT-----GGAGAAAGAT 475
Db 433 ATGAAAAGCTGAGATCTACCTCTCTCACTGTAGTGAAGTTTCTGAGGAGGAGGAAGGAT 492
QY 476 GGTTTTGGCGATGAGAATGAGGGCCA 503
Db 493 GTTTTAATTGCAGTCAGAAATGAGGGCCA 520

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OM nucleic - nucleic search, using sw model

Run on: August 30, 2004, 21:24:28 ; Search time 2049.32 Seconds
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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues
Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: em_esthum.*
3: em_estin.*
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5: em_estov.*
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8: em_htc.*
9: gb_esti.*
10: gb_estc.*
11: gb_htc.*
12: gb_est3.*
13: gb_est4.*
14: gb_est5.*
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28: gb_gssi.*
29: gb_gss2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	307.8	50.5	456	14	CD559532
C 2	307.2	50.4	456	14	CD559686
C 3	303.4	49.7	470	14	CD559687
4	303.4	49.7	492	14	CD559533

5	301	49.3	478	14	CD559534
6	300.8	49.3	463	14	CD559535
7	299.2	49.0	489	14	CD559536
C 8	293	48.0	467	14	CD559688
C 9	292.4	47.9	473	14	CD559689
C 10	292.2	47.9	467	14	CD559690
11	280.2	45.9	405	29	AY412020
12	278.4	45.6	477	14	CD559608
13	277.8	45.5	622	29	CE331159
14	276.2	45.3	405	29	AY412021
15	195	32.0	399	29	AY412022
C 16	164.8	27.0	503	13	BQ598873
C 17	48.2	7.9	1201	9	AL550373
C 18	43.8	7.2	1044	13	EX415231
C 19	43.8	7.2	1101	29	CNS017KX
C 20	42.4	7.0	1025	13	EX441235
C 21	42.4	7.0	1201	13	EX396080
C 22	41.8	6.9	432	9	AA560540
C 23	41.4	6.8	1201	9	AL547091
C 24	40.8	6.7	677	29	CG032226
C 25	40.6	6.7	522	12	BI670794
C 26	40.6	6.7	1026	13	EX461051
C 27	40.6	6.7	1201	13	EX387694
C 28	40.4	6.6	926	28	BH135042
C 29	40.2	6.6	623	28	AQ576964
C 30	40.2	6.6	666	28	AQ326668
C 31	40.2	6.6	1159	13	EX394939
C 32	40.2	6.6	1201	13	EX461310
C 33	40	6.6	317	14	CD087271
C 34	40	6.6	711	29	CC080466
C 35	40	6.6	1101	29	CNS0182P
C 36	39.8	6.5	535	28	AZ370501
C 37	39.8	6.5	565	28	AZ650499
C 38	39.6	6.5	1201	13	EX334478
C 39	39.4	6.5	1101	29	CNS0183C
C 40	39.2	6.4	603	12	BJ328562
C 41	39.2	6.4	619	12	BJ328648
C 42	39.2	6.4	738	28	AQ328856
C 43	39.2	6.4	905	29	CNS00D59
C 44	39	6.4	843	28	BH085356
C 45	39	6.4	948	14	CD242046

ALIGNMENTS

RESULT 1
CD559532
LOCUS
DEFINITION
AGENCY: 14497057 NIH_MGC 195 Homo sapiens cDNA clone
IMAGE: 6971772 5', mRNA sequence.
ACCESSION
CD559532
VERSION
CD559532.1
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 456)
NIH-MGC <http://mgs.nci.nih.gov/>
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NCI
Bldg. 31 Eml0A07 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Narayan Bhat
cDNA Library Preparation: Bhat Laboratory
DNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/ILNL at:

CD559534 AGENCOURT
CD559535 AGENCOURT
CD559536 AGENCOURT
CD559688 AGENCOURT
CD559689 AGENCOURT
CD559690 AGENCOURT
AY412020 Homo sapi
CD559608 AGENCOURT
CE331159 tigr-gs-
AY412021 Pan trogl
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BQ598873 MI-P-B4-a
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EX415231 EX415231
AIU08171 Drosophil
EX441235 EX441235
EX396080 EX396080
AA560540 v119f05.r
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CG032226 PUMU10TB
BI670794 P250a0a
EX461051 EX461051
EX387694 EX387694
BH135042 ENTNM83TF
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AQ326668 nbxb0038G
EX394939 EX394939
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AZ370501 LM0121K03
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EX334478 EX334478
AL108834 Drosophil
BJ328562 BJ328562
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BH085356 RPCI-24-4
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http://image.llnl.gov
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FEATURES
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 /note="Vector: pDNR-Dual; Site 1: loxp-Sali; Site 2: loxp-HindIII; Clones from this library have been PCR-amplified using gene-specific primers to contain the complete open reading frame (based on known gene sequences available from NCBI's RefSeq). Template for PCR is cDNA derived from either pooled cytoplasmic polyA RNA from 30 cells lines or pooled total RNA from 10 different tissues (from BD Biosciences/Clontech and Washington University). PCR products are directionally cloned into the loxp sites of the pDNR-Dual vector. Library constructed by Dr. Narayan Bhat, Earl Bere III and Hongling Liao (Gene Expression Laboratory, Research Technology Program, SAIC Frederick, NCI-Frederick, Frederick, MD 21702). For information on which gene each clone represents, please visit our anonymous ftp site at ftp://image.llnl.gov/image/rearrayed_plates/IRBK.presv.dat a Note: this is a NIH_MGC Library."

ORIGIN

Query Match 50.4%; Score 307.8; DB 14; Length 456;
 Best Local Similarity 79.8%; Pred. No. 3.5e-65;
 Matches 363; Conservative 0; Mismatches 92; Indels 0; Gaps 0;

QY 8 AACACTGAATTCAGAGTATGAGATCTCTCTGAATTTGAGTTGCTAGCTTTGGG 67
 Db |
 1 AAAGCAGAACGTTTTCAGAGCCATGAGGATCTCTCTGATTTGAGTTGCTAGCTTTGGA 60
 QY 68 GCTGCTATGTTCTGCTTGTGTAGAAATCCCATGATAGCTGCTGGCAGAGACC 127
 Db |
 61 GCTGCTATGTTCTGCTTGTGTAGAAATCCCATGATAGCTGCTGGCAGAGACC 120
 QY 128 TTGACACTGCTCTCCACTCATCGAACTTGCTGATAGCGCATGGGAACCTGATTTCT 187
 Db |
 121 TTGCACTGCTTTCTACTCATCGAACTCTGCTGATAGCGCATGGGAACCTGATTTCT 180
 QY 188 ACTCTGAAATATAAATACCACTGCTGATTAAGAGTTTTCAGGGTATAGACACA 247
 Db |
 181 GTTCTCTGATATAAATACCACTGCTGATTAAGAGTTTTCAGGGTATAGACACA 240
 QY 248 TTGAAGAACCAACTGCGCCAGCGGAGCTGTGGATAAATATTCCAAACTTGTCTTTA 307
 Db |
 241 CTGGAGAGTCAACTGTGCAAGGGGTACTGTGGAAGACTATTCAAACTTGTCTTTA 300
 QY 308 ATAAAGAACACATAGAGCCCAAAAAAGGTGTGCGAGGAAGAGATGGAGTGACA 367
 Db |
 301 ATAAAGAAATACATTGACGCGCCCAAAAAAGGTGTGCGAGGAAGAGATGGAGTAAAC 360
 QY 368 AAGTTCTCTAGACTACCTGCAAGTATTCTTGGTGTAAATAAACACCGAGTGGACCGGAA 427
 Db |
 361 CAATTCTAGACTACCTGCAAGTATTCTTGGTGTAAATAAACACCGAGTGGATATAGAA 420
 QY 428 AGTTGAGAACAAACCGGCTTATTGTAGTGAAGAT 462
 Db |
 421 AGTTGAGACTAAACTGTTTGTGTCACCAAGAT 455

RESULT 2

CD559686/c
 LOCUS 456 bp mRNA linear EST 11-JUN-2003
 DEFINITION AGENCOURT_14497093 NIH MGC 195 Homo sapiens cDNA clone
 IMAGE:6971772 3', mRNA sequence.

ACCESSION
 VERSION
 KEYWORDS
 SOURCE

ORGANISM

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT

CD559686
 CD559686.1 GI:31585754

EST.
 Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 456)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Daniela S. Gerhard, Ph.D.

Office of Cancer Genomics

National Cancer Institute / NIH

Bldg. 31 Rm10A07 Bethesda, MD 20892

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Narayan Bhat

cDNA Library Preparation: Bhat Laboratory

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: IRBK1 row: g column: 11

High quality sequence stop: 456.

Location/Qualifiers

1..456

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:6971772"

/tissue_types="mixed"

/lab_host="DH5A (T1 phage-resistant)"

/clone_lib="NIH MGC 195"

/note="Vector: pDNR-Dual; Site 1: loxp-Sali; Site 2: loxp-HindIII; Clones from this library have been PCR-amplified using gene-specific primers to contain the complete open reading frame (based on known gene sequences available from NCBI's RefSeq). Template for PCR is cDNA derived from either pooled cytoplasmic polyA RNA from 30 cells lines or pooled total RNA from 10 different tissues (from BD Biosciences/Clontech and Washington University). PCR products are directionally cloned into the loxp sites of the pDNR-Dual vector. Library constructed by Dr. Narayan Bhat, Earl Bere III and Hongling Liao (Gene Expression Laboratory, Research Technology Program, SAIC Frederick, NCI-Frederick, Frederick, MD 21702). For information on which gene each clone represents, please visit our anonymous ftp site at ftp://image.llnl.gov/image/rearrayed_plates/IRBK.presv.dat a Note: this is a NIH_MGC Library."

FEATURES

source

ORIGIN

Query Match 50.4%; Score 307.2; DB 14; Length 456;
 Best Local Similarity 79.6%; Pred. No. 5e-65;
 Matches 363; Conservative 0; Mismatches 93; Indels 0; Gaps 0;

QY 6 CAACACCTGAACATTTTCAGAGCTATGAGATGCTTCTGAATTTGAGTTTGTAGCTTTG 65
 Db |
 456 CCAAGCAGAACGTTTTCAGAGCCATGAGGATGCTTCTGCAATTTGAGTTTGTAGCTTTG 397
 QY 66 GGGCTGCTATGTTTCTGCTTGTAGAAATCCCATGATAGCTAGCTGGTGGCAGAGA 125
 Db |
 396 GAGCTGCTAGTGTATGCCATCCACAGAAATTCACCAAGTGCATTGGTGAAGAGA 337
 QY 126 CTTTGACACTGCTCTCCACTCATCGAACTTGGGTGATAGCGGATGGGAACCTGATGATTC 185
 Db |
 336 CTTTGACACTGCTTCTACTCATCGAACTCTGCTGATAGCCATGAGACTCTGAGGATTC 277
 QY 186 CTACTCTGAAATATAAATACCAACTGTGCAATTAAGAGTTTTCAGGGTATAGACA 245
 Db |
 276 CTGTTCTGTACATAAATAATACCAACTGTGCACTGAAGAAATCTTTTCAGGGAATAGGCA 217

QY 246 CATTGAAGAACCAACTGCCACGGGAGGCTGTGATTAACCTATTCGAAACCTTGCTTT 305
 Db 216 CACTGGAGAGTCAAACTGTGCAAGGGGTACTGTGGAAGAGCTATTCGAAACCTTGCTTT 157
 QY 306 TAATTAAGAGACACATAGAGCCCAAAAAAAGGTGTGACGAGAAAGATCGAGAGTGA 365
 Db 156 TAATAAGAGAAATACATTGACGGCCAAAAAAGGTGTGAGAGAAAGACCGAGAGTAA 97
 QY 366 CAAAGTTCCTAGACTACCTGCAAGTATTTCTTGTTGTTAATAAACACCGAGTGGACCGG 425
 Db 96 ACCAATTCCTAGACTACCTGCAAGAGTTTCTTGTTGTTAATAAACACCGAGTGGATAATAG 37
 QY 426 AAGTTGAGACAAACCGGCTATTCTAGTGGAGA 461
 Db 36 AAGTTGAGACTAACTGTTGTCAGCCAAAGA 1

RESULT 3
 CD559687/c
 LOCUS
 DEFINITION
 AGENCOURT_14497029 NIH_MGC_195 Homo sapiens cDNA clone
 IMAGE:6971771 5', mRNA sequence.
 CD559687
 CD559687.2 GI:38453484
 EST.
 SOURCE
 Homo sapiens (human)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 470)
 NIH-MGC http://mgi.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 On Jun 10, 2003 this sequence version replaced gi:31585755.
 Contact: Daniela S. Gerhard, Ph.D.
 Office of Cancer Genomics
 National Cancer Institute / NIH
 Bldg. 31 Rm10A07 Bethesda, MD 20892
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: Narayan Bhat
 CDNA Library Preparation: Bhat Laboratory
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov

Plate: IRBK1 row: 9 column: 10
 High quality sequence start: 14
 High quality sequence stop: 470.
 Location/Qualifiers
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 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:6971771"
 /lab_host="DH5A (T1 phage-resistant)"
 /tissue_type="mixed"
 /clone_lib="NIH MGC 195"
 /note="Vector: pDNR-Dual; Site 1: loxP-Sall; Site 2: loxP-HindIII; Clones from this library have been PCR-amplified using gene-specific primers to contain the complete open reading frame (based on known gene sequences available from NCBI's RefSeq). Template for PCR is cDNA derived from either pooled cytoplasmic polyA RNA from 30 cells lines or pooled total RNA from 10 different tissues (from BD Biosciences/Clontech and Washington University). PCR products are directionally cloned into the loxP sites of the pDNR-Dual vector. Library constructed by Dr. Narayan Bhat, Earl Bere III and Hongling Liao (Gene Expression Laboratory, Research Technology Program, SAIC Frederick, NCI-Frederick, Frederick, MD 21702). For information on which gene each clone represents, please visit our anonymous ftp site at

FEATURES

source

CD559533 492 bp mRNA linear EST 26-NOV-2003
 AGENCOURT_14496993 NIH_MGC_195 Homo sapiens cDNA clone
 IMAGE:6971771 5', mRNA sequence.
 CD559533
 CD559533.2 GI:38558947
 EST.
 SOURCE
 Homo sapiens (human)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 492)
 NIH-MGC http://mgi.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 On Jun 10, 2003 this sequence version replaced gi:31585601.
 Contact: Daniela S. Gerhard, Ph.D.
 Office of Cancer Genomics
 National Cancer Institute / NIH
 Bldg. 31 Rm10A07 Bethesda, MD 20892
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: Narayan Bhat
 CDNA Library Preparation: Bhat Laboratory
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: IRBK1 row: 9 column: 10
 High quality sequence start: 14
 High quality sequence stop: 492.

RESULT 4

CD559533

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

ftp://image.llnl.gov/image/rearrayed_plates/IRBK_presv.dat
 a Note: this is a NIH_MGC Library."

ORIGIN

Query Match 49.7%; Score 303.4; DB 14; Length 470;
 Best Local Similarity 80.5%; Pred. No. 4.3e-64;
 Matches 355; Conservative 0; Mismatches 86; Indels 0; Gaps 0;
 QY 6 CAAACACTGAACATTTTCAGAGCTATGAGAAATGCTTCTGAAATTTGAGTTGCTAGCTCTTG 65
 Db 469 CAAACGAGACAGCTTTTCAGAGCCCATGAGAGTCTTCTGCATTTGAGTTGCTAGCTCTTG 410
 QY 66 GGGCTGCTATGTTTCTGCTCTGCTAGAAAATCCCATGAAATCCCATGAAATGCTGTCGACAGA 125
 Db 409 GAGCTGCTAGCTGTATGCCATCCACAGAAATCCCAAGTGCATTGGTGAAGAGAGA 350
 QY 126 CTTTGACACTGCTCTCCACTCATCGAACTTGGCTGTAGCGGATGGGAACTGATGATTC 185
 Db 349 CTTTGGCACTGCTTTCTACTCATCGAACTCTGCTGTATAGCCAATGAGACTCTGAGGATTC 290
 QY 186 CTACTCTGAAATATAAAATCAACCACTGTGCATTAAGAAGTCTTTTCAGGGTATAGACA 245
 Db 289 CTGTTCTCTGTACATAAAATCACCACCTGTGCATCTGCACTGAAGAAATCTTTTCAGGGATAGGCA 230
 QY 246 CATTGAAGAACCAACTGCCACGGGAGGCTGTGGATAAACTATTCGAAACCTTGCTTT 305
 Db 229 CACTGGAGAGTCAAACTGTGCAAGGGGTACTGTGGAAGAGACTATTCAAAAACCTTGCTCT 170
 QY 306 TAATAAAGACACATAGAGCCCAAAAAAAGGTGTGAGGAGAGAGTGGAGAGTGA 365
 Db 169 TAATAAAGAAATACATTGACGGCCAAAAAAGTGTGGAGAGAAAGACCGAGAGTAA 110
 QY 366 CAAAGTTCCTAGACTACCTGCAAGTATTTCTTGTTGTTAATAAACACCGAGTGGACACCGG 425
 Db 109 ACCAATTCCTAGACTACCTGCAAGAGTTTCTTGTTGTTAATAAACACCGAGTGGATAATAG 50
 QY 426 AAGTTGAGACAAACCGGCT 446
 Db 49 AAGTTGAGACTAACTGTT 29

FEATURES
source

Location/Qualifiers
1. .492
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clones="IMAGE:6971771"
/tissue_types="mixed"
/clone_lib="NIH_MGC_195"
/note="Vector: PDNR-Dual; Site 1: loxP-Sali; Site 2: loxP-HindIII; Clones from this library have been PCR-amplified using gene-specific primers to contain the complete open reading frame (based on known gene sequences available from NCBI's RefSeq). Template for PCR is cDNA derived from either pooled cytoplasmic polyA RNA from 30 cells lines or pooled total RNA from 10 different tissues (from BD Biosciences/Clontech and Washington University). PCR products are directionally cloned into the loxP sites of the PDNR-Dual vector. Library constructed by Dr. Narayan Bhat, Earl Bere III and Hongling Liao (Gene Expression Laboratory, Research Technology Program, SAIC Frederick, NCI-Frederick, Frederick, MD 21702). For information on which gene each clone represents, please visit our anonymous ftp site at
ftp://image.llnl.gov/image/rearrayed_plates/IRBK.presv.dat
a Note: this is a NIH_MGC Library."

ORIGIN

Query Match 49.7%; Score 303.4; DB 14; Length 492;
Best Local Similarity 80.5%; Pred. No. 4.3e-64;
Matches 355; Conservative 0; Mismatches 86; Indels 0; Gaps 0;

QY 6 CAACACATGACATTTTCAGAGCTATGAGATGCTTCTGAAATTTGAGTTTGTCTAGCTCTTG 65
DB 33 CAACCGAGAGACGTTTCAGAGCCATGAGGATGCTTCTGCAATTTGAGTTTGTCTAGCTCTTG 92

QY 66 GGGTGTGCTATGTTTCTGCTTCTGCTGTAGAAAATCCCATGAATCCATGACTGGTGGCAGAGA 125
DB 93 GAGCTGCTACGTGTATGCCATCCACAGAAATCCCAAGTGCATTTGGTGAAGAGA 152

QY 126 CTTGACATGCTCTCCACTCATCGAATTTGGTGTATAGCGGATGGAAACCTGATGATTC 185
DB 153 CTTGGCAGCTGCTTCTACTCATCGAATCTGCTGATAGCAATGAGACTCTGAGGATTC 212

QY 186 CTACTCTGTAATAAATAACCACTGTCATTAAGAGATTTTTCAGGGTATAGACA 245
DB 213 CTGTTCTGTACATAAATAACCACTGTCATGAAGAAATCTTTCAGGGAATAGGCA 272

QY 246 CATTGAAGAACCAACTGCCCGGGAGCTGTGGATAAATTTCCAAAATTTGTCTT 305
DB 273 CACTGGAGAGTCAAACTGTGCAAGGGGTACTGTGGAAGACTATTTCAAAATTTGTCTT 332

QY 306 TAATAAGACACATAGACGCCCAAAAAGAGTGTGCAGAGAAAGATGGAGATCA 365
DB 333 TAATAAGAAATACATTGACGGCCAAAAGAAAGTGTGGAGAAGAAAGACCGAGATTA 392

QY 366 CAAAGTTCCTAGACTACCTGCAAGATTTCTTGGTGTATAAACACCGAGTGGACACCGG 425
DB 393 ACCAATTCCTAGACTACCTGCAAGATTTCTTGGTGTATAAACACCGAGTGGATAATAG 452

QY 426 AAAGTTGAGAACAAACCGGCT 446
DB 453 AAAGTTGAGAACTAACTGGTT 473

RESULT 5
LOCUS CD559534
DEFINITION AGENCOURT_14496928 NIH_MGC_195 Homo sapiens cDNA clone
IMAGE:6971770 5', mRNA sequence.
ACCESSION CD559534
VERSION CD559534.2 GI:38558949
KEYWORDS EST.

SOURCE
ORGANISM

Homo sapiens (human)
Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

1. (bases 1 to 478)

NIH-MGC <http://mgc.nci.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

On Jun 10, 2003 this sequence version replaced gi:31585602.

Contact: Daniela S. Gerhard, Ph.D.

Office of Cancer Genomics

National Cancer Institute / NIH

Bldg. 31 Rm10A07 Bethesda, MD 20892

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Narayan Bhat

cDNA Library Preparation: Bhat Laboratory

DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: IRBK1 row: g column: 09

High quality sequence start: 3

High quality sequence stop: 478.

FEATURES

Location/Qualifiers

1. .478

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clones="IMAGE:6971770"

/tissue_types="mixed"

/lab_host="DH5A (T1 phage-resistant)"

/clone_lib="NIH_MGC_195"

/note="Vector: PDNR-Dual; Site 1: loxP-Sali; Site 2:

loxP-HindIII; Clones from this library have been

PCR-amplified using gene-specific primers to contain the

complete open reading frame (based on known gene sequences

available from NCBI's RefSeq). Template for PCR is cDNA

derived from either pooled cytoplasmic polyA RNA from 30

cells lines or pooled total RNA from 10 different tissues

(from BD Biosciences/Clontech and Washington University).

PCR products are directionally cloned into the loxP sites

of the PDNR-Dual vector. Library constructed by Dr.

Narayan Bhat, Earl Bere III and Hongling Liao (Gene

Expression Laboratory, Research Technology Program, SAIC

Frederick, NCI-Frederick, Frederick, MD 21702). For

information on which gene each clone represents, please

visit our anonymous ftp site at

ftp://image.llnl.gov/image/rearrayed_plates/IRBK.presv.dat

a Note: this is a NIH_MGC Library."

ORIGIN

Query Match 49.3%; Score 301; DB 14; Length 478;
Best Local Similarity 80.1%; Pred. No. 1.7e-63;
Matches 366; Conservative 0; Mismatches 90; Indels 1; Gaps 1;

QY 6 CAACACATGACATTTTCAGAGCTATGAGATGCTTCTGAAATTTGAGTTTGTCTAGCTCTTG 65
DB 22 CAACCGAGAGACGTTTCAGAGCCATGAGGATGCTTCTGCAATTTGAGTTTGTCTAGCTCTTG 81

QY 66 GGGTGTGCTATGTTTCTGCTTCTGCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGA 125
DB 82 GAGCTGCTACGTGTATGCCATCCCAAGAAATTTCCACAGTGCATTTGGTGAAGAGA 141

QY 126 CTTGACATGCTCTCCACTCATCGAATTTGGTGTATAGCGGATGGAACTCATGATTC 185
DB 142 CTTGGCAGCTGCTTCTACTCATCGAATCTGCTGTATAGCAATGAGACTCTGAGGATTC 201

QY 186 CTACTCTGTAATAAATAACCACTGTCATTAAGAGATTTTTCAGGGTATAGACA 245
DB 202 CTGTTCTGTACATAAATAACCACTGTCATGAAGAAATCTTTCAGGGAATAGGCA 261

QY 246 CATTGAAGAACCAACTGCCCGGGAGCTGTGGATAAATTTCCAAAATTTGTCTT 305

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Db      262  CACTGGAGAGTCAAACTGTGCAAGGGGGTACTGTGGAAGAGCTATTCAAAAACTTGTCT 321
QY      306  TAATAAAGACACATAGAGCGCCAAAAAAGGTGTCAGGAGAAAGATGAGAGTGA 365
Db      322  TAATAAAGAAATACATGAGCGCCAAAAAAGAA-GTGTGAGAGAGAAAGACGAGAGTAA 380
QY      366  CAAAGTTCTCTAGACTACCTGCAAGTATTTCTTGTTGTAATAAACACCGAGTGACACCG 425
Db      381  ACCAAATCTCTAGACTACCTGCAAGAGTTTCTTGTTGTAATAAACACCGAGTGAGATAATAG 440
QY      426  AAAGTTGAGAACAAACCGGCTTATTGTAGTGGAGAT 462
Db      441  AAAAGTTGAGACTAACTGGTTTGTGAGCCAAAGAT 477

RESULT 6
CD559535 463 bp mRNA linear EST 26-NOV-2003
LOCUS AGENCOURT_14496865 NIH_MGC_195 Homo sapiens cDNA clone
IMAGE:6971769 5', mRNA sequence.
CD559535
ACCESSION CD559535.2 GI:38558950
VERSION
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 463)
NIH-MGC http://mgs.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
On Jun 10, 2003 this sequence version replaced gi:31585603.
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgabs-r@mail.nih.gov
Tissue Procurement: Narayan Bhat
cDNA Library Preparation: Bhat Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: IRBKI row: 9 column: 08
High quality sequence stop: 463.
Location/Qualifiers
1. .463
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clones="IMAGE:6971769"
/tissue_type="mixed"
/lab_host="DH5A (T1 phage-resistant)"
/clone_lib="NIH_MGC_195"
/note="Vector: pDNR-Dual; Site 1: loxP-Sali; Site 2:
loxP-HindIII; Clones from this library have been
PCR-amplified using gene-specific primers to contain the
available from NCI's RefSeq). Template for PCR is cDNA
derived from either pooled cytoplasmic polyA RNA from 30
cells lines or pooled total RNA from 10 different tissues
(from BD Biosciences/Clontech and Washington University).
PCR products are directionally cloned into the loxP sites
of the pDNR-Dual vector. Library constructed by Dr.
Narayan Bhat, Earl Bere III and Hongling Liao (Gene
Expression Laboratory, Research Technology Program, SAIC
Frederick, NCI-Frederick, Frederick, MD 21702). For
information on which gene each clone represents, please
visit our anonymous ftp site at
ftp://image.llnl.gov/image/rearranged_plates/IRBKI.presv.dat
a Note: this is a NIH_MGC library."
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ORIGIN
Query Match 49.3%; Score 300.8; DB 14; Length 463;
Best Local Similarity 79.8%; Pred. No. 1.9e-63;
Matches 367; Conservative 0; Mismatches 92; Indels 1; Gaps 1;
QY      4  GGCAAACTCAACATTCAGAGCTATCAGAAATGCTTCTGAATTTGAGTTTGTAGTCTCT 63
Db      3  GACAACACGCAAGAGTTTCAGAGCCATGAGATGCTTCTGCATTTGAGTTTGTAGTCTCT 62
QY      64  TGGGCTGCTCTATGTTTCTGCTTTTGTGTAGAAAAATCCCATGAATAGACTGGTGGCAGA 123
Db      63  TGGAGCTGCTTACGTGTATGCCATCCCAAGAAATCCCAAGTGCATTTGGTGAAGA 122
QY      124  GACCTTGACATGCTCTCCACTCATCGNACTTGCTGATAGCGGATGGAACTGATGAT 183
Db      123  GACCTTGCACTGCTCTTCTACTCATCGAACTCTCTGATAGCCATGAGACTCTGAGGAT 182
QY      184  TCCCTACTCTGAAATAAAAAATCACCACCTGTGCATTAAAGAAGTTTTTCAGGGTATAGA 243
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QY      244  CACATTTGAAGAACCAAACTGCCCGGAGGCTGTGGATAAACTATTCCAAAACCTTGTCTC 303
Db      243  CACACTGGAGAGTCAAACCTGTGCAAGGGGTACTGTGGAAAGACTATTTCAAAAACTTGTCTC 302
QY      304  TTTAATAAAGAACACATAGAGCGCC-AAAAAAGGTGTGCAGAGAGAAAGATGGAGAG 362
Db      303  CTTAATAAAGAAATACATTTGCGGCCAAAAAAGAAATGTGGAGAAAGACGAGAG 362
QY      363  TGCAAAAGTTCTCAGACTACCTGCAAGTATTCTTTGGTGTATATAAACACCGAGTGGACAC 422
Db      363  TAAACCAATTCCTAGACTACCTGCAAGAGTTCTTTGGTGTATGAACACCGAGTGGATAA 422
QY      423  CGGAAGTTGAGAACAAACCGGCTTATTGTAGTGGAGAT 462
Db      423  TAGAAGTTGAGACTAAACTGGTTTGTGACGCCAAAGAT 462

RESULT 7
CD559536 489 bp mRNA linear EST 26-NOV-2003
LOCUS AGENCOURT_14496804 NIH_MGC_195 Homo sapiens cDNA clone
IMAGE:6971768 5', mRNA sequence.
CD559536
ACCESSION CD559536.2 GI:38558953
VERSION
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 489)
NIH-MGC http://mgs.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
On Jun 10, 2003 this sequence version replaced gi:31585604.
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgabs-r@mail.nih.gov
Tissue Procurement: Narayan Bhat
cDNA Library Preparation: Bhat Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: IRBKI row: 9 column: 07
High quality sequence stop: 17
High quality sequence stop: 489.
Location/Qualifiers
1. .489
source
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/db_xref="taxon:9606"
/clone="IMAGE:6971788"
/tissue_type="mixed"
/lab_host="DHSA (T1 phage-resistant)"
/clone_lib="NIH MGC 195"
/note="Vector: PNR-Dual; Site 1: loxp-Sali; Site 2:
loxP-HindIII; Clones from this library have been
PCR-amplified using gene-specific primers to contain the
complete open reading frame (based on known gene sequences
available from NCBI's RefSeq). Template for PCR is cDNA
derived from either pooled cytoplasmic polyA RNA from 30
cells lines or pooled total RNA from 10 different tissues
(from BD Biosciences/Clontech and Washington University).
PCR products are directionally cloned into the loxp sites
of the pDNR-dual vector. Library constructed by Dr.
Narayan Bhat, Earl Bere III and Hongling Liao (Gene
Expression Laboratory, Research Technology Program, SAIC
Frederick, NCI-Frederick, Frederick, MD 21702). For
information on which gene each clone represents, please
visit our anonymous ftp site at
ftp://image.llnl.gov/image/rearrayed_plates/IRBK_presv.dat
a Note: this is a NIH MGC Library."

ORIGIN

Query Match 47.9%; Score 292.2; DB 14; Length 467;
Best Local Similarity 80.0%; Pred. No. 2.4e-61;
Matches 356; Conservative 0; Mismatches 88; Indels 1; Gaps 1;
QY 6 CAACACTGACATTTGAGAGCTATGAGATGCTTCTGAAATTTGAGTTTCTAGCTCTTG 65
DB 466 CAACACGAGACGTTTCAGAGCCATGAGATGCTTCTGCAATTTGAGTTTCTAGCTCTTG 407
QY 66 GGGTGTCTATGTTTCTGCTTCTGCTAGAAAATCCCATGAATAGACTGGTGGCAGAGA 125
DB 406 GAGTGTCTAGCTGTATGCCATCCACAGANATCCCAAGTGCATTTGGTGAAGAGA 347
QY 126 CTTTGACACTGCTCTCACTCATCGAATCTGGCTGATAGCGGATGGAACTGATGATTC 185
DB 346 CTTTGGCACTGCTTCTACTCATCGAATCTGCTGATAGCAATGAGACTTTGAGGATTC 287
QY 186 CTACTCTGAAATATAAAATCACTGTCATTAAGAGTTTTCAGGGTATAGACA 245
DB 286 CTGTTCTGTATATAAAATCACTGTCATTAAGAGTTTTCAGGGTATAGACA 227
QY 246 CATTGAAGAACCAACTGCCACGGGAGGCTGTGGATAAATTTCCAAAATCTTCTTT 305
DB 226 CACTGGAGAGTCAAACTGTGCAAGGGGTACTGTGGAAGACTATTCAAAAATCTTCTCT 167
QY 306 TAAATAAAGACATAGAGGGCC-AAAAAAGGTGTCAGAGAGAGATGGAGATG 364
DB 166 TAAATAAAGAAATACATTTAGCGGCCAAAAAAGGTGCGAAGAAAGACCGAGAGTA 107
QY 365 ACAAGTTCTTAGACTACCTGCAAGTATTTCTTGGTGTATAAACACCGAGTGCACCG 424
DB 106 AACCAATCTTAGACTACCTGCAAGTATTTCTTGGTGTATAAACACCGAGTGCATAA 47
QY 425 GAAAGTTGAGAACAAACCGGCTTAT 449
DB 46 GAAAGTTGAGACTAACTGGTTTGT 22

RESULT 11

AY412020
LOCUS
DEFINITION Homo sapiens IL5 gene, VIRTUAL TRANSCRIPT, partial sequence,
genomic survey sequence.
ACCESSION AY412020
VERSION AY412020.1 GI:39767985
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 405)
AUTHORS Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Adams, M.D. and Cargill, M.

TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous

gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)

PUBMED

14671302

REFERENCE

2 (bases 1 to 405)
AUTHORS Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Adams, M.D. and Cargill, M.

TITLE Direct Submission

JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,

Rockville, MD 20850, USA

COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment.

FEATURES

source

1..405
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
<1..>405
/gene="IL5"
/locus_tag="HCM4418"

ORIGIN

Query Match 45.9%; Score 280.2; DB 29; Length 405;
Best Local Similarity 80.7%; Pred. No. 2.1e-58;
Matches 327; Conservative 0; Mismatches 78; Indels 0; Gaps 0;
QY 29 ATGAGAACTCTTCAATTTGAGTTTGTAGCTCTTGGGGCTGCTATGTTTCTGCCTTT 88
DB 1 ATGAGAGCTCTTGTGCAATTTGAGTTTGTAGCTCTTGGAGCTGCTAGTGTATGCCATC 60
QY 89 GCTGTAGAAAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACTCAT 148
DB 61 CCCACAGAAATTCACAAAGTGCATTGGTGAAGAGACCTTGGCACTGCTTCTACTCAT 120
QY 149 CGAACTTGGCTGATAGGCGATGGAACTGTGATGATCTTACTCTGCTGAAATAAATCAC 208
DB 121 CGAACTTGGCTGATAGGCGATGGAACTGTGATGATCTTACTCTGCTGATATAAATCAC 180
QY 209 CAACCTGTGCATTAAGAAGTTTTCAGGGTATAGACACATTTGAAGAACCAACTGCCAC 268
DB 181 CAACCTGTGCATTAAGAAGTTTTCAGGGTATAGACACATTTGAAGAACCAACTGTGCAA 240
QY 269 GGGGAGGCTGTGATTAACCTATTCCAAAACCTTGTCTTTTATAAAGAACACATAGAGCGC 328
DB 241 GGGGGTACTGTGGAAAGACTATTCAAAAACCTTGTCTTTTATAAAGAACATATTGAGCGC 300
QY 329 CAAAAAAGAGTGTGAGGAGAAAGATGGAGAGTGACAAAGTTCTCTAGACTACTCTCAA 388
DB 301 CAAAAAAGAGTGTGAGGAGAAAGACGAGAGTAACCAATTTCTAGACTACTCTCAA 360
QY 389 GTATTTCTTGTGTATAAACCACCGAGTGGACACCGGAAAGTTGA 433
DB 361 GAGTTTCTTGTGTATAAACCACCGAGTGGATATAAGAAAGTTGA 405

RESULT 12

CD559608
LOCUS
DEFINITION Homo sapiens IL5 gene, mRNA, linear EST 26-NOV-2003
IMAGE:6971867 5', mRNA sequence.
ACCESSION CD559608
VERSION CD559608.2 GI:38558942
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

US 10 767 362 1.180

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 477)
NIH-MGC <http://mgi.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
On Jun 10, 2003 this sequence version replaced gi:31585676.
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: gsapbs@mail.nih.gov
Tissue Procurement: Narayan Bhat
cDNA Library Preparation: Bhat Laboratory
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: RBK2 row: g column: 10
High quality sequence start: 107
High quality sequence stop: 353.
Location/Qualifiers
source
1. 477
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6971867"
/tissue_type="mixed"
/lab_host="DH5A (T1 phage-resistant)"
/clone_lib="NIH_MGC_195"
/note="vector: pDNR-Dual; Site 1: loxp-SalI; Site 2:
loxP-HindIII; Clones from this library have been
PCR-amplified using gene-specific primers to contain the
complete open reading frame (based on known gene sequences
available from NCBI's RefSeq). Template for PCR is cDNA
derived from either pooled cytoplasmic polyA RNA from 30
cells lines or pooled total RNA from 10 different tissues
(from BD Biosciences/Clontech and Washington University).
PCR products are directionally cloned into the loxp sites
of the pDNR-Dual vector. Library constructed by Dr.
Narayan Bhat, Earl Bere III and Hongling Liao (Gene
Expression Laboratory, Research Technology Program, SAIC
Frederick, NCI-Frederick, Frederick, MD 21702). For
information on which gene each clone represents, please
visit our anonymous ftp site at
ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat
a Note: this is a NIH_MGC Library."

FEATURES
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6971867"
/tissue_type="mixed"
/lab_host="DH5A (T1 phage-resistant)"
/clone_lib="NIH_MGC_195"
/note="vector: pDNR-Dual; Site 1: loxp-SalI; Site 2:
loxP-HindIII; Clones from this library have been
PCR-amplified using gene-specific primers to contain the
complete open reading frame (based on known gene sequences
available from NCBI's RefSeq). Template for PCR is cDNA
derived from either pooled cytoplasmic polyA RNA from 30
cells lines or pooled total RNA from 10 different tissues
(from BD Biosciences/Clontech and Washington University).
PCR products are directionally cloned into the loxp sites
of the pDNR-Dual vector. Library constructed by Dr.
Narayan Bhat, Earl Bere III and Hongling Liao (Gene
Expression Laboratory, Research Technology Program, SAIC
Frederick, NCI-Frederick, Frederick, MD 21702). For
information on which gene each clone represents, please
visit our anonymous ftp site at
ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat
a Note: this is a NIH_MGC Library."

ORIGIN
Query Match 45.6%; Score 278.4; DB 14; Length 477;
Best Local Similarity 78.2%; Pred. No. 6e-58;
Matches 347; Conservative 0; Mismatches 96; Indels 1; Gaps 1;
4 GGCAACACATGACATTTACAGAGCTATGAGA-ATGCTTCTGAAATTTGAGTTGCTAGCTC 62
15 GACTAACGAGAGCTTTACAGCCGTCGAGAGAGCGCTTCTGCAATTTGAGTTGCTAGCTC 74
63 TTGGGGTGCTATGTTTCTGCTTTCTGCTAGAAAATCCCATGAATAGACTGGTGGCAG 122
75 TTGGAGCTGCTAGCTGTATGCCATCCACGGAATTTCCACAAGTCGATTGGTGAAG 134
123 AGACCTTGACATGCTCTCCACTCATCGAACTGGCTGATAGCGGATGGGAACCTGATGA 182
135 AGACCTTGGCACTGCTTCTACTCGTGAACCTGCTGATAGGCAATGAGACTCTGAGGA 194
183 TTCCTACTCTCTGAAATAAATAACCAAACTGTCATTAAGAAAGTTTTCAGGGTATAG 242
195 TTCCTGTTCCGTGATACATAAATAACCAAACTGTCATGAGAAATCTTTCAGGGAATAT 254
243 ACACATGAGAACCAAACTGCCCGGAGGCTGTGGATTAACATTTCCAAAACCTTGT 302
255 GCACATGGAGAGTCAAACTGTGCAAGGGGGTACTGTGGAAGAGCTATTCAAAAACCTTGT 314

QY 303 CTTTATTAAGAACACATAGAGCCCAAAAAAGGTGTGTCAGGAAGATGGAGAG 362
Db 315 CTTTATTAAGAACATACATTCAGCGCCCAAAAAAGCGTGTGAGAAAGACGGAGAG 374
QY 363 TGACAAAAGTTCCTAGACTACCTGCAAGTATTCTTGTGTGTAATAAACACCGAGTGGACAC 422
Db 375 TAAACCAATTCTTAACACTACCTGCAAGAGTTTCTTGTGTGTAATGAACACCGAGTGGATAA 434
QY 423 CGGAAAGTTGAGAACAAACCGGCT 446
Db 435 TATAAAGTTGAGACTAAACTGGTT 458
RESULT 13
CE331159 622 bp DNA linear GSS 26-SEP-2003
LOCUS tigr-gss-dog-17000333986568 Dog Library Canis familiaris genomic,
DEFINITION genomic survey sequence.
ACCESSION CE331159
VERSION CE331159.1 GI:36147469
KEYWORDS GSS
SOURCE Canis familiaris (dog)
ORGANISM Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE 1 (bases 1 to 622)
AUTHORS Kirkness,E.F., Bafna,V., Halpern,A.L., Levy,S., Remington,K.,
Rusch,D.B., Delcher,A.L., Pop,M., Wang,W., Fraser,C.M. and
Venter,J.C.
TITLE The dog genome: survey sequencing and comparative analysis
JOURNAL Science 301 (5641), 1898-1903 (2003)
MEDLINE 22875432
PubMed 14512627
COMMENT Contact: Kirkness EF
The Institute for Genomic Research
Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
Rockville, MD 20850, USA
Tel: 301-838-0200
Fax: 301-838-0208
Email: ekirknes@tigr.org
Class: shotgun.
Location/Qualifiers
1. 622
/organism="Canis familiaris"
/mol_type="genomic DNA"
/strains="Standard Poodle"
/db_xref="taxon:9615"
/clone_lib="Dog Library"
/note="Site 1: BstXI; Libraries were prepared from
peripheral blood"

ORIGIN
Query Match 45.5%; Score 277.8; DB 29; Length 622;
Best Local Similarity 99.3%; Pred. No. 8.6e-58;
Matches 279; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
330 AAAAAAAGGTGTGTCAGGAGAAAGTGGAGATGAGATGACAAAGTTCCTAGACTACCTGCAAG 389
284 AACAGAAAGGTGTGTCAGGAGAAAGTGGAGATGAGATGACAAAGTTCCTAGACTACCTGCAAG 343
390 TATTTCTTGGTGTATAAACCACCGAGTGGACACCGGAAAGTTGAGAACACCGGCTTAT 449
344 TATTTCTTGGTGTATAAACCACCGAGTGGACACCGGAAAGTTGAGAACACCGGCTTAT 403
450 TGTAGTGAAGATTTTGGAGAGAAATGTTTGGCGATGAGATGAGATGAGGCGCAACCAAC 509
404 TGTAGTGAAGATTTTGGAGAGAAATGTTTGGCGATGAGATGAGATGAGGCGCAACCAAC 463
510 AGTAGGGCTTAATGCCAGTATTAAGCTTCAGAGCAAAAGTAAATATTTTCAGGCAT 569
464 AGTAGGGCTTAATGCCAGTATTAAGCTTCAGAGCAAAAGTAAATATTTTCAGGCAT 523
570 CCTACTACTTTATCATCTTCACACAGATGAAATATTTTGGAG 610

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Db 524 CCTACTATTATACACTTCACACAGATGAATATATTGAG 564
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RESULT 14
AY412021 405 bp DNA linear GSS 16-DEC-2003
LOCUS Pan troglodytes IL5 gene, VIRTUAL TRANSCRIPT, partial sequence,
DEFINITION genomic survey sequence.
ACCESSION AY412021
VERSION AY412021.1 GI:39767986
KEYWORDS GSS.
SOURCE Pan troglodytes (chimpanzee)
ORGANISM Pan troglodytes
REFERENCE 1 (bases 1 to 405)
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Adams, M.D. and Cargill, M.
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 405)
AUTHORS Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Adams, M.D. and Cargill, M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment.

FEATURES
Source 1..405
/organism="Pan troglodytes"
/mol_type="Genomic DNA"
/db_xref="taxon:9598"
Gene <1..>405
/gene="IL5"
/locus_tag="HCM4418"

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Best Local Similarity 79.8%; Pred. No. 2.1e-57;
Matches 323; Conservative 0; Mismatches 82; Indels 0; Gaps 0;
QY 29 ATGAGATGCTTCGATTTGAGTTTCTAGCTCTTGGGGCTGCCCTATGTTCTGCCTT 88
DB 1 ATGAGATGCTTCGCAATTTGAGTTTCTAGCTCTTGGAGCTGCCCTAGCTATGCCATC 60
QY 89 GCTGTAGAAATCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCATCAT 148
DB 61 CCCACAGAAATCCCACAAGTGCATTGGTGAAGAGACCTTGGCACTGCTTTCTACTCAT 120
QY 149 CGACTTGGCTGATAGCGGATGGGAACCTGATGTTCTCTACTCTGAAATAAATATCAC 208
DB 121 CGAACTCTGCTAATAGCCATAGACTCTGAGGATTCCTTCTGTATATAAAATCAC 180
QY 209 CAATGTGCTAATGAAGATTTTTCAGGGTATAGACACATTTGAAGAACCAAACTGCCAC 268
DB 181 CAACNNNGCACTGAAGAAATCTTTTCAGGAAATAGGCACACTGGAGAGTCAAACTGTGCA 240
QY 269 GGGAGGCTGTGGTAATCACTATTCCTTCTTAAATAAGAACACATAGAGCGC 328
DB 241 GGGGGTATCTGGGAAGACTATTCAAAACCTTCTCTTAAATAAGAAATACATTTGANGGC 300
QY 329 CAAAAAAGGCTGTGCAGAGAAAGATGGAGAGTGCACAAAGTTCCTAGACTACCTGCA 388
DB 301 CAAAAAAGGCTGTGCAGAGAAAGATGGAGAGTGCACAAATTCCTAGACTACCTGCA 360

QY 389 GTATTTCTTGTGTATAAAACACCGAGTGGACACCGGAAAGTTGA 433
DB 361 GAGTTTCTTGTGTATAACACACCGAGTGGATATAGAAAGTTGA 405
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RESULT 15
AY412022 399 bp DNA linear GSS 16-DEC-2003
LOCUS Mus musculus IL5 gene, VIRTUAL TRANSCRIPT, partial sequence,
DEFINITION genomic survey sequence.
ACCESSION AY412022
VERSION AY412022.1 GI:39767987
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 399)
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Adams, M.D. and Cargill, M.
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 399)
AUTHORS Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Adams, M.D. and Cargill, M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment.

FEATURES
Source 1..399
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/mol_type="Genomic DNA"
/db_xref="taxon:10090"
Gene <1..>399
/gene="IL5"
/locus_tag="HCM4418"

ORIGIN
Query Match 32.0%; Score 195; DB 29; Length 399;
Best Local Similarity 66.7%; Pred. No. 1.9e-37;
Matches 268; Conservative 0; Mismatches 128; Indels 6; Gaps 1;
QY 32 AGAATGCTTCGATTTGAGTTTCTAGCTCTTGGGGCTGCCCTATGTTCTGCCTTGTCT 91
DB 4 AGAATGCTTCGCAATTTGAGTTTCTAGCTCTAG-----CTGTGCTGGGCACTGCC 57
QY 92 GTAGAAATCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCATCATCGA 151
DB 58 ATGAGATTTCCATGAGCACAGTGGTGAAGAGACCTTGACACAGCTGTCCGCTCACCGA 117
QY 152 ACTTGGCTGATAGCGGATGGGAACCTGATGTTCTCTACTCTGAAATAATAATCACCA 211
DB 118 GCTCTGTGACAGCAATGAGNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 177
QY 212 CTGTGCATTAAGAAGTTTTCAGGGTATAGACACATTTGAAGAACCAAACTGCCACGG 271
DB 178 CTATGCAITGGAGAAATCTTTTCAGGGGCTAGACATCTAGAAATCAACTGCTCCGTGG 237
QY 272 GAGGCTGTGGATAAATCTTCCAAAATCTGCTTTTAAATAAGAACACATAGAGCGCAA 331
DB 238 -GGTACTGTGGAATATGCTATTCCAAAACCTGTCTTAAATAAGAAATACATTTGACGCG 297
QY 332 AAAAAAAGGCTGTGCAGGAGAAAGATGGAGAGTGCACAAAGTTCCTAGACTACCTGCAAGTA 391
DB 298 AAGAGAGTGTGGCAGGAGAGACGAGGAGCGAGGAGCGAGGAGTTCCTTGGATTACCTGCAAGAG 357

Qy 392 TTCTTGGTGTAAACACCGAGTGGACACCGGAAAGTTGA 433
Db 358 TTCTTGGTGTAGTACAGAGTGGCAATGGAAGGCTGA 399

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Job time : 2055.32 secs

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OM nucleic - nucleic search, using sw model

Run on: August 30, 2004, 20:51:08 ; Search time 54.4245 Seconds
(without alignments)
6219.989 Million cell updates/sec

Title: US-10-787-382-4
Perfect score: 610
Sequence: 1 caaggaacactgaacatt.....acagatgaatatattgag 610

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0.

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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5: /cgn2_6/ptodata/2/ina/PCTUS COMB.seq.*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	610	100.0	610	4	US-09-322-409-80
2	610	100.0	610	4	US-09-322-409-82
3	610	100.0	610	4	US-09-451-527-80
4	610	100.0	610	4	US-09-451-527-82
5	402	65.9	402	4	US-09-322-409-83
6	402	65.9	402	4	US-09-322-409-84
7	402	65.9	402	4	US-09-451-527-83
8	402	65.9	402	4	US-09-451-527-84
9	401.8	65.9	405	4	US-09-371-615A-1
10	379	62.1	816	3	US-09-079-839-2
11	377.4	61.9	816	4	US-09-023-655-1236
12	345	56.6	345	4	US-09-322-409-85
13	345	56.6	345	4	US-09-322-409-87
14	345	56.6	345	4	US-09-451-527-85
15	345	56.6	345	4	US-09-451-527-87
16	217.6	35.7	1534	3	US-08-629-643A-4
17	217.6	35.7	1534	3	US-09-155-884-4
18	207.4	34.0	377	4	US-09-180-864-1
19	152.4	25.0	3230	3	US-09-280-799-78
20	152.4	25.0	3230	3	US-09-280-799-78
21	90.6	14.9	6727	3	US-08-629-643A-5
22	90.6	14.9	6727	3	US-09-280-799-1
23	90.6	14.9	6727	3	US-09-155-884-5
24	58.2	9.5	7218	1	US-08-232-463-14
25	42.2	6.9	47	1	US-08-466-852-2
26	37.2	6.1	399	4	US-09-621-976-8976
27	34.4	5.6	4843	3	US-08-986-485-1

ALIGNMENTS

RESULT 1

US-09-322-409-80
; Sequence 80, Application US/09322409
; Patent No. 6471957
; GENERAL INFORMATION:
; APPLICANT: Sim, Gek-Kee
; APPLICANT: Yang, Shumin
; APPLICANT: Dreitz, Matthew J.
; APPLICANT: Wonderling, Ramani S.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF
; FILE REFERENCE: IM-2-Cl
; CURRENT APPLICATION NUMBER: US/09/322,409
; EARLIER FILING DATE: 1999-05-28
; EARLIER APPLICATION NUMBER: 60/087,306
; EARLIER FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 154
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 80
; LENGTH: 610
; TYPE: DNA
; ORGANISM: Canis familiaris
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (29)..(430)
US-09-322-409-80

Query Match 100.0%; Score 610; DB 4; Length 610;
Best Local Similarity 100.0%; Pred. No. 3.1e-187;
Matches 610; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	CAAGGCAACACTGACATTTTCAGAGCTATGAGATGCTTCTGATTTGAGTTTCTGCTAGC	60
DB	1	CAAGGCAACACTGACATTTTCAGAGCTATGAGATGCTTCTGATTTGAGTTTCTGCTAGC	60
QY	61	TCTTGGGGCTGCTATGTTTCTGCTTTCCTGCTAGAAAATCCATGAATAGACTGGTGGC	120
DB	61	TCTTGGGGCTGCTATGTTTCTGCTTTCCTGCTAGAAAATCCATGAATAGACTGGTGGC	120
QY	121	AGAGACCTTGAACACTGCTTCTCCATCAGCAATTTGGCTGATAGCGGATGGGAACCTGAT	180
DB	121	AGAGACCTTGAACACTGCTTCTCCATCAGCAATTTGGCTGATAGCGGATGGGAACCTGAT	180
QY	181	GATTCCTCTCTCTGAAAATAAAAATCAACAACCTGTGCATTAAGAAGTTTTTCAGGGTAT	240
DB	181	GATTCCTCTCTCTGAAAATAAAAATCAACAACCTGTGCATTAAGAAGTTTTTCAGGGTAT	240
QY	241	AGACACATTGAAGAACCAAACTGCCACGGGAGGCTGTGGATAAACTATTCCAAAACCTT	300
DB	241	AGACACATTGAAGAACCAAACTGCCACGGGAGGCTGTGGATAAACTATTCCAAAACCTT	300

QY 301 GTCTTTAATAAAGAACACATAGAGCGCCAAAAAAGGTGTGTCAGGAGAAAGATGGAG 360
DB 301 GTCTTTAATAAAGAACACATAGAGCGCCAAAAAAGGTGTGTCAGGAGAAAGATGGAG 360
QY 361 AGTGACAAAGTTCCTAGACTACCTGCAAGTATTTCTTGGTGTATTAACACCCAGTGGAC 420
DB 361 AGTGACAAAGTTCCTAGACTACCTGCAAGTATTTCTTGGTGTATTAACACCCAGTGGAC 420
QY 421 ACCGGAAGTTGAGAACAAACCCGGCTTATTGTAGTGAAGATTTTGGAGAAAGATGGTT 480
DB 421 ACCGGAAGTTGAGAACAAACCCGGCTTATTGTAGTGAAGATTTTGGAGAAAGATGGTT 480
QY 481 TTTGGCGATGAGATGAGGCGCAACCAACAGTAGGGACTTAATGGCCAGTATTAACCTAAGC 540
DB 481 TTTGGCGATGAGATGAGGCGCAACCAACAGTAGGGACTTAATGGCCAGTATTAACCTAAGC 540
QY 541 TTCAGAGACAAAGTAAATATTTTCAGGCATCCTACTCTTATCATTTCACACAGATGAAA 600
DB 541 TTCAGAGACAAAGTAAATATTTTCAGGCATCCTACTACTTTATCATTTCACACAGATGAAA 600
QY 601 TATATTGGAG 610
DB 601 TATATTGGAG 610

RESULT 2

US-09-322-409-82/c
; Sequence 82, Application US/09322409
; Patent No. 6471957
; GENERAL INFORMATION:
; APPLICANT: Sim, Gek-kee
; APPLICANT: Yang, Shumin
; APPLICANT: Dretz, Matthew J.
; APPLICANT: Wonderling, Ramani S.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF
; FILE REFERENCE: IM-2-C1
; CURRENT APPLICATION NUMBER: US/09/322,409
; CURRENT FILING DATE: 1999-05-28
; EARLIER APPLICATION NUMBER: 60/087,306
; EARLIER FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 154
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 82
; LENGTH: 610
; TYPE: DNA
; ORGANISM: Canis familiaris
US-09-322-409-82

Query Match 100.0%; Score 610; DB 4; Length 610;
Best Local Similarity 100.0%; Pred. No. 3.1e-187;
Matches 610; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAAGGCAAACTGACATTCAGAGCTATGAGATGCTTCTGAATTTGAGTTTGTAGC 60
DB 610 CAAGGCAAACTGACATTCAGAGCTATGAGATGCTTCTGAATTTGAGTTTGTAGC 551
QY 61 TCTTGGGGCTGCCTATGTTTCTGCTTGTGTAAGAAATCCCATGAATAGACTGTGGC 120
DB 550 TCTTGGGGCTGCCTATGTTTCTGCTTGTGTAAGAAATCCCATGAATAGACTGTGGC 491
QY 121 AGAGACCTTGACACTGCTTCCACTCATCGAACTTGGCTGATAGGCGATGGAACTGTAT 180
DB 490 AGAGACCTTGACACTGCTTCCACTCATCGAACTTGGCTGATAGGCGATGGAACTGTAT 431
QY 181 GATTCTTACTCTTGAATAAATAACCAACCTGTCATTAAGAGATTTTTCAGGGTAT 240
DB 430 GATTCTTACTCTTGAATAAATAAATAACCAACCTGTCATTAAGAGATTTTTCAGGGTAT 371
QY 241 AGACATTTGAAGAACCAAACTGCCCAACCGGGAGGCTGTGGATAAACTATTTCCAAAACCT 300
DB 370 AGACATTTGAAGAACCAAACTGCCCAACCGGGAGGCTGTGGATAAACTATTTCCAAAACCT 311

QY 301 GTCTTTAATAAAGAACACATAGAGCGCCAAAAAAGGTGTGTCAGGAGAAAGATGGAG 360
DB 310 GTCTTTAATAAAGAACACATAGAGCGCCAAAAAAGGTGTGTCAGGAGAAAGATGGAG 251
QY 361 AGTGACAAAGTTCCTAGACTACCTGCAAGTATTTCTTGGTGTATTAACACCCAGTGGAC 420
DB 250 AGTGACAAAGTTCCTAGACTACCTGCAAGTATTTCTTGGTGTATTAACACCCAGTGGAC 191
QY 421 ACCGGAAGTTGAGAACAAACCCGGCTTATTGTAGTGAAGATTTTGGAGAAAGATGGTT 480
DB 190 ACCGGAAGTTGAGAACAAACCCGGCTTATTGTAGTGAAGATTTTGGAGAAAGATGGTT 131
QY 481 TTTGGCGATGAGATGAGGCGCAACCAACAGTAGGGACTTAATGGCCAGTATTAACCTAAGC 540
DB 130 TTTGGCGATGAGATGAGGCGCAACCAACAGTAGGGACTTAATGGCCAGTATTAACCTAAGC 71
QY 541 TTCAGAGACAAAGTAAATATTTTCAGGCATCCTACTCTTATCATTTCACACAGATGAAA 600
DB 70 TTCAGAGACAAAGTAAATATTTTCAGGCATCCTACTACTTTATCATTTCACACAGATGAAA 11
QY 601 TATATTGGAG 610
DB 10 TATATTGGAG 1

RESULT 3

US-09-451-527-80
; Sequence 80, Application US/09451527
; Patent No. 6482403
; GENERAL INFORMATION:
; APPLICANT: Sim, Gek-kee
; APPLICANT: Yang, Shumin
; APPLICANT: Dretz, Matthew J.
; APPLICANT: Wonderling, Ramani S.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF
; FILE REFERENCE: IM-2-C2
; CURRENT APPLICATION NUMBER: US/09/451,527
; CURRENT FILING DATE: 1999-12-01
; EARLIER APPLICATION NUMBER: 09/322,409
; EARLIER FILING DATE: 1999-05-28
; EARLIER APPLICATION NUMBER: 60/087,306
; EARLIER FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 80
; LENGTH: 610
; TYPE: DNA
; ORGANISM: Canis familiaris
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (29)..(430)
US-09-451-527-80

Query Match 100.0%; Score 610; DB 4; Length 610;
Best Local Similarity 100.0%; Pred. No. 3.1e-187;
Matches 610; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAAGGCAAACTGACATTCAGAGCTATGAGATGCTTCTGAATTTGAGTTTGTAGC 60
DB 1 CAAGGCAAACTGACATTCAGAGCTATGAGATGCTTCTGAATTTGAGTTTGTAGC 60
QY 61 TCTTGGGGCTGCCTATGTTTCTGCTTGTGTAAGAAATCCCATGAATAGACTGTGGC 120
DB 61 TCTTGGGGCTGCCTATGTTTCTGCTTGTGTAAGAAATCCCATGAATAGACTGTGGC 120
QY 121 AGAGACCTTGACACTGCTTCCACTCATCGAACTTGGCTGATAGGCGATGGAACTGTAT 180
DB 121 AGAGACCTTGACACTGCTTCCACTCATCGAACTTGGCTGATAGGCGATGGAACTGTAT 180
QY 181 GATTCTTACTCTTGAATAAATAAATAACCAACCTGTCATTAAGAGATTTTTCAGGGTAT 240

Db 181 GATTCCTACTCTCGAAAAATAAAATCACCACCTGTGCAATTAAGAAGTTTTTCAGGGTAT 240
Qy 241 AGACACATTTGAAGAACCAAACTGCCACGGGGAGGCTGTGGATAAATTTCCAAAACCTT 300
Db 241 AGACACATTTGAAGAACCAAACTGCCACGGGGAGGCTGTGGATAAATTTCCAAAACCTT 300
Qy 301 GTCTTTAATAAAGAACACATAGAGCGCCCAAAAAGAGGTGTGCAGGAGAAAGATGGAG 360
Db 301 GTCTTTAATAAAGAACACATAGAGCGCCCAAAAAGAGGTGTGCAGGAGAAAGATGGAG 360
Qy 361 AGTGACAAAAGTCTCTAGACTACCTGCAAGTATTTCTTGGTGTAAATAAACCACCGAGTGGAC 420
Db 361 AGTGACAAAAGTCTCTAGACTACCTGCAAGTATTTCTTGGTGTAAATAAACCACCGAGTGGAC 420
Qy 421 ACCGGAAGTTGAGAACCAAAACCGGCTTATTTGTAGTGAAGATTTTGGAGAAGATGGTTT 480
Db 421 ACCGGAAGTTGAGAACCAAAACCGGCTTATTTGTAGTGAAGATTTTGGAGAAGATGGTTT 480
Qy 481 TTTGGCGATCAGATGAGGCGCCCAACCAAGTAGGACTTAAATGGCCAGTATAACTAAGC 540
Db 481 TTTGGCGATCAGATGAGGCGCCCAACCAAGTAGGACTTAAATGGCCAGTATAACTAAGC 540
Qy 541 TTCAGAGACAAAAGTAAATATTTTCCAGCATCCTACTACTTTATCATTTCACAGATGAAA 600
Db 541 TTCAGAGACAAAAGTAAATATTTTCCAGCATCCTACTACTTTATCATTTCACAGATGAAA 600
Qy 601 TATATTTGAG 610
Db 601 TATATTTGAG 610

RESULT 4
US-09-451-527-82/c
; Sequence 82, Application US/09451527
; Patent No. 6482403
; GENERAL INFORMATION:
; APPLICANT: Yang, Gek-Ke
; APPLICANT: Yang, Shumin
; APPLICANT: Dreitz, Matthew J.
; APPLICANT: Wondorling, Ramani S.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; FILE REFERENCE: IM-2-C2
; CURRENT APPLICATION NUMBER: US/09/451.527
; EARLIER FILING DATE: 1999-12-01
; EARLIER FILING DATE: 1999-05-28
; EARLIER FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 82
; LENGTH: 610
; TYPE: DNA
; ORGANISM: Canis familiaris
US-09-451-527-82

Query Match 100.0%; Score 610; DB 4; Length 610;
Best Local Similarity 100.0%; Pred. No. 3.1e-187;
Matches 610; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CAAGGCAAACTGAACTTTGAGAGCTATGAGATGCTTCTGAAATTTGATTTGCTAGC 60
Db 610 CAAGGCAAACTGAACTTTGAGAGCTATGAGATGCTTCTGAAATTTGATTTGCTAGC 551
Qy 61 TCTTTGGGCTGCTCTATGCTTCTGCTTTGCTGTAGAAAATCCCAATGATAGCTTGGTGGC 120
Db 550 TCTTTGGGCTGCTCTATGCTTCTGCTTTGCTGTAGAAAATCCCAATGATAGCTTGGTGGC 491
Qy 121 AGAGACCTTGACCTGCTCTCCACTCATPCGAATTTGGCTGATGGCGATGGAACTCTGAT 180
Db 490 AGAGACCTTGACCTGCTCTCCACTCATPCGAATTTGGCTGATGGCGATGGAACTCTGAT 431

Qy 181 GATTCCTACTCTCGAAAAATAAAATCACCACCTGTGCAATTAAGAAGTTTTTCAGGGTAT 240
Db 430 GATTCCTACTCTCGAAAAATAAAATCACCACCTGTGCAATTAAGAAGTTTTTCAGGGTAT 371
Qy 241 AGACACATTTGAAGAACCAAACTGCCACGGGGAGGCTGTGGATAAATTTCCAAAACCTT 300
Db 370 AGACACATTTGAAGAACCAAACTGCCACGGGGAGGCTGTGGATAAATTTCCAAAACCTT 311
Qy 301 GTCTTTAATAAAGAACACATAGAGCGCCCAAAAAGAGGTGTGCAGGAGAAAGATGGAG 360
Db 310 GTCTTTAATAAAGAACACATAGAGCGCCCAAAAAGAGGTGTGCAGGAGAAAGATGGAG 251
Qy 361 AGTGACAAAAGTCTCTAGACTACCTGCAAGTATTTCTTGGTGTAAATAAACCACCGAGTGGAC 420
Db 250 AGTGACAAAAGTCTCTAGACTACCTGCAAGTATTTCTTGGTGTAAATAAACCACCGAGTGGAC 191
Qy 421 ACCGGAAGTTGAGAACCAAAACCGGCTTATTTGTAGTGAAGATTTTGGAGAAGATGGTTT 480
Db 190 ACCGGAAGTTGAGAACCAAAACCGGCTTATTTGTAGTGAAGATTTTGGAGAAGATGGTTT 131
Qy 481 TTTGGCGATCAGATGAGGCGCCCAACCAAGTAGGACTTAAATGGCCAGTATAACTAAGC 540
Db 130 TTTGGCGATCAGATGAGGCGCCCAACCAAGTAGGACTTAAATGGCCAGTATAACTAAGC 71
Qy 541 TTCAGAGACAAAAGTAAATATTTTCCAGCATCCTACTACTTTATCATTTCACAGATGAAA 600
Db 70 TTCAGAGACAAAAGTAAATATTTTCCAGCATCCTACTACTTTATCATTTCACAGATGAAA 11
Qy 601 TATATTTGAG 610
Db 10 TATATTTGAG 1

RESULT 5
US-09-322-409-83
; Sequence 83, Application US/09322409
; Patent No. 6471957
; GENERAL INFORMATION:
; APPLICANT: Yang, Gek-Ke
; APPLICANT: Yang, Shumin
; APPLICANT: Dreitz, Matthew J.
; APPLICANT: Wondorling, Ramani S.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; FILE REFERENCE: IM-2-C1
; CURRENT APPLICATION NUMBER: US/09/322.409
; EARLIER FILING DATE: 1999-05-28
; EARLIER FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 154
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 83
; LENGTH: 402
; TYPE: DNA
; ORGANISM: Canis familiaris
US-09-322-409-83

Query Match 65.9%; Score 402; DB 4; Length 402;
Best Local Similarity 100.0%; Pred. No. 4.1e-120;
Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 29 ATGAGATGCTTCTGAAATTTGAGTTTGTAGCTCTTGGGCTGCTCTATGTTTCTGCTTT 88
Db 1 ATGAGATGCTTCTGAAATTTGAGTTTGTAGCTCTTGGGCTGCTCTATGTTTCTGCTTT 60
Qy 89 GCTGTAGAAAATCCCAATGATAGACTGGTGGCAGAGACTTGACACTGCTCTCCACTCAT 148
Db 61 GCTGTAGAAAATCCCAATGATAGACTGGTGGCAGAGACTTGACACTGCTCTCCACTCAT 120
Qy 149 CGAAGCTTGCTGATAGGCGATGGGAACCTGATGATCTCTACTCTCGAAAATAAATAATCAC 208
Db 121 CGAAGCTTGCTGATAGGCGATGGGAACCTGATGATCTCTACTCTCGAAAATAAATAATCAC 180

```

RESULT 7
US-09-451-527-83
; Sequence 83, Application US/09451527
; Patent No. 6482403
; GENERAL INFORMATION:
; APPLICANT: Sim, Gek-kee
; APPLICANT: Yang, Shumin
; APPLICANT: Wongderling, Ramani S.
; APPLICANT: Dreitz, Matthew J.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF
; FILE REFERENCE: IM-2-C2
; CURRENT APPLICATION NUMBER: US/09/451,527
; CURRENT FILING DATE: 1999-12-01
; EARLIER APPLICATION NUMBER: 09/322,409
; EARLIER FILING DATE: 1999-05-28
; EARLIER APPLICATION NUMBER: 60/087,306
; EARLIER FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 83
; LENGTH: 402
; TYPE: DNA
; ORGANISM: Canis familiaris
US-09-451-527-83

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US-09-322-409-84/c

	Query Match	65.98;	Score 402;	DB 4;	Length 402;
	Best Local Similarity	100.0%;	Pred. No. 4.1e-120;		
	Matches 402;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0
QY	29	ATGGAATGCTTCGAATTTGAGTTTGTCTAGCTCTTGGGGCTGCCTATGTTTCTGCCCTTT	88		
DB	1	ATGGAATGCTTCGAATTTGAGTTTGTCTAGCTCTTGGGGCTGCCTATGTTTCTGCCCTTT	60		
QY	89	GCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACTCAT	148		
DB	61	GCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACTCAT	120		
QY	149	CGAATCTGGCTGATAGCGATGGGABCCCTGATCTTCTTACCTCTGAGAAATGAAAATCAT	208		

Db	121	CGAACTTGGCTGATAGCGGATGGGAACCTGATGATTCCTTCTGAAATAAATAAC	CAC	180
QY	209	CAACTGTGCATTAAAGAAGTTTTTTCAGGGTATAGACACATTGAAGAACCAAACTGCCAC	268	
Db	181	CAACTGTGCATTAAAGAAGTTTTTTCAGGGTATAGACACATTGAAGAACCAAACTGCCAC	240	
QY	269	GGGAGAGCTGTGGATAAAGCTATTTCCTAAACTTGTCTTTTAAATAAAGAACAACATAGAGCGC	328	
Db	241	GGGAGAGCTGTGGATAAAGCTATTTCCTAAACTTGTCTTTTAAATAAAGAACAACATAGAGCGC	300	
QY	329	CAAAAAAAGAGTGTGCAGAGAGAAAGATGGAGAGTGACAAAGTTCCTAGACTACCTGCAA	388	
Db	301	CAAAAAAAGAGTGTGCAGAGAGAAAGATGGAGAGTGACAAAGTTCCTAGACTACCTGCAA	360	
QY	389	GTATTTCTTGGTGTATATAACACCGAGTGGACACCGGAAAGT	430	
Db	361	GTATTTCTTGGTGTATATAACACCGAGTGGACACCGGAAAGT	402	

RESULT 8
 US-09-451-527-84/c
 ; Sequence 84, Application US/09451527
 ; Patent No. 6482403
 ; GENERAL INFORMATION:
 ; APPLICANT: Sim, Gek-Kee
 ; APPLICANT: Yang, Shumin
 ; APPLICANT: Dreitz, Matthew J.
 ; APPLICANT: Wonderling, Ramani S.
 ; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
 ; TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF
 ; FILE REFERENCE: IN-2-C2
 ; CURRENT APPLICATION NUMBER: US/09/451-527

Qy	89	GCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACACTGCTCTCCACTCAT	144
Db	61	GCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACACTGCTCTCCACTCAT	120
Qy	149	CGAACTTGGCTGATAGCGCATGGGAACCTGATGATTCTCTACTCTCTGAAAATATAAATAC	208
Db	121	CGAACTTGGCTGATAGCGCATGGGAACCTGATGATTCTCTACTCTCTGAAAATATAAATAC	180
Qy	209	CAACTGTGCATTAAGAAGTTTTTCAGGGTATAGACACATTTGAAGAACCAAACTGCCAC	268
Db	181	CAACTGTGCATTAAGAAGTTTTTCAGGGTATAGACACATTTGAAGAACCAAACTGCCAC	240
Qy	269	GGGGAGCTGTGGATAAACTATTTCAAAACTTTGTTCTTTAATAAAGAACACATAGAGCGC	328
Db	241	GGGGAGCTGTGGATAAACTATTTCAAAACTTTGTTCTTTAATAAAGAACACATAGAGCGC	300
Qy	329	CAAAAAAAGGTGTCGAGAGAAAGATGGAGAGTGACAAAGTCTCTAGACTACCTGCAA	388
Db	301	CAAAAAAAGGTGTCGAGAGAAAGATGGAGAGTGACAAAGTCTCTAGACTACCTGCAA	360
Qy	389	GTATTTCTTGGTCTAATAAACACCGAGTGGACACCGGAAAGTTGA	433
Db	361	GTATTTCTTGGTCTAATAAACACCGAGTGGACATGGAAGTTGA	405
RESULT 10			
US-09-079-839-2			
; Sequence 2, Application US/09079839			
; Patent No. 6048726			
; GENERAL INFORMATION:			
; APPLICANT: Weltman, Joel K.			
; APPLICANT: Karim, Aftab S.			
; TITLE OF INVENTION: INHIBITION OF EOSINOPHILIC INFLAMMATION			
; FILE REFERENCE: 09998/002001			
; CURRENT APPLICATION NUMBER: US/09/079,839			
; NUMBER OF SEQ ID NOS: 2			
; SOFTWARE: FastSeq for Windows Version 3.0			
; SEQ ID NO 2			
; LENGTH: 816			
; TYPE: DNA			
; ORGANISM: Homo sapiens			
US-09-079-839-2			
Query Match 62.1%; Score 379; DB 3; Length 816;			
Best Local Similarity 79.1%; Pred. No. 1.6e-112;			
Matches 463; Conservative 0; Mismatches 120; Indels 2; Gaps 1			
Qy	2	AAGCAAAACACTGAACTTTCAGAGCTATGAGAAATGCTTCTGAATTTGAGTTGCTAGCT	61
Db	18	AAGCAAAACAGCAGAACGTTTCAGAGCCATGAGAGTCTTCTCATTTGAGTTGCTAGCT	77
Qy	62	CTTGGGCTGCTCTATGTTTCTGCTTTGCTGTAGAAAATCCCATGAATAGACTGGTGGCA	121
Db	78	CTTGGAGCTGCTCTACGTTATGCCATCCCAACAGAAATCCCAAGTGCAATGGTGGAA	137
Qy	122	GAGACCTTGACACTGCTCTCCACTATCGAACTTGGCTGATAGGGGATGGGAACCTGATG	181
Db	138	GAGACCTTGACACTGCTCTCTACTCATCGAACTTCTGCTGATGACCAATGAGACTCTGAGG	197
Qy	182	ATTCTCTACTCCTGAAATATAAATACCAACTGTGCATTAAGAAAGTTTTTCAGGGTATA	241
Db	198	ATTCTCTGTTCTCTGATATAAATACCAACTGTGCATGAGAAATCTTTTCAGGAATA	257
Qy	242	GACACATTTGAAGAACCAAACTGCCACGGGGGCTGTGGATAAATCTATTCAAAACTTG	301
Db	258	GGCACACTGGAGAGTCAAACTGTGCAAGGGGTACTGTGAAAAGACTATTCAAAACTTG	317
Qy	302	TCCTTAATAAAGAACACATAGAGCCCAAAAAAAGGTGTCGAGAGAAAGATGGAGA	361
Db	318	TCCTTAATAAAGAAATACATTTGACGCCCAAAAAAAGGTGTCGAGAGAAAGATGGAGA	377
Qy	362	GTGACAAAGTTCTGACACTACCTGCAAGTATTTCTTGGTGTATAAACAACCGAGTGGCA	421

Db 378 GTAACCAATCTCTAGACTACTCTCAAGAGTTCTTGGTGTAATGAACACCGAGTGGATA 437
 Qy 422 CCGAAAGTTGAGAACAAACCGGCTTATTGTAGTGAAGAATTTTGGAGAGAATG--GTT 479
 Db 438 ATAGAAAGTTGAGACTAAACTGGTTTGTTCAGCCAAAGATTTTGGAGGAGAGGACATT 497
 Qy 480 TTTTGGCGATCAGATCAGGGCCCAACCAACAGTAGGAGCTTAATGCCAGTAACTAAG 539
 Db 498 TTACTGAGTGAGATGAGGCCCAAGAAAGAGTCAGGCCCTTAATTTCAATATAATTTAA 557
 Qy 540 CTTGAGAGCAAAATAAATTTTTCAGGCATCCTACTACTTATCA 584
 Db 558 CTTGAGAGGAAAGTAAATATTTTCAGGCATCTACTGACACTTTGCA 602

RESULT 11

US-09-023-655-1236
 ; Sequence 1236, Application US/09023655
 ; Patent No. 6607879

GENERAL INFORMATION:

APPLICANT: Cocks, Benjamin G.
 APPLICANT: Susan G. Stuart
 APPLICANT: Jeffrey J. Sellhauer
 TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
 TITLE OF INVENTION: EXPRESSION
 NUMBER OF SEQUENCES: 1508
 CORRESPONDENCE ADDRESS:

ADDRESSEE: INCYTE PHARMACEUTICALS, INC.

STREET: 3174. FORTER DRIVE

CITY: PALO ALTO

STATE: CALIFORNIA

COUNTRY: USA

ZIP: 94304

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/023,655

FILING DATE: HEREWITH

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Zeller, Karen J.

REGISTRATION NUMBER: 37,071

REFERENCE/DOCKET NUMBER: PA-0001 US

TELECOMMUNICATION INFORMATION:

TELEPHONE: (650) 855-0555

TELEFAX: (650) 845-4166

INFORMATION FOR SEQ ID NO: 1236:

SEQUENCE CHARACTERISTICS:

LENGTH: 816 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

IMMEDIATE SOURCE:

LIBRARY: GENEANK

CLONE: Q288309

US-09-023-655-1236

Query Match

Best Local Similarity 61.9%; Score 377.4; DB 4; Length 816;

Matches 462; Conservative 0; Mismatches 121; Indels 2; Gaps 1;

Qy 2 AAGCAACACTGACATTTTCAGAGCTATGAGATGCTTCTGATTTGAGTTTGCTAGCT 61

Db 18 AAGCAACAGCAGAACGTTTCAGAGCCATGAGGATGCTTCTGATTTGAGTTTGCTAGCT 77

Qy 62 CTTGGGGTGCTATGTTTCTGCGCTTCTCTAGAAAATCCCATGAATAGACTGCTGGCA 121
 Db 78 CTTGGAGCTGCTACGTTGATGCCATCCCAACAGAAATCCCAAGTGCATTTGGTGA 137
 Qy 122 GAGACCTTTGACACTGCTCTCCACTCATCGAACTTGGCTGATAGCGGATGGAACTGATG 181
 Db 138 GAGACCTTTGGCACCTGCTTCTACTCATCGAACTCTGCTGATAGCAATGAGACTCTCAGG 197
 Qy 182 ATTCTACTCTCTGAAAATAAAAAATCAACCACTGTGCATTAAGAAGTTTTTTCAGGTTATA 241
 Db 198 ATTCTGTCTCTGTACATAAAAAATCACCAACTGTGCATGAAGAAATCTTTTCAGGGAATA 257
 Qy 242 GACACATTGAAGAAACCAAACTGCCACGGGGAGGCTGTGGATAACTATTTCAAAACTTG 301
 Db 258 GGCACACTGGAGAGTCAAACTGTGCAAGGGGTACTGTGGAAGACTATTTCMAAACTTG 317
 Qy 302 TCTTTAATAAAGAAACACATAGAGCGCCAAAAAAGGTTGTGAGGAGAAAGATGGAGA 361
 Db 318 TCCTTAATAAAGAAATACATTGACGGCCAAAAAAGGTTGTGAGAGAAAGACGGAGA 377
 Qy 362 GTGACAAAGTTCTTAGACTACCTGCAAGTATTTCTCTGTGTGTAATAAACACCGAGTGGACA 421
 Db 378 GTAACCAATCTCTAGACTACTCTGCAAGAGTTTCTTGTGTAATGAACACCGAGTGGATA 437
 Qy 422 CCGAAAGTTGAGAACAAACCGGCTTATTGTAGTGAAGAATTTTGGAGAGAATG--GTT 479
 Db 438 ATAGAAAGTTGAGACTAAACTGGTTTGTTCAGCCAAAGATTTTGGAGGAGAGGACATT 497
 Qy 480 TTTTGGCGATCAGATGAGGCCCAACCAACAGTAGGAGCTTAATGGCCAGCTTAAG 539
 Db 498 TTACTGAGTGAGATGAGGCCCAAGAAAGAGTCAGGCCCTTAATTTTCAATATAATTTAA 557
 Qy 540 CTTGAGAGCAAAAGTAAATATTTTCAGGCATCCTACTACTTTATCA 584
 Db 558 CTTGAGAGGAAAGTAAATATTTTCAGGCATCTACTGACACTTTGCA 602

RESULT 12

US-09-322-409-85

; Sequence 85, Application US/09322409

; Patent No. 6471957

; GENERAL INFORMATION:

; APPLICANT: Sim, Gek-kee

; APPLICANT: Yang, Shumin

; APPLICANT: Dreitz, Matthew J.

; APPLICANT: Wonderling, Ramani S.

; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC

; FILE REFERENCE: IM-2-C1

; CURRENT APPLICATION NUMBER: US/09/322,409

; CURRENT FILING DATE: 1999-05-28

; EARLIER APPLICATION NUMBER: 60/087,306

; EARLIER FILING DATE: 1998-05-29

; NUMBER OF SEQ ID NOS: 154

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 85

; LENGTH: 345

; TYPE: DNA

; ORGANISM: Canis familiaris

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (1)..(345)

US-09-322-409-85

Query Match

Best Local Similarity 56.6%; Score 345; DB 4; Length 345;

Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 86 TTTCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACT 145

Db 1 TTTCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACT 60

Qy 146 CATCGAACTTGGCTGTAGTGGGAACTCTGATGATTCCTCTCTGAAAAATAAAAT 205

Db 61 CATCGAACTTGGCTGTAGTGGGAACTGATGATTTCTACTCTGTAATAAATAAAT 120
Qy 206 CACCAACTGTGCATTAAAGAAAGTTTTTCAGGGTATAGACACATTGAAGAACCAAACTGCC 265
Db 121 CACCAACTGTGCATTAAAGAAAGTTTTTCAGGGTATAGACACATTGAAGAACCAAACTGCC 180
Qy 266 CACGGGAGGCTGTGGATAAATCTTCCAAAACCTGTCTTTAATAAAGAACACATAGAG 325
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Db 241 CGCCAAAAAAGGTTGTCAGGAGAAAGATGGAGAGTGACAAAGTTCTCTAGACTACCTG 300
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Db 301 CAAGTATTCTTGGTGTAAATAAACACCGAGTGGACACCGGAAAGT 345

RESULT 13
US-09-322-409-87/c
; Sequence 87, Application US/09322409
; Patent No. 6471957
; GENERAL INFORMATION:
; APPLICANT: Sim, Gek-Kee
; APPLICANT: Yang, Shumin
; APPLICANT: Dreitz, Matthew J.
; APPLICANT: Wonderling, Ramani S.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; FILE REFERENCE: IM-2-C1
; CURRENT APPLICATION NUMBER: US/09/322,409
; EARLIER FILING DATE: 1999-05-28
; EARLIER APPLICATION NUMBER: 60/087,306
; EARLIER FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 154
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 87
; LENGTH: 345
; TYPE: DNA
; ORGANISM: Canis familiaris
US-09-322-409-87

Query Match 56.6%; Score 345; DB 4; Length 345;
Best Local Similarity 100.0%; Pred. No. 9.9e-102;
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 146 CATCGAACTTGGCTGTAGGCGATGGAACTCATGATTCCTACTCTGAAAATAAATAAAT 205
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Qy 206 CACCAACTGTGCATTAAAGAAAGTTTTTCAGGGTATAGACACATTGAAGAACCAAACTGCC 265
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Qy 266 CACGGGAGGCTGTGGATAAATCTTCCAAAACCTGTCTTTAATAAAGAACACATAGAG 325
Db 165 CACGGGAGGCTGTGGATAAATCTTCCAAAACCTGTCTTTAATAAAGAACACATAGAG 106
Qy 326 CGCCAAAAAAGGTTGTCAGGAGAAAGATGGAGAGTGACAAAGTTCTCTAGACTACCTG 385
Db 105 CGCCAAAAAAGGTTGTCAGGAGAAAGATGGAGAGTGACAAAGTTCTCTAGACTACCTG 46
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Db 45 CAAGTATTCTTGGTGTAAATAAACACCGAGTGGACACCGGAAAGT 1

RESULT 14
US-09-451-527-85
; Sequence 85, Application US/09451527
; Patent No. 6482403
; GENERAL INFORMATION:
; APPLICANT: Sim, Gek-Kee
; APPLICANT: Yang, Shumin
; APPLICANT: Dreitz, Matthew J.
; APPLICANT: Wonderling, Ramani S.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; FILE REFERENCE: IM-2-C2
; CURRENT APPLICATION NUMBER: US/09/451,527
; EARLIER FILING DATE: 1999-12-01
; EARLIER APPLICATION NUMBER: 60/087,306
; EARLIER FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 85
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; TYPE: DNA
; ORGANISM: Canis familiaris
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; NAME/KEY: CDS
; LOCATION: (1)..(345)
US-09-451-527-85

Query Match 56.6%; Score 345; DB 4; Length 345;
Best Local Similarity 100.0%; Pred. No. 9.9e-102;
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 301 CAAGTATTCTTGGTGTAAATAAACACCGAGTGGACACCGGAAAGT 345

RESULT 15
US-09-451-527-87/c
; Sequence 87, Application US/09451527
; Patent No. 6482403
; GENERAL INFORMATION:
; APPLICANT: Sim, Gek-Kee
; APPLICANT: Yang, Shumin
; APPLICANT: Dreitz, Matthew J.
; APPLICANT: Wonderling, Ramani S.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; FILE REFERENCE: IM-2-C2
; CURRENT APPLICATION NUMBER: US/09/451,527
; EARLIER FILING DATE: 1999-12-01
; EARLIER APPLICATION NUMBER: 60/087,306

; EARLIER FILING DATE: 1999-05-28
; EARLIER APPLICATION NUMBER: 60/087,306
; EARLIER FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 87
; LENGTH: 345
; TYPE: DNA
; ORGANISM: Canis familiaris
US-09-451-527-87

Query Match 56.6%; Score 345; DB 4; Length 345;
Best Local Similarity 100.0%; Pred. No. 9.9e-102;
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 86 TTGCTGTAGAAAATCCCATGAAATAGACTGGTGGCAGAGACCTTGACACTGTCTCTCCACT 145
Db 345 TTGCTGTAGAAAATCCCATGAAATAGACTGGTGGCAGAGACCTTGACACTGTCTCTCCACT 286
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Db 285 CATCGAACTTGGCTGATAGGCGATGGGAACCTGATGATTCCTACTCCTGAAAAATAAAAT 226
Qy 206 CACCAACTGTGCATTAAAGAAGTTTTTCAGGGTATAGACACATTGAAGAACCAAACTGCC 265
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Qy 266 CACGGGAGGCTGTGGATAAACTATTCCAAAACCTGTCTTTAATAAAAGAACACATAGAG 325
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Db 45 CAAGTATTTCTTGGTGTAAATAAACCCGAGTGGACACCCGAAAGT 1

Search completed: August 31, 2004, 06:34:44
Job time : 58.4245 secs

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OM nucleic - nucleic search, using sw model

Run on: August 31, 2004, 01:25:57 ; Search time 360.942 Seconds
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Title: US-10-787-382-4

Perfect score: 610

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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 332720 seqs, 246071050 residues

Total number of hits satisfying chosen parameters: 6474540

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:

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17: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:
18: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:
19: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Score	Match	Length	DB	ID	Description
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C 2	610	100.0	610	9	US-09-755-633-6	Sequence 6, Appli
3	610	100.0	610	15	US-10-218-654-80	Sequence 80, Appli
C 4	610	100.0	610	15	US-10-218-654-82	Sequence 82, Appli
5	610	100.0	610	15	US-10-262-439-80	Sequence 80, Appli
C 6	610	100.0	610	15	US-10-262-439-82	Sequence 82, Appli
7	402	65.9	402	9	US-09-755-633-7	Sequence 7, Appli
C 8	402	65.9	402	9	US-09-755-633-8	Sequence 8, Appli
9	402	65.9	402	15	US-10-218-654-83	Sequence 83, Appli
C 10	402	65.9	402	15	US-10-218-654-84	Sequence 84, Appli
11	402	65.9	402	15	US-10-262-439-83	Sequence 83, Appli
C 12	402	65.9	402	15	US-10-262-439-84	Sequence 84, Appli
13	379	62.1	816	16	US-10-191-997-90	Sequence 90, Appli
C 14	377.4	61.9	816	17	US-10-641-643-1236	Sequence 1236, Ap

15 345 56.6 345 9 US-09-755-633-9 Sequence 9, Appli
C 16 345 56.6 345 9 US-09-755-633-11 Sequence 11, Appli
17 345 56.6 345 15 US-10-218-654-85 Sequence 85, Appli
C 18 345 56.6 345 15 US-10-218-654-87 Sequence 87, Appli
19 345 56.6 345 15 US-10-262-439-85 Sequence 85, Appli
C 20 345 56.6 345 15 US-10-262-439-87 Sequence 87, Appli
21 299 49.0 671 9 US-09-755-633-21 Sequence 21, Appli
22 276.6 45.3 858 15 US-10-295-074-8 Sequence 8, Appli
23 275.6 45.2 858 15 US-10-295-074-10 Sequence 10, Appli
24 232.4 38.1 864 15 US-10-295-074-14 Sequence 14, Appli
25 231.4 37.9 864 15 US-10-295-074-12 Sequence 12, Appli
26 171.8 28.2 1658 9 US-09-755-633-18 Sequence 18, Appli
C 27 170.2 27.9 1658 9 US-09-755-633-19 Sequence 19, Appli
28 152.4 25.0 3230 9 US-09-800-629A-78 Sequence 78, Appli
29 152.4 25.0 3230 17 US-10-679-532-78 Sequence 17, Appli
30 90.6 14.9 6727 9 US-09-800-629A-1 Sequence 1, Appli
31 90.6 14.9 6727 17 US-10-679-532-1 Sequence 1, Appli
32 81.4 13.3 5397 15 US-10-311-455-1017 Sequence 1017, Ap
C 33 79.8 13.1 5397 15 US-10-311-455-1018 Sequence 1018, Ap
34 42.6 7.0 65 10 US-09-908-975-2631 Sequence 2631, Ap
35 42 6.9 3673778 15 US-10-312-841-2 Sequence 2, Appli
36 40.6 6.7 60 10 US-09-908-975-11360 Sequence 11360, A
37 38.8 6.4 2196 13 US-10-424-599-100905 Sequence 100905,
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41 37.2 6.1 594 15 US-10-146-731-10 Sequence 10, Appli
42 37.2 6.1 594 15 US-10-140-472-10 Sequence 10, Appli
43 37.2 6.1 594 15 US-10-141-761-10 Sequence 10, Appli
44 37.2 6.1 594 15 US-10-142-855-10 Sequence 10, Appli
45 37.2 6.1 594 15 US-10-158-790-10 Sequence 10, Appli

ALIGNMENTS

RESULT 1

US-09-755-633-4
; Sequence 4, Application US/09755633
; Patent No. US20020127200A1
; GENERAL INFORMATION:
; APPLICANT: Yang, Shumin
; APPLICANT: McCall, Catherine A.
; APPLICANT: Weber, Eric R.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; FILE REFERENCE: IM-2-C1-C1
; FILE REFERENCE: IM-2-C1-C1
; CURRENT APPLICATION NUMBER: US/09755,633
; CURRENT FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: 09/322,409
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/087,306
; PRIOR FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 610
; TYPE: DNA
; ORGANISM: Canis familiaris
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (29)..(430)
US-09-755-633-4

Query Match 100.0%; Score 610; DB 9; Length 610;

Best Local Similarity 100.0%; Pred. No. 4.5e-181;

Matches 610; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAAGGCAACACTGACATTTTCAGAGCTATGAGATGCTTCTGAAATTTGAGTTGCTTCTAGC 60

Db 1 CAAGGCAACACTGACATTTTCAGAGCTATGAGATGCTTCTGAAATTTGAGTTGCTTCTAGC 60

QY 61 TCTTGGGGCTGCTATGTTTCTGCTTTCCTTGTGTAGAAAATCCCATGAATAGACTGGTGGC 120

Db 61 TCCTGGGCTGCCCTATGTTCTGCTTTGCTGTAGAAAATCCCATGATAGCTGGTGGC 120
Qy 121 AGAGACCTTGACACTGCTCTCCATCATCGAACTTGGCTGATAGGCGATGGGAACCTGAT 180
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Qy 181 GATTCCTACTCTGAAAATATAAATACCAACTGCGAGGCTGTGGATAAACTATTCCAAAACCTT 240
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Qy 241 AGACACATTGAAGAACCAAACTGCCACGGGAGGCTGTGGATAAACTATTCCAAAACCTT 300
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Qy 361 AGTCACAAAGTTCCTAGACTACCTGCAAGTATTCTTTGGTGTATAAAACACCGAGTGGAC 420
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Db 421 ACCGGAAGTTGAGAACAAACCGGCTTATTGTAGTGAAGATTTTGGAGAGAAATGGTTT 480
Qy 481 TTTGGCGATGAGATGAGGCGCAACCAAGTGGGACTTAATGCGCAGTATAACTAAGC 540
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Qy 601 TATATTGAG 610
Db 601 TATATTGAG 610

RESULT 2

US-09-755-633-6/c
; Sequence 6, Application US/09755633
; Patent No. US20020127200A1
; GENERAL INFORMATION:
; APPLICANT: Yang, Shumin
; APPLICANT: McCall, Catherine A.
; APPLICANT: Weber, Eric R.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; FILE REFERENCE: IM-2-C1-C1
; CURRENT APPLICATION NUMBER: US/09/755,633
; PRIOR FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: 09/322,409
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/087,306
; PRIOR FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; TYPE: DNA
; ORGANISM: Canis familiaris
US-09-755-633-6

Query Match 100.0%; Score 610; DB 9; Length 610;
Best Local Similarity 100.0%; Pred. No. 4.5e-181;
Matches 610; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 130 ACCGGAAGTTGAGAACAAACCGGCTTATTGTAGTGAAGATTTTGGAGAGAAATGGTTT 131
Qy 481 TTTGGCGATGAGATGAGGCGCAACCAAGTGGGACTTAATGCGCAGTATAACTAAGC 540
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Db 70 TTCAGACAAAGTAAATATTTCAGGCATCCTACTACTTATCATTACATTCACACAGATGAAA 11
Qy 601 TATATTGAG 610
Db 10 TATATTGAG 1

RESULT 3

US-10-218-654-80
; Sequence 80, Application US/10218654
; Publication No. US20030099609A1
; GENERAL INFORMATION:
; APPLICANT: Sim, Gek-Kee
; APPLICANT: Yang, Shumin
; APPLICANT: Dreitz, Matthew J.
; APPLICANT: Wonderling, Ramani S.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; FILE REFERENCE: IM-2-C1
; CURRENT APPLICATION NUMBER: US/10/218,654
; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: US/09/322,409
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/087,306
; PRIOR FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 154
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 80
; LENGTH: 610
; TYPE: DNA
; ORGANISM: Canis familiaris
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (29)..(430)
US-10-218-654-80

Query Match 100.0%; Score 610; DB 15; Length 610;
Best Local Similarity 100.0%; Pred. No. 4.5e-181;
Matches 610; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 4
 US-10-218-654-82/c
 ; Sequence 82, Application US/10218654
 ; Publication No. US20030099609A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Sim, Gek-Kee
 ; APPLICANT: Yang, Shumin
 ; APPLICANT: Dreitz, Matthew J.
 ; APPLICANT: Wonderling, Ramani S.
 ; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
 ; TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF
 ; FILE REFERENCE: IM-2-C1
 ; CURRENT APPLICATION NUMBER: US/10/218,654
 ; CURRENT FILING DATE: 2002-08-13
 ; PRIOR APPLICATION NUMBER: US/09/322,409
 ; PRIOR FILING DATE: 1999-05-28
 ; PRIOR APPLICATION NUMBER: 60/087,306
 ; PRIOR FILING DATE: 1998-05-29
 ; NUMBER OF SEQ ID NOS: 154
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 82
 ; LENGTH: 610
 ; TYPE: DNA
 ; ORGANISM: Canis familiaris
 US-10-218-654-82

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RESULT 5
US-10-262-439-80
; Sequence 80, Application US/10262439
; Publication No. US20030143196A1
; GENERAL INFORMATION:
; APPLICANT: Sim, Gek-Kee
; APPLICANT: Yang, Shumin
; APPLICANT: Dreitz, Matthew J.
; APPLICANT: Wonderling, Ramani S.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF
; FILE REFERENCE: IM-2-C2
; CURRENT APPLICATION NUMBER: US/10/262,439
; CURRENT FILING DATE: 2002-09-30
; PRIORITY APPLICATION NUMBER: US/09/451,527
; PRIORITY FILING DATE: 1999-12-01
; PRIORITY APPLICATION NUMBER: 09/322,409
; PRIORITY FILING DATE: 1999-05-28
; PRIORITY APPLICATION NUMBER: 60/087,306
; PRIORITY FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 80
; LENGTH: 610
; TYPE: DNA

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US-10-262-439-80
; Sequence 80, Application US/10262439
; Publication No. US20030143196A1
; GENERAL INFORMATION:
; APPLICANT: Sim, Gek-Kee
; APPLICANT: Yang Shumin
; APPLICANT: Dreitz, Matthew J.
; APPLICANT: Wonderling, Ramani S.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF
; FILE REFERENCE: IM-2-C2
; CURRENT APPLICATION NUMBER: US/10/262,439
; CURRENT FILING DATE: 2002-09-30
; PRIOR APPLICATION NUMBER: US/09/451,527
; PRIOR FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: 09/322,409
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/087,306
; PRIOR FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 80
; LENGTH: 610
; TYPE: DNA

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PRIOR FILING DATE: 1999-05-28
PRIOR APPLICATION NUMBER: 60/087,306
PRIOR FILING DATE: 1998-05-29
NUMBER OF SEQ ID NOS: 21
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 7
LENGTH: 402
TYPE: DNA
ORGANISM: Canis familiaris
US-09-755-633-7

Query Match
Best Local Similarity 65.9%; Score 402; DB 9; Length 402;
Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 29 ATGAGATGCTTCTGAATTTGAGTTTGTAGTCTTTGGGGTGGCTGCTATGTTTCTGCTTT 88
DB 402 ATGAGATGCTTCTGAATTTGAGTTTGTAGTCTTTGGGGTGGCTGCTATGTTTCTGCTTT 343
QY 89 GCTGTAGAAAATCCCATGAATAGACTGCTGGCAGAGACCTTGACACTGCTCTCCACTCAT 148
DB 342 GCTGTAGAAAATCCCATGAATAGACTGCTGGCAGAGACCTTGACACTGCTCTCCACTCAT 283
QY 149 CGAACTTGGCTGATAGGCGATGGGAACCTGATGATTTCTTCTGAAAAATAAAATCAC 208
DB 282 CGAACTTGGCTGATAGGCGATGGGAACCTGATGATTTCTTCTGAAAAATAAAATCAC 223
QY 209 CAACTGTGCATTAAGAAATTTTTCAGGGTATAGACACATTTGAAGAACCAACTGCCAC 268
DB 222 CAACTGTGCATTAAGAAATTTTTCAGGGTATAGACACATTTGAAGAACCAACTGCCAC 163
QY 269 GGGGAGGCTGTGATAAACTATTCCAAAACCTTGTCTTTAAATAAAGAACACATAGAGCGC 328
DB 162 GGGGAGGCTGTGATAAACTATTCCAAAACCTTGTCTTTAAATAAAGAACACATAGAGCGC 103
QY 329 CAAAAAAGAGTGTGCAGGAGAAAGATGGAGAGTGACAAAGTTCTTAGACTACCTGCAA 388
DB 102 CAAAAAAGAGTGTGCAGGAGAAAGATGGAGAGTGACAAAGTTCTTAGACTACCTGCAA 43
QY 389 GTATTTCTTGGTGTATTAACACCGAGTGGACACCGGAAAGT 430
DB 42 GTATTTCTTGGTGTATTAACACCGAGTGGACACCGGAAAGT 1

RESULT 9
US-10-218-654-83
Sequence 83, Application US/10216654
Publication No. US20030099609A1
GENERAL INFORMATION:
APPLICANT: Yang, Shumin
APPLICANT: Yang, Gek-Kee
APPLICANT: Yang, Shumin
APPLICANT: Dreitz, Matthew J.
APPLICANT: Wonderting, Ramani S.
TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF
FILE REFERENCE: IM-2-C1
CURRENT APPLICATION NUMBER: US/10/218,654
CURRENT FILING DATE: 2002-08-13
PRIOR APPLICATION NUMBER: US/09/322,409
PRIOR FILING DATE: 1999-05-28
PRIOR APPLICATION NUMBER: 60/087,306
PRIOR FILING DATE: 1998-05-29
NUMBER OF SEQ ID NOS: 154
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 83
LENGTH: 402
TYPE: DNA
ORGANISM: Canis familiaris
US-10-218-654-83

Query Match 65.9%; Score 402; DB 15; Length 402;
Best Local Similarity 100.0%; Pred. No. 1e-115;
Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 29 ATGAGATGCTTCTGAATTTGAGTTTGTAGTCTTTGGGGTGGCTGCTATGTTTCTGCTTT 88
DB 1 ATGAGATGCTTCTGAATTTGAGTTTGTAGTCTTTGGGGTGGCTGCTATGTTTCTGCTTT 60
QY 89 GCTGTAGAAAATCCCATGAATAGACTGCTGGCAGAGACCTTGACACTGCTCTCCACTCAT 148
DB 61 GCTGTAGAAAATCCCATGAATAGACTGCTGGCAGAGACCTTGACACTGCTCTCCACTCAT 120
QY 149 CGAACTTGGCTGATAGGCGATGGGAACCTGATGATTTCTTCTGAAAAATAAAATCAC 208
DB 121 CGAACTTGGCTGATAGGCGATGGGAACCTGATGATTTCTTCTGAAAAATAAAATCAC 180
QY 209 CAACTGTGCATTAAGAAATTTTTCAGGGTATAGACACATTTGAAGAACCAACTGCCAC 268
DB 181 CAACTGTGCATTAAGAAATTTTTCAGGGTATAGACACATTTGAAGAACCAACTGCCAC 240
QY 269 GGGGAGGCTGTGATAAACTATTCCAAAACCTTGTCTTTAAATAAAGAACACATAGAGCGC 328
DB 241 GGGGAGGCTGTGATAAACTATTCCAAAACCTTGTCTTTAAATAAAGAACACATAGAGCGC 300
QY 329 CAAAAAAGAGTGTGCAGGAGAAAGATGGAGAGTGACAAAGTTCTTAGACTACCTGCAA 388
DB 301 CAAAAAAGAGTGTGCAGGAGAAAGATGGAGAGTGACAAAGTTCTTAGACTACCTGCAA 360
QY 389 GTATTTCTTGGTGTATTAACACCGAGTGGACACCGGAAAGT 430
DB 361 GTATTTCTTGGTGTATTAACACCGAGTGGACACCGGAAAGT 402

RESULT 8
US-09-755-633-8/c
Sequence 8, Application US/09755633
Patent No. US20020127200A1
GENERAL INFORMATION:
APPLICANT: Yang, Shumin
APPLICANT: McCall, Catherine A.
APPLICANT: Weber, Eric R.
TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF
FILE REFERENCE: IM-2-C1-C1
CURRENT APPLICATION NUMBER: US/09/755,633
CURRENT FILING DATE: 2001-01-05
PRIOR APPLICATION NUMBER: 09/322,409
PRIOR FILING DATE: 1999-05-28
PRIOR APPLICATION NUMBER: 60/087,306
PRIOR FILING DATE: 1998-05-29
NUMBER OF SEQ ID NOS: 21
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 8
LENGTH: 402
TYPE: DNA
ORGANISM: Canis familiaris
US-09-755-633-8

Query Match 65.9%; Score 402; DB 9; Length 402;
Best Local Similarity 100.0%; Pred. No. 1e-115;
Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 181 CAACCTGTGCATTAAGAAGATTTTTCAGGGTATAGACACATTTGAAGAACCACCAACTGCCAC 240
Qy 269 GGGGAGGCTGGGATAAACTATTCAAACCTTGTCTTTAATAAAGAACACATAGAGCGC 328
Db 241 GGGGAGGCTGGGATAAACTATTCAAACCTTGTCTTTAATAAAGAACACATAGAGCGC 300
Qy 329 CAAAAAAGAGTGTGAGGAGAAAGATGGAGAGTGCACAAAGTTCCTAGACTACCTGCAA 388
Db 301 CAAAAAAGAGTGTGAGGAGAAAGATGGAGAGTGCACAAAGTTCCTAGACTACCTGCAA 360
Qy 389 GTATTTCTTGTGTAATAAACACCGAGTGGACACCGGAAAGT 430
Db 361 GTATTTCTTGTGTAATAAACACCGAGTGGACACCGGAAAGT 402

RESULT 10
US-10-218-654-84/c
; Sequence 84, Application US/10218654
; Publication No. US20030099609A1
; GENERAL INFORMATION:
; APPLICANT: Sim, Gek-Kee
; APPLICANT: Yang, Shumin
; APPLICANT: Dreitz, Matthew J.
; APPLICANT: Wonderling, Ramani S.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; FILE REFERENCE: IM-2-C1
; CURRENT APPLICATION NUMBER: US/10/218,654
; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: US/09/322,409
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/087,306
; PRIOR FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 154
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 84
; TYPE: DNA
; ORGANISM: Canis familiaris
US-10-218-654-84

Query Match 65.9%; Score 402; DB 15; Length 402;
Best Local Similarity 100.0%; Pred. No. 1e-115;
Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 29 ATGAGATGCTTCTGAAATTTGAGTTTCTAGCTTTGGGCTGCTATGTTCTGCTTT 88
Db 402 ATGAGATGCTTCTGAAATTTGAGTTTCTAGCTTTGGGCTGCTATGTTCTGCTTT 343
Qy 89 GCTGTAGAAAATCCCATGATAGACTGGTGGGAGAGACTTGACATGCTCTCCATCAT 148
Db 342 GCTGTAGAAAATCCCATGATAGACTGGTGGGAGAGACTTGACATGCTCTCCATCAT 283
Qy 149 CGAACTTGGCTGATAGCGGATGGAACTGATGTTCTACTCTCTGAAATTAATAATC 208
Db 282 CGAACTTGGCTGATAGCGGATGGAACTGATGTTCTACTCTCTGAAATTAATAATC 223
Qy 209 CAACCTGTGCATTAAGAAGTTCCTAGGGTATAGACACATTTGAAGAACCAAACTGCCAC 268
Db 222 CAACCTGTGCATTAAGAAGTTCCTAGGGTATAGACACATTTGAAGAACCAAACTGCCAC 163
Qy 269 GGGGAGGCTGGGATAAACTATTCCAAAAGTTCCTTTAATAAAGAACACATAGAGCGC 328
Db 162 GGGGAGGCTGGGATAAACTATTCCAAAAGTTCCTTTAATAAAGAACACATAGAGCGC 103
Qy 329 CAAAAAAGAGTGTGAGGAGAAAGATGGAGAGTGCACAAAGTTCCTAGACTACCTGCAA 388
Db 102 CAAAAAAGAGTGTGAGGAGAAAGATGGAGAGTGCACAAAGTTCCTAGACTACCTGCAA 43
Qy 389 GTATTTCTTGTGTAATAAACACCGAGTGGACACCGGAAAGT 430
Db 42 GTATTTCTTGTGTAATAAACACCGAGTGGACACCGGAAAGT 1

RESULT 11
US-10-262-439-83
; Sequence 83, Application US/10262439
; Publication No. US20030143196A1
; GENERAL INFORMATION:
; APPLICANT: Sim, Gek-Kee
; APPLICANT: Yang, Shumin
; APPLICANT: Dreitz, Matthew J.
; APPLICANT: Wonderling, Ramani S.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; FILE REFERENCE: IM-2-C2
; CURRENT APPLICATION NUMBER: US/10/262,439
; CURRENT FILING DATE: 2002-09-30
; PRIOR APPLICATION NUMBER: US/09/451,527
; PRIOR FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: 09/322,409
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/087,306
; PRIOR FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 83
; LENGTH: 402
; TYPE: DNA
; ORGANISM: Canis familiaris
US-10-262-439-83

Query Match 65.9%; Score 402; DB 15; Length 402;
Best Local Similarity 100.0%; Pred. No. 1e-115;
Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 29 ATGAGATGCTTCTGAAATTTGAGTTTCTAGCTTTGGGCTGCTATGTTCTGCTTT 88
Db 1 ATGAGATGCTTCTGAAATTTGAGTTTCTAGCTTTGGGCTGCTATGTTCTGCTTT 60
Qy 89 GCTGTAGAAAATCCCATGATAGACTGGTGGGAGAGACTTGACATGCTCTCCATCAT 148
Db 61 GCTGTAGAAAATCCCATGATAGACTGGTGGGAGAGACTTGACATGCTCTCCATCAT 120
Qy 149 CGAACTTGGCTGATAGCGGATGGAACTGATGTTCTACTCTCTGAAATTAATAATC 208
Db 121 CGAACTTGGCTGATAGCGGATGGAACTGATGTTCTACTCTCTGAAATTAATAATC 180
Qy 209 CAACCTGTGCATTAAGAAGTTCCTAGGGTATAGACACATTTGAAGAACCAAACTGCCAC 268
Db 181 CAACCTGTGCATTAAGAAGTTCCTAGGGTATAGACACATTTGAAGAACCAAACTGCCAC 240
Qy 269 GGGGAGGCTGGGATAAACTATTCCAAAAGTTCCTTTAATAAAGAACACATAGAGCGC 328
Db 241 GGGGAGGCTGGGATAAACTATTCCAAAAGTTCCTTTAATAAAGAACACATAGAGCGC 300
Qy 329 CAAAAAAGAGTGTGAGGAGAAAGATGGAGAGTGCACAAAGTTCCTAGACTACCTGCAA 388
Db 301 CAAAAAAGAGTGTGAGGAGAAAGATGGAGAGTGCACAAAGTTCCTAGACTACCTGCAA 360
Qy 389 GTATTTCTTGTGTAATAAACACCGAGTGGACACCGGAAAGT 430
Db 361 GTATTTCTTGTGTAATAAACACCGAGTGGACACCGGAAAGT 402

RESULT 12
US-10-262-439-84/c
; Sequence 84, Application US/10262439
; Publication No. US20030143196A1
; GENERAL INFORMATION:
; APPLICANT: Sim, Gek-Kee
; APPLICANT: Yang, Shumin
; APPLICANT: Dreitz, Matthew J.
; APPLICANT: Wonderling, Ramani S.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; FILE REFERENCE: IM-2-C2
; CURRENT APPLICATION NUMBER: US/10/262,439
; CURRENT FILING DATE: 2002-09-30
; PRIOR APPLICATION NUMBER: US/09/451,527
; PRIOR FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: 09/322,409
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/087,306
; PRIOR FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 83
; LENGTH: 402
; TYPE: DNA
; ORGANISM: Canis familiaris
US-10-262-439-84

APPLICATION NUMBER: <Unknown>
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0001 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1236:
SEQUENCE CHARACTERISTICS:
LENGTH: 816 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GENBANK
CLONE: g288309
SEQUENCE DESCRIPTION: SEQ ID NO: 1236 :

US-10-641-643-1236

Query Match 61.98; Score 377.4; DB 17; Length 816;
Best Local Similarity 79.08; Pred. No. 8.9e-108;
Matches 462; Conservative 0; Mismatches 121; Indels 2; Gaps 1;
QY 2 AAGCCAAACACTGAACATTTTCAGAGCTATGAGAAATGCTTCTGAATTTGAGTTTGCTAGCT 61
DB 18 AAGCCAAACCGAGACGTTTCAGAGCATGAGATGCTTCTGATTTGAGTTTGCTAGCT 77
QY 62 CTTGGGGCTCCCTATGTTTCTGCTTGTGTAGAAAATCCCATGAAATAGACTGTGGCA 121
DB 78 CTTGGAGCTCCCTACGTGTATGCCATCCCAACAGAAATCCCAAGTGCATTTGGTGA 137
QY 122 GAGACCTTGACACTGCTCCACTCATCGAATCTGCTGATGAGGCGATGGAACTGTG 181
DB 138 GAGACCTTGACACTGCTCTTCTCTCATCGAATCTGCTGATGAGGCGATGGAACTGTG 197
QY 182 ATTCTCTACTCCTGAAATATAATCAACCACTGTGCATTAAGAAAGTTTTCAGGGTATA 241
DB 198 ATTCTCTCTCTGTACATAAATATCAACCACTGTGCATTAAGAAATCTTTCAGGGATA 257
QY 242 GACACATTGAGAACCAACTGCCACGGGAGGCTGTGTAATACTATTCCAAACCTTG 301
DB 258 GGCACACTGGAGAGTCAAACTGTGCAAGGGGCTACTGTGAAAGACTATTGAAACCTTG 317
QY 302 TCTTTAATAAAGAACACATAGAGCGCCAAATAAAGAGTGTGAGGAGAAAGATGGAGA 361
DB 318 TCCTTAATAAAGAAATACATTGACGCGCAATAAAGAGTGTGAGGAGAAAGATGGAGA 377
QY 362 GTGACAAAGTTCTAGACTACTGCAAGATATTTCTGGTGTATATAACACCGAGTGGACA 421
DB 378 GTAAACCAATTCCTAGACTACTGCAAGAGTTTCTGGTGTATATAACACCGAGTGGATA 437
QY 422 CCGGAAAGTTGAGAACCAACCGGCTTATTTAGTGAAGATTTTGAGAGGAATG - GTT 479
DB 438 ATAGAAAGTTGAGACTTAAGTGTGTTGTCAGCCAAAGATTTTGAGGAGAAAGACATT 497
QY 480 TTTTGGCGATGAGAAATGAGGGCCAAACACAGTAGGACTTTAATGGCCAGTATAACTAAG 539
DB 498 TTTACTGAGTGAATGAGGGCCCAAGAAAGAGTCAAGCCCTTAATTTTCAATATAATTAA 557
QY 540 CTTTCAGAGCAAGTAATATTTTCAGGCATCTTACTACTTTATCA 584
DB 558 CTTTCAGAGGAAAGTAATATTTTCAGGCATCTTACTACTTTGCCA 602

RESULT 15

US-09-755-633-9
; Sequence 9, Application US/09755633
; Patent No. US20020127200A1
; GENERAL INFORMATION:
; APPLICANT: Yang, Shumin
; APPLICANT: McCall, Catherine A.

APPLICANT: Weber, Eric R.
TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
FILE OF INVENTION: ACID MOLECULES, AND USES THEREOF
FILE REFERENCE: IM-2-C1-C1
CURRENT APPLICATION NUMBER: US/09/755,633
CURRENT FILING DATE: 2001-01-05
PRIOR APPLICATION NUMBER: 09/322,409
PRIOR FILING DATE: 1999-05-28
PRIOR APPLICATION NUMBER: 60/087,306
PRIOR FILING DATE: 1998-05-29
NUMBER OF SEQ ID NOS: 21
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 9
LENGTH: 345
TYPE: DNA
ORGANISM: Canis familiaris
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(345)
US-09-755-633-9

Query Match 56.63; Score 345; DB 9; Length 345;
Best Local Similarity 100.0%; Pred. No. 8.4e-98;
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 86 TTTGCTGTAGAAAATCCCATGATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACT 145
DB 1 TTTGCTGTAGAAAATCCCATGATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACT 60
QY 146 CATCGAACTTGGCTGATAGGCGATGGGAACCTGATGATTCCTTCTCTGAAAAATAAAAT 205
DB 61 CATCGAACTTGGCTGATAGGCGATGGGAACCTGATGATTCCTTCTCTGAAAAATAAAAT 120
QY 206 CACCAACTGTGCATTAAGAAAGTTTTCAGGGTATAGACATTTGAAGACCAAACTGCC 265
DB 121 CACCAACTGTGCATTAAGAAAGTTTTCAGGGTATAGACATTTGAAGACCAAACTGCC 180
QY 266 CACGGGAGGCTGTGGATAAACTATTCAAAACTTGTCTTTAATAAAGAACACATAGAG 325
DB 181 CACGGGAGGCTGTGGATAAACTATTCAAAACTTGTCTTTAATAAAGAACACATAGAG 240
QY 326 CGCCAAAAAAGGTTGTGAGGAGAAAGATGGAGAGTGCACAAAGTTCTTAGACTACCTG 385
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DB 301 CAAGTATTTCTTGGTGTAAATAAACACCGAGTGGACACCGGAAAGT 345

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Job time : 364.942 secs

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Run on: August 30, 2004, 16:21:12 ; Search time 1737.73 Seconds
(without alignments)
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Perfect score: 402
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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

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Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 2: gb_htg.*
- 3: gb_in.*
- 4: gb_om.*
- 5: gb_ov.*
- 6: gb_pat.*
- 7: gb_ph.*
- 8: gb_pl.*
- 9: gb_pr.*
- 10: gb_ro.*
- 11: gb_sts.*
- 12: gb_sy.*
- 13: gb_un.*
- 14: gb_vi.*
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- 37: em_htg_vrt.*
- 38: em_sy.*
- 39: em_htgo_hum.*
- 40: em_htgo_mus.*
- 41: em_htgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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4	402	100.0	402	6	AR254495
5	402	100.0	402	6	BD211560
6	402	100.0	402	6	BD211561
7	402	100.0	610	4	AF331919
8	402	100.0	610	6	AR241536
9	402	100.0	610	6	AR241537
10	402	100.0	610	6	AR254492
11	402	100.0	610	6	AR254493
12	402	100.0	610	6	BD211558
13	402	100.0	610	6	BD211559
14	398.8	99.2	405	6	AR300436
15	398.8	99.2	405	6	AX083939
16	345	85.8	345	6	AR241540
17	345	85.8	345	6	AR241541
18	345	85.8	345	6	AR254496
19	345	85.8	345	6	AR254497
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21	345	85.8	345	6	BD211563
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23	338.6	84.2	405	4	AF068770
24	335.4	83.4	405	4	ECU91947
25	329.8	82.0	356	4	AF091133
26	326.8	81.3	405	4	BTINTLEUS
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32	277.2	69.0	816	6	EO1639
33	277.2	69.0	816	6	E13591
34	277.2	69.0	816	9	HSILSR
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36	275.6	68.6	816	9	HSBCDPIA
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38	275.6	68.6	858	6	AX766523
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ALIGNMENTS

RESULT 1
AR241538

LOCUS

DEFINITION

AR241538

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

AR241538
Sequence 83 from patent US 6471957.
402 bp
DNA
linear
PAT 20-DEC-2002
Unknown.
Unclassified.
1 (bases 1 to 402)
Sim.G.-K., Yang,S., Dretz,M.J. and Wonderling,R.S.
Canine IL-4 immunoregulatory proteins and uses thereof
Patent: US 6471957-A 83 29-OCT-2002;
Location/Qualifiers

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/organism="unknown"
/mol_type="genomic DNA"
ORIGIN
Query Match 100.0%; Score 402; DB 6; Length 402;
Best Local Similarity 100.0%; Pred. No. 6e-101;
Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ATGAGAAATGCTTCGAAATTTGAGTTTCTAGCTCTTGGGCTGCCCTATGTTCTGCCTTT 60
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Qy 61 GCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACTCAT 120
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Qy 121 CGAACTTGGCTGTAGTAGGCGATGGAACTGATGATTCCTACTCTGAAATAAAATATCAC 180
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Qy 361 GTATTTCTTGGTGTAAATAAACACCGAGTGGACCCGGAAGT 402
Db 361 GTATTTCTTGGTGTAAATAAACACCGAGTGGACCCGGAAGT 402
RESULT 2
AR241539/c
LOCUS AR241539 402 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 84 from patent US 6471957.
ACCESSION AR241539
VERSION AR241539.1 GI:27287248
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 402)
AUTHORS Sim,G.-K., Yang,S., Dreitz,M.J. and Wonderling,R.S.
TITLE Canine IL-4 immunoregulatory proteins and uses thereof
JOURNAL Patent: US 6471957-A 84 29-OCT-2002;
FEATURES
source 1..402
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN
Query Match 100.0%; Score 402; DB 6; Length 402;
Best Local Similarity 100.0%; Pred. No. 6e-101;
Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ATGAGAAATGCTTCGAAATTTGAGTTTCTAGCTCTTGGGCTGCCCTATGTTCTGCCTTT 60
Db 402 ATGAGAAATGCTTCGAAATTTGAGTTTCTAGCTCTTGGGCTGCCCTATGTTCTGCCTTT 343
Qy 61 GCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACTCAT 120
Db 342 GCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACTCAT 283
Qy 121 CGAACTTGGCTGTAGTAGGCGATGGAACTGATGATTCCTACTCTGAAATAAAATATCAC 180
Db 282 CGAACTTGGCTGTAGTAGGCGATGGAACTGATGATTCCTACTCTGAAATAAAATATCAC 223

Qy 181 CAACCTGTCATTAAGAAGTTTTCAGGGTATAGACACATTTGAAGAACCAACTGCCAC 240
Db 222 CAACCTGTCATTAAGAAGTTTTCAGGGTATAGACACATTTGAAGAACCAACTGCCAC 163
Qy 241 GGGGAGGCTGGGATAAATATCCAAACTTGTCTTTAATAAAGAACACATAGAGCGC 300
Db 162 GGGGAGGCTGGGATAAATATCCAAACTTGTCTTTAATAAAGAACACATAGAGCGC 103
Qy 301 CAAAAAAGGTTGTCAGGAGAAAGATGGAGAGTGAACAAAGTTCTCTAGACTACCTGCAA 360
Db 102 CAAAAAAGGTTGTCAGGAGAAAGATGGAGAGTGAACAAAGTTCTCTAGACTACCTGCAA 43
Qy 361 GTATTTCTTGGTGTAAATAAACACCGAGTGGACCCGGAAGT 402
Db 42 GTATTTCTTGGTGTAAATAAACACCGAGTGGACCCGGAAGT 1
RESULT 3
AR254494
LOCUS AR254494 402 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 83 from patent US 6482403.
ACCESSION AR254494
VERSION AR254494.1 GI:27303382
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 402)
AUTHORS Sim,G.-K., Yang,S., Dreitz,M.J. and Wonderling,R.S.
TITLE Canine IL-13 immunoregulatory proteins and uses thereof
JOURNAL Patent: US 6482403-A 83 19-NOV-2002;
FEATURES
source 1..402
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN
Query Match 100.0%; Score 402; DB 6; Length 402;
Best Local Similarity 100.0%; Pred. No. 6e-101;
Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ATGAGAAATGCTTCGAAATTTGAGTTTCTAGCTCTTGGGCTGCCCTATGTTCTGCCTTT 60
Db 1 ATGAGAAATGCTTCGAAATTTGAGTTTCTAGCTCTTGGGCTGCCCTATGTTCTGCCTTT 60
Qy 61 GCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACTCAT 120
Db 61 GCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACTCAT 120
Qy 121 CGAACTTGGCTGTAGTAGGCGATGGAACTGATGATTCCTACTCTGAAATAAAATATCAC 180
Db 121 CGAACTTGGCTGTAGTAGGCGATGGAACTGATGATTCCTACTCTGAAATAAAATATCAC 180
Qy 181 CAACCTGTCATTAAGAAGTTTTCAGGGTATAGACACATTTGAAGAACCAACTGCCAC 240
Db 181 CAACCTGTCATTAAGAAGTTTTCAGGGTATAGACACATTTGAAGAACCAACTGCCAC 240
Qy 241 GGGGAGGCTGGGATAAATATCCAAACTTGTCTTTAATAAAGAACACATAGAGCGC 300
Db 241 GGGGAGGCTGGGATAAATATCCAAACTTGTCTTTAATAAAGAACACATAGAGCGC 300
Qy 301 CAAAAAAGGTTGTCAGGAGAAAGATGGAGAGTGAACAAAGTTCTCTAGACTACCTGCAA 360
Db 301 CAAAAAAGGTTGTCAGGAGAAAGATGGAGAGTGAACAAAGTTCTCTAGACTACCTGCAA 360
Qy 361 GTATTTCTTGGTGTAAATAAACACCGAGTGGACCCGGAAGT 402
Db 361 GTATTTCTTGGTGTAAATAAACACCGAGTGGACCCGGAAGT 402
RESULT 4
AR254495/c

LOCUS AR254495 402 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 84 from patent US 6482403.
ACCESSION AR254495
VERSION AR254495.1 GI:27303383
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 402)
AUTHORS Sim,G.-K., Yang,S., Dreitz,M.J. and Wonderling,R.S.
TITLE Canine IL-13 immunoregulatory proteins and uses thereof
JOURNAL Patent: US 6482403-A 84 19-NOV-2002;
FEATURES
source Location/Qualifiers
1..402
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN
Query Match 100.0%; Score 402; DB 6; Length 402;
Best Local Similarity 100.0%; Pred. No. 6e-101;
Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ATGAGAAATGCTTCTGAATTTGAGTTTCTAGCTTTGGGCTGCTGCTATGTTTCTGCTTT 60
Db 402 ATGAGAAATGCTTCTGAATTTGAGTTTCTAGCTTTGGGCTGCTGCTATGTTTCTGCTTT 343
Qy 61 CTTGTAGAAATCCCATGATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACTCAT 120
Db 342 CTTGTAGAAATCCCATGATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACTCAT 283
Qy 121 CGAACTTGGCTGATAGCGGATGGAACTGATGATTTCTACTCTGAAATATAAAATCAAC 180
Db 282 CGAACTTGGCTGATAGCGGATGGAACTGATGATTTCTACTCTGAAATATAAAATCAAC 223
Qy 181 CAACCTGTCATTAAGAAGTTTTCAGGCTATAGACACATGAGAACCAAACTGCCAC 240
Db 222 CAACCTGTCATTAAGAAGTTTTCAGGCTATAGACACATGAGAACCAAACTGCCAC 163
Qy 241 GGGAGAGCTGTGGATAAATCTTCCAAACTTGTCTTTTAAATAAAGAACACATAGAGCGC 300
Db 162 GGGAGAGCTGTGGATAAATCTTCCAAACTTGTCTTTTAAATAAAGAACACATAGAGCGC 103
Qy 301 CAAAAAAGAGTGTGAGGAGAAAGATGAGAGTGACAAAGTTCTCTAGACTACCTGCAA 360
Db 102 CAAAAAAGAGTGTGAGGAGAAAGATGAGAGTGACAAAGTTCTCTAGACTACCTGCAA 43
Qy 361 GTATTTCTTGTGTAATAAACACCGAGTGACACCGGAAAGT 402
Db 42 GTATTTCTTGTGTAATAAACACCGAGTGACACCGGAAAGT 1
RESULT 5
LOCUS BD211560 402 bp DNA linear PAT 17-JUL-2003
DEFINITION Canine and feline immunoregulatory proteins, nucleic acid molecules and method of using the same.
ACCESSION BD211560
VERSION BD211560.1 GI:33021330
KEYWORDS JP 2002516104-A/66.
SOURCE Canis familiaris (dog)
ORGANISM Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE 1 (bases 1 to 402)
AUTHORS Sim,G., Yang,S., Dreitz,M.J. and Wonderling,R.S.
TITLE Canine and feline immunoregulatory proteins, nucleic acid molecules and method of using the same
JOURNAL Patent: JP 2002516104-A 66 04-JUN-2002;
COMMENT OS Canis familiaris (dog)
PN JP 2002516104-A/66
PD 04-JUN-2002
PF 28-MAY-1999 JP 2000551002

PR 29-MAY-1998 US 60/087306
PI GEKKEE SIM,SHUMIN YANG,MATTHEW J DREITZ,RAMANI S WONDERLING PC
C12N15/09,A61K31/7088,A61K38/00,A61K39/00,A61K39/395,
PC A61K39/395,
PC A61K45/00,A61K48/00,A61P37/02,A61P37/04,C07K14/475,C07K14/535,
PC C07K14/54,
PC C07K14/56,C07K14/705,C07K16/24,C07K16/28,C12N1/21,C12N5/10, PC
G01N33/15,
PC G01N33/50,C12N15/00,A61K37/02,A61K37/66,C12N5/00 CC Canine
and feline immunoregulatory proteins, nucleic acid CC
molecules and
CC method of using the same
FH Key Location/Qualifiers
FT source 1..402
/organism="Canis familiaris (dog)".
FEATURES
source Location/Qualifiers
1..402
/organism="Canis familiaris"
/mol_type="genomic DNA"
/db_xref="taxon:9615"
ORIGIN
Query Match 100.0%; Score 402; DB 6; Length 402;
Best Local Similarity 100.0%; Pred. No. 6e-101;
Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ATGAGAAATGCTTCTGAATTTGAGTTTCTAGCTTTGGGCTGCTGCTATGTTTCTGCTTT 60
Db 1 ATGAGAAATGCTTCTGAATTTGAGTTTCTAGCTTTGGGCTGCTGCTATGTTTCTGCTTT 60
Qy 61 CTTGTAGAAATCCCATGATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACTCAT 120
Db 61 CTTGTAGAAATCCCATGATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACTCAT 120
Qy 121 CGAACTTGGCTGATAGCGGATGGAACTGATGATTTCTACTCTGAAATATAAAATCAAC 180
Db 121 CGAACTTGGCTGATAGCGGATGGAACTGATGATTTCTACTCTGAAATATAAAATCAAC 180
Qy 181 CAACCTGTCATTAAGAAGTTTTCAGGCTATAGACACATGAGAACCAAACTGCCAC 240
Db 181 CAACCTGTCATTAAGAAGTTTTCAGGCTATAGACACATGAGAACCAAACTGCCAC 240
Qy 241 GGGAGAGCTGTGATAAATCTTCCAAACTTGTCTTTTAAATAAAGAACACATAGAGCGC 300
Db 241 GGGAGAGCTGTGATAAATCTTCCAAACTTGTCTTTTAAATAAAGAACACATAGAGCGC 300
Qy 301 CAAAAAAGAGTGTGAGGAGAAAGATGAGAGTGACAAAGTTCTCTAGACTACCTGCAA 360
Db 301 CAAAAAAGAGTGTGAGGAGAAAGATGAGAGTGACAAAGTTCTCTAGACTACCTGCAA 360
Qy 361 GTATTTCTTGTGTAATAAACACCGAGTGACACCGGAAAGT 402
Db 361 GTATTTCTTGTGTAATAAACACCGAGTGACACCGGAAAGT 402
RESULT 6
LOCUS BD211561/c 402 bp DNA linear PAT 17-JUL-2003
DEFINITION Canine and feline immunoregulatory proteins, nucleic acid molecules and method of using the same.
ACCESSION BD211561
VERSION BD211561.1 GI:33021331
KEYWORDS JP 2002516104-A/67.
SOURCE Canis familiaris (dog)
ORGANISM Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE 1 (bases 1 to 402)
AUTHORS Sim,G., Yang,S., Dreitz,M.J. and Wonderling,R.S.
TITLE Canine and feline immunoregulatory proteins, nucleic acid molecules and method of using the same
JOURNAL Patent: JP 2002516104-A 67 04-JUN-2002;
HESKA CORP

COMMENT OS Canis familiaris (dog)
 PN JP 2002516104-A/67
 PD 04-JUN-2002
 PF 28-MAY-1999 JP 2000551002
 PR 29-MAY-1998 US 60/087306
 PI GEKKEE SIM, SHUMIN YANG, MATTHEW J DREITZ, RAMANI S WONDERLING PC
 C12N15/09, A61K31/7088, A61K38/00, A61K39/00, A61K39/395,
 PC A61K39/395,
 PC A61K45/00, A61K48/00, A61P37/02, A61P37/04, C07K14/475, C07K14/535,
 PC C07K14/54,
 PC C07K14/56, C07K14/705, C07K16/24, C07K16/28, C12N1/21, C12N5/10, PC
 G01N33/15
 PC G01N33/50, C12N15/00, A61K37/02, A61K37/66, C12N5/00 CC Canine
 and feline immunoregulatory proteins, nucleic acid CC
 molecules and
 CC method of using the same
 FH Key Location/Qualifiers
 FT source 1..402
 FT /organism="Canis familiaris (dog)".
 FEATURES source Location/Qualifiers
 1..402
 /organism="Canis familiaris"
 /mol_type="genomic DNA"
 /db_xref="taxon:9615"

ORIGIN

Query Match 100.0%; Score 402; DB 6; Length 402;
 Best Local Similarity 100.0%; Pred. No. 6e-101;
 Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGATGCTTCGAAATTTGAGTTTCTAGCTCTTGGGCTGCCTATGTTTCTGCCTTT 60
 DB 402 ATGAGATGCTTCGAAATTTGAGTTTCTAGCTCTTGGGCTGCCTATGTTTCTGCCTTT 343

QY 61 GCTGTAGAAAATCCCATGAATAGACTGGTGGGAGACCTTGACACTGCTCTCCACTCAT 120
 DB 342 GCTGTAGAAAATCCCATGAATAGACTGGTGGGAGACCTTGACACTGCTCTCCACTCAT 283

QY 121 CGAACTTGGCTGATAGCGGATGGGAACCTGATGATTCCTACTCTGAAATATAAATCAC 180
 DB 282 CGAACTTGGCTGATAGCGGATGGGAACCTGATGATTCCTACTCTGAAATATAAATCAC 223

QY 181 CAACCTGTGCATTAAGAAGTTTTTTCAGGGTATAGACACATTGAAGAACCAAACTGCCAC 240
 DB 222 CAACCTGTGCATTAAGAAGTTTTTTCAGGGTATAGACACATTGAAGAACCAAACTGCCAC 163

QY 241 GGGGAGCTGTGGATTAACCTATTCCTAAACTTGTCTTTTATAAAGAACACATAGAGCG 300
 DB 162 GGGGAGCTGTGGATTAACCTATTCCTAAACTTGTCTTTTATAAAGAACACATAGAGCG 103

QY 301 CAAAAAAGAGGTGTGCAGAGAAAGATGGAGAGTGACAAAGTTCTAGACTACCTGCAA 360
 DB 102 CAAAAAAGAGGTGTGCAGAGAAAGATGGAGAGTGACAAAGTTCTAGACTACCTGCAA 43

QY 361 GTATTTCTTGGTGTAAATCAACCGAGTGGACACCGGAAAGT 402
 DB 42 GTATTTCTTGGTGTAAATCAACCGAGTGGACACCGGAAAGT 1

RESULT 7
 AF331919
 LOCUS AF331919 610 bp mRNA linear MAM 04-OCT-2001
 DEFINITION Canis familiaris interleukin-5 mRNA, complete cds.
 ACCESSION AF331919
 VERSION AF331919.1 GI:15919180
 KEYWORDS Canis familiaris (dog)
 SOURCE Canis familiaris
 ORGANISM Canis familiaris
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 1 (bases 1 to 610)
 Yang, S., Sellins, K.S., Weber, E. and McCall, C.
 Canine interleukin-5: molecular characterization of the gene and
 expression of biologically active recombinant protein
 J. Interferon Cytokine Res. 21 (6), 361-367 (2001)

JOURNAL expression of biologically active recombinant protein
 MEDLINE J. Interferon Cytokine Res. 21 (6), 361-367 (2001)
 21334408
 PUBMED 11440633
 REFERENCE 2 (bases 1 to 610)
 AUTHORS Yang, S.
 Direct Submission
 TITLE Submitted (22-DEC-2000) Immunology, Heska Corporation, 1613
 JOURNAL Prospect Parkway, Ft Collins, CO 80525, USA
 FEATURES Location/Qualifiers
 1..610
 /organism="Canis familiaris"
 /mol_type="mRNA"
 /db_xref="taxon:9615"
 1..28
 29..433
 /note="IL-5"
 /codon_start=1
 /product="interleukin-5"
 /protein_id="AAL10715.1"
 /db_xref="GI:15919181"
 /translation="MRMLNLSLALGAAVYSAFAPVENPMNRLVAETLTLLSTHRTWL
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 433..610

3'UTR
 ORIGIN

Query Match 100.0%; Score 402; DB 4; Length 610;
 Best Local Similarity 100.0%; Pred. No. 5.9e-101;
 Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGATGCTTCGAAATTTGAGTTTCTAGCTCTTGGGCTGCCTATGTTTCTGCCTTT 60
 DB 29 ATGAGATGCTTCGAAATTTGAGTTTCTAGCTCTTGGGCTGCCTATGTTTCTGCCTTT 88

QY 61 GCTGTAGAAAATCCCATGAATAGACTGGTGGGAGACCTTGACACTGCTCTCCACTCAT 120
 DB 89 GCTGTAGAAAATCCCATGAATAGACTGGTGGGAGACCTTGACACTGCTCTCCACTCAT 148

QY 121 CGAACTTGGCTGATAGCGGATGGGAACCTGATGATTCCTACTCTGAAATATAAATCAC 180
 DB 149 CGAACTTGGCTGATAGCGGATGGGAACCTGATGATTCCTACTCTGAAATATAAATCAC 208

QY 181 CAACCTGTGCATTAAGAAGTTTTTTCAGGGTATAGACACATTGAAGAACCAAACTGCCAC 240
 DB 209 CAACCTGTGCATTAAGAAGTTTTTTCAGGGTATAGACACATTGAAGAACCAAACTGCCAC 268

QY 241 GGGGAGCTGTGGATTAACCTATTCCTAAACTTGTCTTTTATAAAGAACACATAGAGCG 300
 DB 269 GGGGAGCTGTGGATTAACCTATTCCTAAACTTGTCTTTTATAAAGAACACATAGAGCG 328

QY 301 CAAAAAAGAGGTGTGCAGAGAAAGATGGAGAGTGACAAAGTTCTAGACTACCTGCAA 360
 DB 329 CAAAAAAGAGGTGTGCAGAGAAAGATGGAGAGTGACAAAGTTCTAGACTACCTGCAA 388

QY 361 GTATTTCTTGGTGTAAATCAACCGAGTGGACACCGGAAAGT 402
 DB 389 GTATTTCTTGGTGTAAATCAACCGAGTGGACACCGGAAAGT 430

RESULT 8
 AR241536
 LOCUS AR241536 610 bp DNA linear PAT 20-DEC-2002
 DEFINITION Sequence 80 from patent US 6471957.
 ACCESSION AR241536
 VERSION AR241536.1 GI:27287245
 KEYWORDS Unknown.
 SOURCE Unknown.
 ORGANISM Unknown.
 1 (bases 1 to 610)
 Sim, G.-K., Yang, S., Dreitz, M.J. and Wonderling, R.S.
 Canine IL-4 immunoregulatory proteins and uses thereof
 TITLE

Query Match	100.0%	Score 402;	DB 6;	Length 610;
Best Local Similarity	100.0%;	Pred. No. 5.9e-101;		
Matches 402;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0
QY	1	ATGAGAATGCTCTCGAAATTTGAGTTTGTCTAGCTCTTTGGGCTGCCCTATGTTTCTGCTTT	60	
DB	29	ATGAGAAATGCTCTCGAAATTTGAGTTTGTCTAGCTCTTTGGGCTGCCCTATGTTTCTGCTTT	88	
QY	61	GTTGTAGAAAAATCCCATGAATAGACTGGTGGCGAGACCTTGTGACACTGCTCTCCATCAT	120	
DB	89	GCTGTAGAAAAATCCCATGAATAGACTGGTGGCGAGACCTTGTGACACTGCTCTCCATCAT	148	
QY	121	CGAACTTGGCTGATAGGCGATGGGAACTCGATGATTCCTACTCTCGAAATAAAAAATCAC	180	
DB	149	CGAACTTGGCTGATAGGCGATGGGAACTCGATGATTCCTACTCTCGAAATAAAAAATCAC	208	
QY	181	CACACTGTGCATTTAAAGAAAGTTTTTCAGGGTATAGACACATTTGAAGAACCCAAATGCCCCAC	240	
DB	209	CACACTGTGCATTTAAAGAAAGTTTTTCAGGGTATAGACACATTTGAAGAACCCAAATGCCCCAC	268	
QY	241	GGGGAGGCTGTGGATAAACTATTCGAAAACTTGTGCTTTTAATAAAGAACACATAGAGGC	300	
DB	269	GGGGAGGCTGTGGATAAACTATTCGAAAACTTGTGCTTTTAATAAAGAACACATAGAGGC	328	
QY	301	CAAAAAAAAAGGTGTGCAGGAGAAAGATGGAGAGTGACAAAAGTTCTCTAGACTACCTGC	360	
DB	329	CAAAAAAAAAGGTGTGCAGGAGAAAGATGGAGAGTGACAAAAGTTCTCTAGACTACCTGC	388	
QY	361	GTATTTCTTGTTGTTAATAAAACCCAGTGTGACACCGGAAAGT	402	
DB	389	GTATTTCTTGTTGTTAATAAAACCCAGTGTGACACCGGAAAGT	430	

RESULT 9
 AR241537/c
 LOCUS
 DEFINITION
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 UNCLASSIFIED
 1 (bases 1 to 610)
 Sim,G.-K., Yang,S., Dreitz,M.J. and Wonderling,R.S.
 Canine IL-4 immunoregulatory proteins and uses thereof
 Patent: US 6471957-A 82 29-OCT-2002;
 Location/Qualifiers
 1. .610
 /organism="unknown"
 /mol_type="genomic DNA"
 source
 ORIGIN
 Query Match 100.0%; Score 402; DB 6; Length 610;
 Best Local Similarity 100.0%; Pred. No. 5.9e-101;
 Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ATGAGAAATGCTTCTGAATTGAGTTTGCTAGCTCTGGGGCTGCCTATGTTTCTGCCTTT 60
 Db 582 ATGAGAAATGCTTCTGAATTGAGTTTGCTAGCTCTGGGGCTGCCTATGTTTCTGCCTTT 523
 QY 61 GCTGTAGAAAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACTGCTCTCCACTCAT 120
 522 GCTGTCCTCAATATGCTCATATATACAGCTGTGCGAGAGCTTTGACATGCTCTTCATCAT 463

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RESULT 11
AR254493/c
LOCUS AR254493 610 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 82 from patent US 6482403.
ACCESSION AR254493
VERSION AR254493.1 GI:27303381
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
  1 (bases 1 to 610)
AUTHORS Sim,G.-K., Yang,S., Dreitz,M.J. and Wonderling,R.S.
TITLE Canine IL-13 immunoregulatory proteins and uses thereof
JOURNAL Patent: US 6482403-A 82 19-NOV-2002;
FEATURES
  source
    location/Qualifiers
    1..610
    /organism="unknown"
    /mol_type="genomic DNA"
ORIGIN
  Query Match 100.0%; Score 402; DB 6; Length 610;
  Best Local Similarity 100.0%; Pred. No. 5.9e-101;
  Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
  QY 1 ATGGAATGCTCTCGAATTGAGTTTGTAGTCTTGGGCTGCTATGTTCTGCTTT 60
  Db 582 ATGGAATGCTCTCGAATTGAGTTTGTAGTCTTGGGCTGCTATGTTCTGCTTT 523
  QY 61 GCTGTAGAAAATCCCATGAATAGACTGGTGGCAGACCTTGACACGCTCTCCATCAT 120
  Db 522 GCTGTAGAAAATCCCATGAATAGACTGGTGGCAGACCTTGACACGCTCTCCATCAT 463
  QY 121 CGAATCTGGCTGATAGGCGATGGAACTGATGATTTCTTCTTAAAGAAACACATAGAGCGC 300
  Db 462 CGAATCTGGCTGATAGGCGATGGAACTGATGATTTCTTCTTAAAGAAACACATAGAGCGC 403
  QY 181 CAATCTGTCATTAAGAAGTTTTTCAGGGTATAGACATTTGAAGACCAACTGCCAC 240
  Db 402 CAATCTGTCATTAAGAAGTTTTTCAGGGTATAGACATTTGAAGACCAACTGCCAC 343
  QY 241 GGGAGGCTGGGATAAATCTTCCAAACTTGTCTTTTAAAGAAACACATAGAGCGC 300
  Db 342 GGGAGGCTGGGATAAATCTTCCAAACTTGTCTTTTAAAGAAACACATAGAGCGC 283
  QY 301 CAAAAAAGGCTGGCAGAGAAAGATGGAGAGTGACAAAGTTCTAGACTACCTGCAA 360
  Db 282 CAAAAAAGGCTGGCAGAGAAAGATGGAGAGTGACAAAGTTCTAGACTACCTGCAA 223
  QY 361 GTATTTCTTGTGTAATAAACACCGAGTGGACACCGGAAAGT 402
  Db 222 GTATTTCTTGTGTAATAAACACCGAGTGGACACCGGAAAGT 181

RESULT 12
BD211558
LOCUS BD211558 610 bp DNA linear PAT 17-JUL-2003
DEFINITION Canine and feline immunoregulatory proteins, nucleic acid molecules
  and method of using the same.
ACCESSION BD211558
VERSION BD211558.1 GI:33021328
KEYWORDS JP 2002516104-A/64.
SOURCE Canis familiaris (dog)
ORGANISM Canis familiaris
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
  1 (bases 1 to 610)
  Sim,G., Yang,S., Dreitz,M.J. and Wonderling,R.S.
  Canine and feline immunoregulatory proteins, nucleic acid molecules
  and method of using the same
  Patent: JP 2002516104-A 64 04-JUN-2002;
  HESKA CORP
  OS Canis familiaris (dog)
  PN JP 2002516104-A/64

RESULT 13
BD211559/c
LOCUS BD211559 610 bp DNA linear PAT 17-JUL-2003
DEFINITION Canine and feline immunoregulatory proteins, nucleic acid molecules
  and method of using the same.
ACCESSION BD211559
VERSION BD211559.1 GI:33021329
KEYWORDS JP 2002516104-A/65.
SOURCE Canis familiaris (dog)
ORGANISM Canis familiaris
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
  1 (bases 1 to 610)
  Sim,G., Yang,S., Dreitz,M.J. and Wonderling,R.S.
  Canine and feline immunoregulatory proteins, nucleic acid molecules
  and method of using the same
  Patent: JP 2002516104-A 65 04-JUN-2002;
  HESKA CORP
  OS Canis familiaris (dog)
  PN JP 2002516104-A/65

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JOURNAL	Patent: US 6537781-A 1 25-MAR-2003;
FEATURES	Location/Qualifiers
source	1. .405
	/organism="unknown"
	/mol_type="genomic DNA"
ORIGIN	
	Query Match 99.2%; Score 398.8; DB 6; Length 405;
	Best Local Similarity 99.5%; Pred. No. 4.6e-100;
	Matches 400; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY	1 ATGAGAAATGCTTCGAATTTGAGTTTGCTAGCTCTTGGGGCTGCCATGTTTCTGCCTTT 60
Db	1 ATGAGAAATGCTTCGAATTTGAGTTTGCTAGCTCTTGGGGCTGCCATGTTTCTGCCTTT 60
QY	61 GCTCTAGAAATCCCATGAATAGACTGGTGGCAGAGACCTTGGACACTGCTCTCCACTCAT 120
Db	61 GCTGTAGAAATCCCATGAATAGACTGGTGGCAGAGACCTTGGACACTGCTCTCCACTCAT 120
QY	121 CGAACTTGGCTGTAGGCGATGGGAACCTGATGATTCCTACTCCTGAAATATAAATCAT 180
Db	121 CGAACTTGGCTGTAGGCGATGGGAACCTGATGATTCCTACTCCTGAAATATAAATCAT 180
QY	181 CAACCTGTGCATTAAGAAAGTTTTTCAGGGTATAGACACATTGAAGAACCAAACTGCCAC 240
Db	181 CAACCTGTGCATTAAGAAAGTTTTTCAGGGTATAGACATTTGAAGAACCAAACTGCCAC 240

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ORIGIN
Query Match          99.2%; Score 398.8; DB 6; Length 405;
Best Local Similarity 99.5%; Pred. No. 4.6e-100;
Matches 400; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1  ATGAGAAATGCTTCTGAAATTGAGTTTGCTAGCTCTTTGGGGCTGCCTAATGTTCTGCCTTT 60
      |||
Db      1  ATGAGAAATGCTTCTGAAATTGAGTTTGCTAGCTCTTTGGGGCTGCCTAATGTTCTGCCTTT 60

Qy      61  GCTGTAGAAAATCCCATGAATAGACTGCTGGCAGAGACCTTGACACTGCTCTCCACTCAT 120

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Db      ||||| 61 GCTGTAGAAATCCCATGATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACTCAT 120
QY      ||||| 121 CGAAGCTTCGGCTGATAGGCGATGGGAACCTGATGATTCCTACTCCTGGAATATAAATCAC 180
Db      ||||| 121 CGAAGCTTCGGCTGATAGGCGATGGGAACCTGATGATTCCTACTCCTGGAATATAAATCAC 180
QY      ||||| 181 CAAGCTGTGCATTAAAGAGTTCAGGGTATAGACACATTTGAAGAACCAAACTGCCAC 240
Db      ||||| 181 CAAGCTGTGCATTAAAGAGTTCAGGGTATAGACACATTTGAAGAACCAAACTGCCAC 240
QY      ||||| 241 GGGGAGGCTGTGGATAAAGTATTCGAAACTTGTCTTTAATAAAGAACACATAGAGCGC 300
Db      ||||| 241 GGGGAGGCTGTGGATAAAGTATTCGAAACTTGTCTTTAATAAAGAACACATAGAGCGC 300
QY      ||||| 301 CAAAAAAGGTGTGCAGGAGAAAGATGGAGAGTGACAAAGTTCTTAGACTACCTGCCAA 360
Db      ||||| 301 CAAAAAAGGTGTGCAGGAGAAAGATGGAGAGTGACAAAGTTCTTAGACTACCTGCCAA 360
QY      ||||| 361 GTATTCTTGTGTAAATAAACCCGAGTGGACACCGGAAAGT 402
Db      ||||| 361 GTATTCTTGTGTAAATAAACCCGAGTGGACAAATGGAAAGT 402
```

Search completed: August 31, 2004, 01:25:41
Job time : 1737.73 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 30, 2004, 15:56:41 ; Search time 191.733 Seconds
(without alignments)
8907.036 Million cell updates/sec

Title: US-10-787-382-7

Perfect score: 402
Sequence: 1 atgagaatgcttctgaattt.....ccgagtgacaccgaaagt 402

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 3373863 segs, 2124093041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_29Jan04:.*
1: Geneseqn1980s:.*
2: Geneseqn1990s:.*
3: Geneseqn2000s:.*
4: Geneseqn2001as:.*
5: Geneseqn2001bs:.*
6: Geneseqn2002s:.*
7: Geneseqn2003as:.*
8: Geneseqn2003bs:.*
9: Geneseqn2003cs:.*
10: Geneseqn2004s:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	402	100.0	402	3	Aaz55548 Canine in
2	402	100.0	402	3	Aaz55549 Canine in
3	402	100.0	610	3	Aaz55546 Canine in
4	402	100.0	610	3	Aaz55547 Canine in
5	398.8	99.2	405	4	Aaf74300 Canine in
6	345	85.8	345	3	Aaz55550 Canine ma
7	345	85.8	345	3	Aaz55551 Canine ma
8	344.4	85.7	838	3	Aaz44265 Porcine I
9	316.2	78.7	520	2	Aat50755 Ovine IL-
10	311.8	77.6	399	2	Aat50756 Ovine IL-
11	287.4	71.5	393	4	Aaf74306 Canine in
12	277.2	69.0	816	3	Aaa34857 Human ade
13	277.2	69.0	816	3	Aaal3338 Human int
14	277.2	69.0	816	3	Aaf20979 Human low
15	277.2	69.0	816	7	Aaz96673 Human nuc
16	277.2	69.0	816	7	Aaf63368 Human int
17	277.2	69.0	4057	3	Aaa34858 Human ade
18	277.2	69.0	4057	3	Aaf20980 Human low
19	277.2	69.0	4057	7	Aaz96674 Human nuc
20	275.6	68.6	402	1	Aan81380 A human B
21	275.6	68.6	858	8	Aal61293 hIL5-P2-P
22	275.6	68.6	858	8	Aal61294 hIL5-P30-
23	252	62.7	252	4	Aaf74305 Canine in

24	231.4	57.6	864	8	AAL61296
25	231.4	57.6	864	8	AAL61295
26	229.4	57.1	385	3	AAA43842
27	224.6	55.9	370	1	AAV91647
28	206.4	51.3	399	2	AAV64061
29	206.4	51.3	402	2	AAT14921
30	206.4	51.3	1533	1	AAV82431
31	206.4	51.3	1534	2	AAT88013
32	206.4	51.3	1623	2	AAT14925
33	206.4	51.3	1623	2	AAV64062
34	206.2	51.3	377	2	AAV01595
35	201	50.0	1945	9	ADB53890
36	200	49.8	481	1	AAV80461
37	196.4	48.9	348	2	AAT14922
38	194.6	48.4	342	2	AAT14923
39	194.2	48.3	339	2	AAT14924
40	178.4	44.4	375	3	AAC68870
41	175.6	43.7	357	3	AAC68871
42	169.2	42.1	381	3	AAC68867
43	166.4	41.4	399	3	AAC68873
44	166	41.3	444	3	AAC68875
45	165.6	41.2	375	3	AAC68872

ALIGNMENTS

RESULT 1

AAZ55548
ID AAZ55548 standard; cDNA; 402 BP.

XX AC AAZ55548;

XX DT 14-MAR-2000 (first entry)

XX DE Canine interleukin-5 (IL-5) cDNA coding region.

XX KW Interleukin-5; IL-5; antibody; canine; inhibitor; immune response;
XX KW immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.

XX OS Canis familiaris.

XX PN WO9961618-A2.

XX PD 02-DEC-1999.

XX PF 28-MAY-1999; 99WO-US011942.

XX PR 29-MAY-1998; 98US-0087306P.

XX (HESK-) HESKA CORP.

XX PI Sim G, Yang S, Dreitz MJ, Wonderling RS;

XX DR WPI; 2000-072623/06.

XX DR P-PSDB; AAY58219.

XX PT Nucleic acids encoding immunoregulatory proteins from cats or dogs,
XX PT useful for treating or preventing e.g. tumors or autoimmune disease.

XX PS Claim 1b; Page 225; 264pp; English.

XX Sequences AAZ55546-255551 represent cDNA sequences encoding canine interleukin-5 (IL-5). The invention relates to canine IL-4, canine or feline IL-5 (IL-5), canine or feline CD40, canine or feline CD154 (CD40 ligand), canine IL-5, canine IL-13, feline interferon-alpha (IFN-alpha) and feline granulocyte macrophage colony-stimulating factor (GM-CSF), and nucleotides which encode these immunoregulatory proteins. The proteins, their associated nucleic acids, specific antibodies and inhibitors may be used as vaccines for therapeutic or prophylactic regulation of an immune response in animals (particularly cats, dogs, horses and humans). They may be used to treat autoimmune or infectious diseases including allergies, tumours, inflammation and graft rejection, and to increase the

CC response from a co-administered antigen. The nucleotide sequences can
 CC also be used for the recombinant production of a protein, while
 CC nucleotide fragments are useful as probes, as amplification primers and
 CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).
 CC The proteins may be used to raise antibodies and to screen for modulators
 CC of activity, while the antibodies may be used in detection, and in drug
 CC targeting

XX Sequence 402 BP; 129 A; 79 C; 93 G; 101 T; 0 U; 0 Other;

Query Match 100.0%; Score 402; DB 3; Length 402;
 Best Local Similarity 100.0%; Pred. No. 2.3e-110;
 Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGATGCTTCTGAATTTGAGTTTGTGCTAGCTCTTGGGCTGCTATGTTCTGCGCTTT 60
 DB 1 ATGAGATGCTTCTGAATTTGAGTTTGTGCTAGCTCTTGGGCTGCTATGTTCTGCGCTTT 60
 QY 61 GCTGTAGAAAATCCCATGAATAGACTGGTGCAGAGACCTTGACACTGCTCTCCACTCAT 120
 DB 61 GCTGTAGAAAATCCCATGAATAGACTGGTGCAGAGACCTTGACACTGCTCTCCACTCAT 120
 QY 121 CGAATCTGGCTGTAGGCGATGGGAACCTGATGATTCCTACTCTGAAAATAAAAAATCAC 180
 DB 121 CGAATCTGGCTGTAGGCGATGGGAACCTGATGATTCCTACTCTGAAAATAAAAAATCAC 180
 QY 181 CAATCTGTCATTAAGAAGTTTTTCAGGGTATGACACATTAAGACCAACTGCCAC 240
 DB 181 CAATCTGTCATTAAGAAGTTTTTCAGGGTATGACACATTAAGACCAACTGCCAC 240
 QY 241 GGGAGGCTGTGGATAAATTTCCAAAACCTTGTCTTTAATAAAGAACACATAGAGCGC 300
 DB 241 GGGAGGCTGTGGATAAATTTCCAAAACCTTGTCTTTAATAAAGAACACATAGAGCGC 300
 QY 301 CAAAAAAGGCTGTGAGAGAAAGATGGAGAGTGACAAAGTTCTAGACTACCTGCAA 360
 DB 301 CAAAAAAGGCTGTGAGAGAAAGATGGAGAGTGACAAAGTTCTAGACTACCTGCAA 360
 QY 361 GTATTTCTTGGTGTAAATACACCGAGTGGACACCGGAAAGT 402
 DB 361 GTATTTCTTGGTGTAAATACACCGAGTGGACACCGGAAAGT 402

RESULT 2
 AAZ55549/c
 ID AAZ55549 standard; cDNA; 402 BP.

XX AAZ55549;

XX 14-MAR-2000 (first entry)

XX Canine interleukin-5 (IL-5) cDNA coding region complement.

XX Interleukin-5; IL-5; antibody; canine; inhibitor; immune response;
 XX immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.

XX Canis familiaris.

XX WO9961618-A2.

XX 02-DEC-1999.

XX 28-MAY-1999; 99WO-US011942.

XX 29-MAY-1998; 98US-0087306P.

XX (HESK-) HESKA CORP.

XX Sim G, Yang S, Dreitz MJ, Wonderling RS;

XX WPI; 2000-072623/06.

XX P-PSDB; AAY58219.

PT Nucleic acids encoding immunoregulatory proteins from cats or dogs,
 PT useful for treating or preventing e.g. tumors or autoimmune disease.

XX Claim 1h; Page 226; 264pp; English.

XX Sequences AAZ55546-425551 represent cDNA sequences encoding canine
 CC interleukin-5 (IL-5). The invention relates to canine IL-4, canine or
 CC feline Flt-3 ligand, canine or feline CD40, canine or feline CD154 (CD40
 CC ligand), canine IL-5, canine IL-13, feline interferon-alpha (IFN-alpha)
 CC and feline granulocyte macrophage colony-stimulating factor (GM-CSF), and
 CC nucleotides which encode these immunoregulatory proteins. The proteins,
 CC their associated nucleic acids, specific antibodies and inhibitors may be
 CC used as vaccines for therapeutic or prophylactic regulation of an immune
 CC response in animals (particularly cats, dogs, horses and humans). They
 CC may be used to treat autoimmune or infectious diseases including
 CC allergies, tumours, inflammation and graft rejection, and to increase the
 CC response from a co-administered antigen. The nucleotide sequences can
 CC also be used for the recombinant production of a protein, while
 CC nucleotide fragments are useful as probes, as amplification primers and
 CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).
 CC The proteins may be used to raise antibodies and to screen for modulators
 CC of activity, while the antibodies may be used in detection, and in drug
 CC targeting

XX Sequence 402 BP; 101 A; 93 C; 79 G; 129 T; 0 U; 0 Other;

Query Match 100.0%; Score 402; DB 3; Length 402;

Best Local Similarity 100.0%; Pred. No. 2.3e-110;

Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGATGCTTCTGAATTTGAGTTTGTGCTAGCTCTTGGGCTGCTATGTTCTGCGCTTT 60
 DB 402 ATGAGATGCTTCTGAATTTGAGTTTGTGCTAGCTCTTGGGCTGCTATGTTCTGCGCTTT 343
 QY 61 GCTGTAGAAAATCCCATGAATAGACTGGTGCAGAGACCTTGACACTGCTCTCCACTCAT 120
 DB 342 GCTGTAGAAAATCCCATGAATAGACTGGTGCAGAGACCTTGACACTGCTCTCCACTCAT 283
 QY 121 CGAATCTGGCTGTAGGCGATGGGAACCTGATGATTCCTACTCTGAAAATAAAAAATCAC 180
 DB 282 CGAATCTGGCTGTAGGCGATGGGAACCTGATGATTCCTACTCTGAAAATAAAAAATCAC 223
 QY 181 CAATCTGTCATTAAGAAGTTTTTCAGGGTATGACACATTAAGACCAACTGCCAC 240
 DB 222 CAATCTGTCATTAAGAAGTTTTTCAGGGTATGACACATTAAGACCAACTGCCAC 163
 QY 241 GGGAGGCTGTGGATAAATTTCCAAAACCTTGTCTTTAATAAAGAACACATAGAGCGC 300
 DB 162 GGGAGGCTGTGGATAAATTTCCAAAACCTTGTCTTTAATAAAGAACACATAGAGCGC 103
 QY 301 CAAAAAAGGCTGTGAGAGAAAGATGGAGAGTGACAAAGTTCTAGACTACCTGCAA 360
 DB 102 CAAAAAAGGCTGTGAGAGAAAGATGGAGAGTGACAAAGTTCTAGACTACCTGCAA 43
 QY 361 GTATTTCTTGGTGTAAATACACCGAGTGGACACCGGAAAGT 402
 DB 42 GTATTTCTTGGTGTAAATACACCGAGTGGACACCGGAAAGT 1

RESULT 3

AAZ55546

ID AAZ55546 standard; cDNA; 610 BP.

XX AAZ55546;

XX 14-MAR-2000 (first entry)

XX Canine interleukin-5 (IL-5) cDNA.

XX Interleukin-5; IL-5; antibody; canine; inhibitor; immune response;

XX immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.

XX Canis familiaris.


```

XX FH      Location/Qualifiers
XX FT      29..433
XX FT      /*tag= a
XX FT      /product= "Canine IL-5"
XX
XX PN      WO9961618-A2.
XX
XX PD      02-DEC-1999.
XX
XX PF      28-MAY-1999; 99WO-US011942.
XX
XX PR      29-MAY-1998; 98US-0087306P.
XX
XX PA      (HESK-) HESKA CORP.
XX
XX PI      Sim G, Yang S, Dreitz MJ, Wonderling RS;
XX
XX DR      WPI: 2000-072623/06.
XX
XX DR      P-PSDB; AAY58219.
XX
XX PT      Nucleic acids encoding immunoregulatory proteins from cats or dogs,
XX      useful for treating or preventing e.g. tumors or autoimmune disease.
XX
XX PS      Claim 1h; Page 223-224; 264pp; English.
XX
XX CC      Sequences AAZ55546-Z55551 represent cDNA sequences encoding canine
XX      interleukin-5 (IL-5). The invention relates to canine IL-4, canine or
XX      feline Flt-3 ligand, canine or feline CD40, canine or feline CD134 (CD40
XX      ligand), canine IL-5, canine IL-13, feline interferon-alpha (IFN-alpha)
XX      and feline granulocyte macrophage colony-stimulating factor (GM-CSF), and
XX      nucleotides which encode these immunoregulatory proteins. The proteins,
XX      their associated nucleic acids, specific antibodies and inhibitors may be
XX      used as vaccines for therapeutic or prophylactic regulation of an immune
XX      response in animals (particularly cats, dogs, horses and humans). They
XX      may be used to treat autoimmune or infectious diseases including
XX      allergies, tumours, inflammation and graft rejection, and to increase the
XX      response from a co-administered antigen. The nucleotide sequences can
XX      also be used for the recombinant production of a protein, while
XX      nucleotide fragments are useful as probes, as amplification primers and
XX      as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).
XX      The proteins may be used to raise antibodies and to screen for modulators
XX      of activity, while the antibodies may be used in detection, and in drug
XX      targeting
XX
XX SQ      Sequence 610 BP; 202 A; 114 C; 139 G; 155 T; 0 U; 0 Other;

Query Match      100.0%; Score 402; DB 3; Length 610;
Best Local Similarity 100.0%; Pred. No. 2.7e-110;
Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ATGAGAAATGCTTCGAATTTGAGTTTCTAGCTTCTGGGGCTGGCTATGTTCTGCTCTT 60
DB      29 ATGAGAAATGCTTCGAATTTGAGTTTCTAGCTTCTGGGGCTGGCTATGTTCTGCTCTT 88
QY      61 GCTTAGAAAATCCATGAATAGACTGGTGGCAGAGACCTTGACATGCTCTCACTCAT 120
DB      89 GCTGTAGAAAATCCATGAATAGACTGGTGGCAGAGACCTTGACATGCTCTCACTCAT 148
QY      121 CGAACTGGCTGATAGCGATGGGAACCTCATGATTTCTACTCTGAAATATAAAATCAC 180
DB      149 CGAACTGGCTGATAGCGATGGGAACCTCATGATTTCTACTCTGAAATATAAAATCAC 208
QY      181 CAACCTGTGCATTAAGAAGTTTTTTCAGGGTATAGACATTTGAAGAACCAAACTGCCAC 240
DB      209 CAACCTGTGCATTAAGAAGTTTTTTCAGGGTATAGACATTTGAAGAACCAAACTGCCAC 268
QY      241 GGGAGAGCTGTGGATAACTATTTCCAAACTGTCTTTAATAAAGACACATAGAGCCG 300
DB      269 GGGAGAGCTGTGGATAACTATTTCCAAACTGTCTTTAATAAAGACACATAGAGCCG 328
QY      301 CAAAAAAAAGGTGTGAGAGAGAAAGATGGAGAGTGACAAAGTTCTCTAGACTACCTGCAA 360

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DB      329 CAAAAAAAAGGTGTGAGAGAGAAAGATGGAGAGTGACAAAGTTCTCTAGACTACCTGCAA 388
QY      361 GTATTTCTTGTGTAATAAACAACCGAGTGGACACCGGAAAGT 402
DB      389 GTATTTCTTGTGTAATAAACAACCGAGTGGACACCGGAAAGT 430

RESULT 4
AAZ55547/c
ID      AAZ55547 standard; cDNA; 610 BP.
XX
XX AC      AAZ55547;
XX
XX DT      14-MAR-2000 (first entry)
XX
XX DE      Canine interleukin-5 (IL-5) cDNA complement.
XX
XX KW      Interleukin-5; IL-5; antibody; canine; inhibitor; immune response;
XX      immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.
XX
XX OS      Canis familiaris.
XX
XX FH      Key
XX CDS      Location/Qualifiers
XX FT      complement(178..582)
XX FT      /*tag= a
XX FT      /product= "Canine IL-5"
XX
XX PN      WO9961618-A2.
XX
XX PD      02-DEC-1999.
XX
XX PF      28-MAY-1999; 99WO-US011942.
XX
XX PR      29-MAY-1998; 98US-0087306P.
XX
XX PA      (HESK-) HESKA CORP.
XX
XX PI      Sim G, Yang S, Dreitz MJ, Wonderling RS;
XX
XX DR      WPI: 2000-072623/06.
XX
XX DR      P-PSDB; AAY58219.
XX
XX PT      Nucleic acids encoding immunoregulatory proteins from cats or dogs,
XX      useful for treating or preventing e.g. tumors or autoimmune disease.
XX
XX PS      Claim 1h; Page 224-225; 264pp; English.
XX
XX CC      Sequences AAZ55546-Z55551 represent cDNA sequences encoding canine
XX      interleukin-5 (IL-5). The invention relates to canine IL-4, canine or
XX      feline Flt-3 ligand, canine or feline CD40, canine or feline CD134 (CD40
XX      ligand), canine IL-5, canine IL-13, feline interferon-alpha (IFN-alpha)
XX      and feline granulocyte macrophage colony-stimulating factor (GM-CSF), and
XX      nucleotides which encode these immunoregulatory proteins. The proteins,
XX      their associated nucleic acids, specific antibodies and inhibitors may be
XX      used as vaccines for therapeutic or prophylactic regulation of an immune
XX      response in animals (particularly cats, dogs, horses and humans). They
XX      may be used to treat autoimmune or infectious diseases including
XX      allergies, tumours, inflammation and graft rejection, and to increase the
XX      response from a co-administered antigen. The nucleotide sequences can
XX      also be used for the recombinant production of a protein, while
XX      nucleotide fragments are useful as probes, as amplification primers and
XX      as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).
XX      The proteins may be used to raise antibodies and to screen for modulators
XX      of activity, while the antibodies may be used in detection, and in drug
XX      targeting
XX
XX SQ      Sequence 610 BP; 155 A; 139 C; 114 G; 202 T; 0 U; 0 Other;

Query Match      100.0%; Score 402; DB 3; Length 610;
Best Local Similarity 100.0%; Pred. No. 2.7e-110;
Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ATGAGAAATGCTTCGAATTTGAGTTTCTAGCTTCTGGGGCTGGCTATGTTCTGCTCTT 60

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Db 582 ATGAGATGCTTCTGAAATTTGAGTTTGTAGCTCTTGGGCTGCCTATGTTTCTGCGTTT 523
QY 61 GCTGTAGAAATCCCATGATAGACTGGTGCAGAGACCTTGACACTGCTCCACTCAT 120
Db 522 GCTGTAGAAATCCCATGATAGACTGGTGCAGAGACCTTGACACTGCTCCACTCAT 463
QY 121 CGAACTTGGCTGTAGAGCGATGGGAACCTGATGATTTCTTCTCTGAAAAATAAAATCAC 180
Db 462 CGAACTTGGCTGTAGAGCGATGGGAACCTGATGATTTCTTCTCTGAAAAATAAAATCAC 403
QY 181 CAACGTGTCATTAAGAAGTTTTCAGGGTATAGACACATTAAGAACCAAACTGCCAC 240
Db 402 CAACGTGTCATTAAGAAGTTTTCAGGGTATAGACACATTAAGAACCAAACTGCCAC 343
QY 241 GGGGAGGCTGTGGATAAACTATTCCAAAACCTTGTCTTTAATAAAGAACACATAGAGCGC 300
Db 342 GGGGAGGCTGTGGATAAACTATTCCAAAACCTTGTCTTTAATAAAGAACACATAGAGCGC 283
QY 301 CAAAAAAGAGTGTGAGGAGAAAGATGGAGAGTGACAAAGTTCTTAGACTACCTGCAA 360
Db 282 CAAAAAAGAGTGTGAGGAGAAAGATGGAGAGTGACAAAGTTCTTAGACTACCTGCAA 223
QY 361 GTATTCTTGTGTAATAAACCAGAGTGGACACCGGAAAGT 402
Db 222 GTATTCTTGTGTAATAAACCAGAGTGGACACCGGAAAGT 181

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RESULT 5

AAF74300
ID AAF74300 standard; DNA; 405 BP.

AC AAF74300;

DT 04-MAY-2001 (first entry)

DE Canine interleukin-5 coding sequence #1.

KW Dog; interleukin-5; IL-5; allergy; cancer; gene therapy;
KW inflammatory reaction; ds.

OS Canis sp.

FN WO20011049-A2.

PD 15-FEB-2001.

PF 09-AUG-2000; 2000WO-US021651.

PR 10-AUG-1999; 99US-00371615.

PA (INDEX-) IDEXX LAB INC.

PI Guo H, Lawton R, Mermer B, Aliyappa AP;

DR WPI; 2001-191542/19.

DR P-PSDB; AAB72615.

PT Novel canine interleukin 5 polynucleotide and polypeptides are used for
PT generating antibodies which are useful in treating allergies in dogs.

PS Claim 31; Page 46; 48pp; English.

XX The present invention provides the protein and coding sequences of the
XX canine interleukin-5 (IL-5) protein. This can be used to treat allergies,
XX cancer and inflammatory reactions in dogs. The present sequence is one
XX version of the IL-5 coding sequence shown in the specification

SQ Sequence 405 BP; 131 A; 77 C; 94 G; 103 T; 0 U; 0 Other;

Query Match 99.2%; Score 398.8; DB 4; Length 405;

Best Local Similarity 99.5%; Pred. No. 2.1e-109;

Matches 400; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 1 ATGAGATGCTTCTGAAATTTGAGTTTGTAGCTCTTGGGCTGCCTATGTTTCTGCGTTT 60
Db 1 ATGAGATGCTTCTGAAATTTGAGTTTGTAGCTCTTGGGCTGCCTATGTTTCTGCGTTT 60
QY 61 GCTGTAGAAATCCCATGATAGACTGGTGCAGAGACCTTGACACTGCTCCACTCAT 120
Db 61 GCTGTAGAAATCCCATGATAGACTGGTGCAGAGACCTTGACACTGCTCCACTCAT 120
QY 121 CGAACTTGGCTGTAGAGCGATGGGAACCTGATGATTTCTTCTCTGAAAAATAAAATCAC 180
Db 121 CGAACTTGGCTGTAGAGCGATGGGAACCTGATGATTTCTTCTCTGAAAAATAAAATCAC 180
QY 181 CAACGTGTCATTAAGAAGTTTTCAGGGTATAGACACATTAAGAACCAAACTGCCAC 240
Db 181 CAACGTGTCATTAAGAAGTTTTCAGGGTATAGACACATTAAGAACCAAACTGCCAC 240
QY 241 GGGGAGGCTGTGGATAAACTATTCCAAAACCTTGTCTTTAATAAAGAACACATAGAGCGC 300
Db 241 GGGGAGGCTGTGGATAAACTATTCCAAAACCTTGTCTTTAATAAAGAACACATAGAGCGC 300
QY 301 CAAAAAAGAGTGTGAGGAGAAAGATGGAGAGTGACAAAGTTCTTAGACTACCTGCAA 360
Db 301 CAAAAAAGAGTGTGAGGAGAAAGATGGAGAGTGACAAAGTTCTTAGACTACCTGCAA 360
QY 361 GTATTCTTGTGTAATAAACCAGAGTGGACACCGGAAAGT 402
Db 361 GTATTCTTGTGTAATAAACCAGAGTGGACACCGGAAAGT 402

```

RESULT 6

AZ55550
ID AZ55550 standard; cDNA; 345 BP.

AC AZ55550;

DT 14-MAR-2000 (first entry)

DE Canine mature interleukin-5 (IL-5) cDNA.

KW Interleukin-5; IL-5; antibody; canine; inhibitor; immune response;
KW immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.

OS Canis familiaris.

FN WO9961618-A2.

PD 02-DEC-1999.

PF 28-MAY-1999; 99WO-US011942.

PR 29-MAY-1998; 98US-0087306P.

PA (HESK-) HESKA CORP.

PI Sim G, Yang S, Dreitz MJ, Wonderling RS;

DR WPI; 2000-072623/06.

DR P-PSDB; AAY58220.

PT Nucleic acids encoding immunoregulatory proteins from cats or dogs,
PT useful for treating or preventing e.g. tumors or autoimmune disease.

PS Claim 1h; Page 226-227; 264pp; English.

XX Sequences AA255546-255551 represent cDNA sequences encoding canine
XX interleukin-5 (IL-5). The invention relates to canine IL-4, canine or
XX feline Flt-3 ligand, canine or feline CD40, canine or feline CD134 (CD40
XX ligand), canine IL-5, canine IL-13, feline interferon-alpha (IFN-alpha)
XX and feline granulocyte macrophage colony-stimulating factor (GM-CSF), and
XX nucleotides which encode these immunoregulatory proteins. The proteins,
XX their associated nucleic acids, specific antibodies and inhibitors may be
XX used as vaccines for therapeutic or prophylactic regulation of an immune

CC response in animals (particularly cats, dogs, horses and humans). They
CC may be used to treat autoimmune or infectious diseases including
CC allergies, tumours, inflammation and graft rejection, and to increase the
CC response from a co-administered antigen. The nucleotide sequences can
CC also be used for the recombinant production of a protein, while
CC nucleotide fragments are useful as probes, as amplification primers and
CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).
CC The proteins may be used to raise antibodies and to screen for modulators
CC of activity, while the antibodies may be used in detection, and in drug
CC targeting
XX
SQ Sequence 345 BP; 120 A; 68 C; 78 G; 79 T; 0 U; 0 Other;

Query Match 85.8%; Score 345; DB 3; Length 345;
Best Local Similarity 100.0%; Pred. No. 2.7e-93;
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 TTGCTGTAGAAATCCCATGATAGACTGGTGGCAGAGACCTTGACCTGCTCTCCACT 60

QY 118 CATCGAACTTGGCTGTAGTGGGATGGGAACCTGATGATTCCTCTGAAAAATAAAAT 177
DB 61 CATCGAACTTGGCTGTAGTGGGATGGGAACCTGATGATTCCTCTGAAAAATAAAAT 120

QY 178 CACCACTGTGCATTAAAGAGTTTTCRGGGTATAGACATTTGAGACCAACTGCC 237
DB 121 CACCACTGTGCATTAAAGAGTTTTCRGGGTATAGACATTTGAGACCAACTGCC 180

QY 238 CACGGGAGGCTGTGGATAAACTATTCCTGAACTTGTCTTTTAAATAAAGAACACATAGAG 297
DB 181 CACGGGAGGCTGTGGATAAACTATTCCTGAACTTGTCTTTTAAATAAAGAACACATAGAG 240

QY 298 CGCCAAAAAAGGTGTGAGGAGAAAGATGAGAGTGACAAAGTTCCTAGACTACCTG 357
DB 241 CGCCAAAAAAGGTGTGAGGAGAAAGATGAGAGTGACAAAGTTCCTAGACTACCTG 300

QY 358 CAAGTATTTCTTGGTGTAAATAACACCGAGTGACACCGGAAAGT 402
DB 301 CAAGTATTTCTTGGTGTAAATAACACCGAGTGACACCGGAAAGT 345

RESULT 7
AAZ5551/c
ID AAZ5551 standard; cDNA; 345 BP.
AC AAZ5551;
XX
XX 14-MAR-2000 (first entry)
DT Canine mature interleukin-5 (IL-5) cDNA complement.
DE Interleukin-5; IL-5; antibody; canine; inhibitor; immune response;
KW immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.
XX
XX Canis familiaris.
XX WO961618-A2.
XX
XX 02-DEC-1999.
XX
XX 28-MAY-1999; 99WO-US011942.
XX
XX 29-MAY-1998; 98US-0087306P.
XX
XX (HESK-) HESKA CORP.
XX
XX Sim G, Yang S, Dreitz MJ, Wonderling RS;
FI WPI; 2000-072623/06.
XX P-PSDB; AAY58220.
DR
XX Nucleic acids encoding immunoregulatory proteins from cats or dogs,
PT

PT useful for treating or preventing e.g. tumors or autoimmune disease.
XX
XX Claim 1h; Page 228; 264pp; English.
XX
XX Sequences AAZ5551-25551 represent cDNA sequences encoding canine
CC interleukin-5 (IL-5). The invention relates to canine IL-4, canine or
CC feline Flt-3 ligand, canine or feline CD40, canine or feline CD135 (CD40
CC ligand), canine IL-5, canine IL-13, feline interferon-alpha (IFN-alpha)
CC and feline granulocyte macrophage colony-stimulating factor (GM-CSF), and
CC nucleotides which encode these immunoregulatory proteins. The proteins,
CC their associated nucleic acids, specific antibodies and inhibitors may be
CC used as vaccines for therapeutic or prophylactic regulation of an immune
CC response in animals (particularly cats, dogs, horses and humans). They
CC may be used to treat autoimmune or infectious diseases including
CC allergies, tumours, inflammation and graft rejection, and to increase the
CC response from a co-administered antigen. The nucleotide sequences can
CC also be used for the recombinant production of a protein, while
CC nucleotide fragments are useful as probes, as amplification primers and
CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).
CC The proteins may be used to raise antibodies and to screen for modulators
CC of activity, while the antibodies may be used in detection, and in drug
CC targeting
XX
SQ Sequence 345 BP; 79 A; 78 C; 68 G; 120 T; 0 U; 0 Other;

Query Match 85.8%; Score 345; DB 3; Length 345;
Best Local Similarity 100.0%; Pred. No. 2.7e-93;
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 58 TTGCTGTAGAAATCCCATGATAGACTGGTGGCAGAGACCTTGACCTGCTCTCCACT 117
DB 345 TTGCTGTAGAAATCCCATGATAGACTGGTGGCAGAGACCTTGACCTGCTCTCCACT 286

QY 118 CACCACTGTGCATTAAAGAGTTTTCAGGGTATAGACATTTGAGACCAACTGCC 237
DB 295 CACCACTGTGCATTAAAGAGTTTTCAGGGTATAGACATTTGAGACCAACTGCC 226

QY 178 CACCACTGTGCATTAAAGAGTTTTCAGGGTATAGACATTTGAGACCAACTGCC 237
DB 225 CACCACTGTGCATTAAAGAGTTTTCAGGGTATAGACATTTGAGACCAACTGCC 166

QY 238 CACGGGAGGCTGTGGATAAACTATTCCTGAACTTGTCTTTTAAATAAAGAACACATAGAG 297
DB 165 CACGGGAGGCTGTGGATAAACTATTCCTGAACTTGTCTTTTAAATAAAGAACACATAGAG 106

QY 298 CGCCAAAAAAGGTGTGAGGAGAAAGATGAGAGTGACAAAGTTCCTAGACTACCTG 357
DB 105 CGCCAAAAAAGGTGTGAGGAGAAAGATGAGAGTGACAAAGTTCCTAGACTACCTG 46

QY 358 CAAGTATTTCTTGGTGTAAATAACACCGAGTGACACCGGAAAGT 402
DB 45 CAAGTATTTCTTGGTGTAAATAACACCGAGTGACACCGGAAAGT 1

RESULT 8
AAZ44265
ID AAZ44265 standard; DNA; 838 BP.
XX
XX AAZ44265;
XX
XX 31-MAR-2000 (first entry)
DT Porcine IL-5 DNA.
DE
XX Pig; vaccine; cysticercosis; protective antigen; cC1; cC3; cC4;
KW tenial cysticercus; gamma interferon; IFN-gamma; interleukin 5; IL-5; ss.
XX
XX Sus scrofa.
XX
XX CN1231339-A.
XX
XX 13-OCT-1999.
XX

PF 29-JAN-1999; 99CN-00113447.
 XX
 PR 29-JAN-1999; 99CN-00113447.
 XX
 XX (UVTW-) UNIV NO 2 MILITARY MEDICAL PLA.
 PA
 XX Sun S, Dai J;
 PI
 XX WPI; 2000-087904/08.
 DR
 XX Nucleic acid vaccine for cysticercosis co-contracted by human and pig.
 PT
 XX
 PS Claim 3; Page 9; 21pp; Chinese.
 XX
 CC This invention describes a novel nucleic acid vaccine for preventing and
 CC curing human and pork cysticercosis. The invention involves the formation
 CC of a eukaryotic expression plasmid from fusion transcript expression unit
 CC consisting of three protective antigen genes (cCl, cC3 and cC4) of pig
 CC tenial cysticercus and coexpression unit of related cell factor gamma
 CC interferon (IFN-gamma) and pork interleukin 5 (IL-5)) genes. The
 CC production and purification process of said nucleic acid vaccine is
 CC simple and convenient, the physical and chemical properties of the
 CC vaccine are stable, and the vaccine is easy to store and transport, and
 CC possesses effective immunological protective function for human and pig
 CC cysticercosis. This sequence represents the pig IL-5 gene used in the
 CC method of the invention
 XX
 XX Sequence 838 BP; 280 A; 148 C; 171 G; 239 T; 0 U; 0 Other;
 SQ
 Query Match 85.7%; Score 344.4; DB 3; Length 838;
 Best Local Similarity 91.0%; Pred. No. 5.8e-93;
 Matches 366; Conservative 0; Mismatches 36; Indels 0; Gaps 0;
 QY 1 ATGGAATGCTTCTGAATTTGAGTTTCTAGCTTTGGGGCTGCTTCTGCTTTTCTGCTTT 60
 DB 45 ATGGAATGCTTCTGCAATTTGAGTTTCTAGCTTTGGGGCTGCTTCTGCTTTTCTGCTTT 104
 QY 61 GCTGTAGAAATCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACTCAT 120
 DB 105 GCTGTACAACTCCATGAATAGCTGGTGGCAGAGACCTTGACACTGCTCTCCACTCAT 164
 QY 121 CGAATCTGGCTGATAGCGGATGGGAACCTGATGATTCCTTCTGAAATATAAATACAC 180
 DB 165 CGAATCTGATGATGCGGACGGGAACCTGATGATTCCTTCTGAAATATAAATACAC 224
 QY 181 CAATGTGCAATTAAGAAGTTTTCAGGGTATAGACACATTTGAAGAACCAACTGCCAC 240
 DB 225 CAATGTGCAATTAAGAAGTTTTCAGGGTATAGACACATTTGAAGAACCAACTGCCAC 284
 QY 241 GGGAGGCTGTGGATAAATATTCCTGCTTTTATATAAAGAACACATAGAGCGC 300
 DB 285 GGGGATGCTGTGGAAGAGCTTTTCGGAAGCTTTTATATAAAGAACACATAGAGCGC 344
 QY 301 CAAAAAAGGCTGTGAGAGAGAGTGGAGAGTGCAGAGTTCCTAGACTACCTGCA 360
 DB 345 CAAAAAAGGCTGTGAGAGAGAGTGGAGAGTGCAGAGTTCCTAGACTACCTGCA 404
 QY 361 GTATTTCTTGGTGTATATAACACCGAGTGGACACCGGAAAGT 402
 DB 405 GTGTTTCTTGGTGTATATAACACTGAGTGGACCAATGGAAGT 446
 RESULT 9
 AAT50755
 ID AAT50755 standard; DNA; 520 BP.
 XX
 AC AAT50755;
 XX
 DT 17-OCT-2003 (revised)
 DT 24-SEP-1997 (first entry)
 XX
 DE Ovine IL-5 gene.

KW Cytokine; ovine; sheep; interleukin-5; interleukin-12; IL-5; IL-12;
 KW livestock; cow; stress; transport; vaccine adjuvant; veterinary; cancer;
 KW immunosuppression; allergy; reproductive system; growth; early maturity;
 KW antibody; diagnosis; immunopotentiator;
 KW early haematopoietic progenitor cell; cytotoxic cell; thymocyte;
 KW secretion; IGM; IGA; bacterial endotoxin; gamma-interferon; ss.
 XX
 OS Ovis aries.
 XX
 FH Key Location/Qualifiers
 XX CDS 46..444
 FT /*tag= a
 FT /product= "Ovine_IL-5"
 FT 46..183
 FT exon /*tag= b
 FT 184..216
 FT exon /*tag= c
 FT 217..345
 FT exon /*tag= d
 FT 346..480
 FT exon /*tag= e
 FT 481..520
 XX
 PN W09700321-A1.
 XX
 PD 03-JAN-1997.
 XX
 PF 14-JUN-1996; 96WO-AU000360.
 XX
 PR 14-JUN-1995; 95AU-00003502.
 PR 27-OCT-1995; 95AU-00006244.
 XX
 XX (CSIR) COMMONWEALTH SCI & IND RES ORG.
 XX
 PI Seow H, Wood P;
 XX
 DR WPI; 1997-077528/07.
 DR P-PSDB; AAW08479.
 XX
 PT Nucleic acid encoding ovine interleukin-5 or -12 - used as vaccine
 PT adjuvants and to treat or prevent microbial infections in livestock.
 XX
 PS Claim 6; Page 39-40; 78pp; English.
 CC The sequences given in AAT50755-56 encode ovine interleukin-5 (IL-5).
 CC Ovine IL-5 or IL-12 are used to treat and/or prevent infections in
 CC livestock (esp. cows and sheep), particularly where the animals are
 CC stressed, e.g. during transport. IL-5 and IL-12 can also be used as
 CC adjuvants in vaccines for veterinary use (partic. weakly immunogenic
 CC subunit or synthetic peptide vaccines). They may also be used to treat
 CC cancer, immunosuppression and allergy, to enhance/suppress the
 CC reproductive system and to promote growth or early maturity. Optionally
 CC interleukin can be delivered from constructs or delivery cells and
 CC antibodies are useful in enzyme immunoassays for rapid diagnosis of
 CC infection. The interleukins are immunopotentiators, especially IL-5
 CC promotes growth of early haematopoietic progenitor cells and generation
 CC of cytotoxic cells from thymocytes, also it stimulates production and
 CC secretion of IGM and IGA (in synergism with bacterial endotoxin). IL-12
 CC induces production of gamma-interferon by, and proliferation of, T and NK
 CC cells and increases the (non-)specific cytolytic lymphocyte response. The
 CC genetic constructs can also be used for in vitro production of IL-5 or -
 CC 12. (Updated on 17-OCT-2003 to standardise OS field)
 XX
 SQ Sequence 520 BP; 166 A; 99 C; 124 G; 131 T; 0 U; 0 Other;
 Query Match 78.7%; Score 316.2; DB 2; Length 520;
 Best Local Similarity 86.8%; Pred. No. 1.4e-84;
 Matches 348; Conservative 0; Mismatches 53; Indels 0; Gaps 0;
 QY 1 ATGGAATGCTTCTGAAATTTGAGTTTCTAGCTTTGGGGCTGCTTCTGCTTTTCTGCTTT 60

PA (IDEX-) IDEXX LAB INC.
 XX Guo H, Lawton R, Mermer B, Aiyappa AP;
 XX WPI; 2001-191542/19.
 XX Novel canine interleukin 5 polynucleotide and polypeptides are used for
 PT generating antibodies which are useful in treating allergies in dogs.
 XX Claim 1; Page 35; 48pp; English.
 XX The present invention provides the protein and coding sequences of the
 CC canine interleukin-5 (IL-5) protein. This can be used to treat allergies,
 CC cancer and inflammatory reactions in dogs. The present sequence is one
 CC version of the IL-5 coding sequence shown in the specification
 XX
 XX Sequence 393 BP; 128 A; 82 C; 86 G; 97 T; 0 U; 0 Other;
 Query Match 71.5%; Score 287.4; DB 4; Length 393;
 Best Local Similarity 99.7%; Pred. No. 5.5e-76;
 Matches 288; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 103 ACATGCTCTCCACTCATCGAAGCTTGCTGATAGGCGATGGAACTGATGATCTCTACT 162
 Db 1 ACATGCTCTCCACTCATCGAAGCTTGCTGATAGGCGATGGAACTGATGATCTCTACT 60
 QY 163 CCTGAAATAAATAACCAACTGTCATTAAAGAAAGTTTTTCAGGATATAGACACATTG 222
 Db 61 CCTGAAATAAATAACCAACTGTCATTAAAGAAAGTTTTTCAGGATATAGACACATTG 120
 QY 223 AAGAACCAACTGCGCGGGAGGCTGTGATTAAGTATTCCTGTTTAAATA 282
 Db 121 AAGAACCAACTGCGCGGGAGGCTGTGATTAAGTATTCCTGTTTAAATA 190
 QY 283 AAAGAACACATAGAGCGCCCAAAAGGTTGTCAGGAGAAAGATGAGAGTGACAAAG 342
 Db 181 AAAGAACACATAGAGCGCCCAAAAGGTTGTCAGGAGAAAGATGAGAGTGACAAAG 240
 QY 343 TTCTAGACTACCTGCAAGTATTTCTTGGTGTAATAAACACCGAGTGGA 391
 Db 241 TTCTAGACTACCTGCAAGTATTTCTTGGTGTAATAAACACCGAGTGGA 289
 RESULT 12
 ID AAA34857 standard; DNA; 816 BP.
 XX AC AAA34857;
 XX
 DT 28-JUL-2000 (first entry)
 XX
 DE Human adenosine receptor related polynucleotide SEQ ID NO:2546.
 XX
 KW Human; adenosine receptor; low adenosine antisense oligonucleotide;
 KW phosphorothioate; impaired respiration; inflammation; allergy;
 KW allergic disease; bronchoconstriction; inhibitor; anti-inflammatory;
 KW antiallergic; anticholinergic; cytoskeletal; analgesic; impaired airway;
 KW lung disease; ischemic condition; pulmonary vasoconstriction; asthma;
 KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;
 KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
 KW cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.
 XX
 OS Homo sapiens.
 XX
 XX WO200009525-A2.
 XX
 PD 24-FEB-2000.
 XX
 XX 03-AUG-1999; 99WO-US017712.
 XX
 XX 03-AUG-1998; 98US-0095212P.
 XX
 XX (UYEC-) UNIV EAST CAROLINA.

XX Nyce JW.
 XX WPI; 2000-205971/18.
 XX New antisense oligonucleotides useful for treating e.g. pulmonary
 PT vasoconstriction, inflammation, allergies, asthma, hypertension,
 PT bronchitis, emphysema, respiratory distress syndrome, ischemia or
 PT cancers.
 XX
 PS Disclosure; Page 716; 1343pp; English.
 XX
 CC The present invention describes a new composition comprising an antisense
 CC oligonucleotide (ON) with low adenosine (up to 15%), which targets
 CC nucleic acids involved in bronchoconstriction, allergies, and/or
 CC inflammation. The ON can have antiinflammatory, antiallergic,
 CC anticholinergic, cytoskeletal and analgesic activities. The compositions are
 CC useful for the treatment of diseases associated with inflammation,
 CC impaired airways, including lung disease and diseases whose secondary
 CC effects afflict the lungs of a subject. They can be used for treating
 CC e.g. ischemic conditions, pulmonary vasoconstriction, allergies, asthma,
 CC impaired respiration, respiratory distress syndrome, pain, cystic
 CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive
 CC pulmonary disease (COPD), and cancers such as leukemias, lymphomas,
 CC carcinomas, and cancers which may metastasize to the lungs, including
 CC breast and prostate cancer. The reduction of the adenosine content of the
 CC ONs reduces side effects. The A-containing ONs break down with the
 CC release of deoxyadenosine which activates adenosine receptors causing
 CC bronchoconstriction and inflammation. AAA32313 to AAA35312 represent the
 CC nucleotide sequences given in the sequence listing from the present
 CC invention, which correspond to SEQ ID NO:1 to 2815, and then the last 185
 CC sequences are also called SEQ ID NO:1 to 185, but the sequences differ
 CC from the previously named sequences. SEQ ID NO:11 to 1680 (AAA32323 to
 CC AAA33992) are specifically claimed ONs from the present invention. N.B.
 CC sequences given in the disclosure of the present invention do not match
 CC up with their corresponding SEQ ID NO: sequences given in the sequence
 CC listing
 XX
 SQ Sequence 816 BP; 277 A; 137 C; 164 G; 238 T; 0 U; 0 Other;
 Query Match 69.0%; Score 277.2; DB 3; Length 816;
 Best Local Similarity 80.6%; Pred. No. 8.4e-73;
 Matches 324; Conservative 0; Mismatches 78; Indels 0; Gaps 0;
 QY 1 ATGAGATGCTTCTGAATTTGAGTTTGTCTAGCTCTTGGGGTGCCTATGTTTCTGCCTTT 60
 Db 45 ATGAGGATGCTTCTGCATTTTGTCTAGCTCTTGGAGCTGCTACGTGTATGCCATC 104
 QY 61 GCTGTAGAAAATCCCATGATAGACTGCTGTCAGAGACCTTGACACTGCTCTCCACTCAT 120
 Db 105 CCCACAGAAATCCCAAGTGCATTTGTTGAAAGAGACCTTGGACCTGTTCTACTCAT 164
 QY 121 CGAACTTGGCTGATAGCGGATGGAACTGATGATTTCTACTCTGTAATAATAAATCAC 180
 Db 165 CGAACTTGTGTATAGCAATAGACACTCTGAGGATTCCTGTTCTGTACATAAATAATCAC 224
 QY 181 CAACCTGTGCATTAAGAAGTTTTTCAGGTTATAGACACTTGAAGACCAACTGCCAC 240
 Db 225 CACTGTGCTCTGAAGAATACTTTTCAGGAAATAGGCACCTGGAGATCAACTGTGCAA 284
 QY 241 GGGGAGGCTGTGGATAAACTATTCCAAAACCTGTTTAAATAAAGAACACATAGAGCGC 300
 Db 285 GGGGCTACTGTGGAAGACACTATTCAAAAACCTTGTCTTAAATAAAGAAATACATTGCGGC 344
 QY 301 CAAAAAAGGTTGTCAGGAGAAAGATGGAGTGTGCAAGTTCTTAGACTACCTGCAA 360
 Db 345 CAAAAAAGGTTGTCAGGAGAAAGATGGAGTGTGCAAGTTCTTAGACTACCTGCAA 404
 QY 361 GTATTTCTTGGTGAATAAATAACCCAGTGGACACCGGAAAGT 402
 Db 405 GAGTTTCTTGGTGAATAAATAACCCAGTGGATGATATAGAAAGT 446

[illegible]

RESULT 14	
AAF20979	
ID	AAF20979 standard; DNA; 816 BP.
XX	
XX	
XX	AAF20979;
XX	
XX	
DT	14-MAR-2001 (first entry)
DE	
XX	Human low adenosine antisense oligonucleotide related sequence #2546.
XX	
KW	Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
KW	human; airway disorder; bronchoconstriction; lung inflammation;
KW	surfactant depletion; respiratory; bronchodilator; antiinflammatory;
KW	immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic;
KW	respiratory obstruction; pulmonary obstruction; impeded respiration;
KW	surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
KW	respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
KW	pulmonary hypertension; emphysema; pulmonary transplantation rejection;
KW	chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
XX	cancer; ss.
XX	
OS	Homo sapiens.
XX	
XX	WC200062736-A2.
PN	
XX	
PD	26-OCT-2000.
XX	
PF	24-MAR-2000; 2000WO-US008020.
XX	
PR	06-APR-1999; 99US-0127958P.
XX	
XX	{UYEC-} UNIV EAST CAROLINA.
PA	(NYCE/) NYCE J W.
XX	
XX	
PI	Nyce JW;
XX	
XX	
DR	WPI; 2000-679539/66.
XX	
PT	Low adenosine (A) content antisense oligonucleotides which do not trigger
XX	adenosine receptors during metabolism, useful e.g. for treating cancers
PT	and respiratory obstructions.
XX	
PS	Disclosure; Page 788; 1592pp; English.

The present invention describes low adenosine (A) content antisense oligonucleotides and compositions (I) comprising them. In the antisense oligonucleotides the A is replaced by a 'Universal' or alternative base. (I) can have respiratory, bronchodilator, antiinflammatory, analgesic, immunosuppressive, antiasthmatic, hypotensive and cytostatic activities. The antisense oligonucleotides and (I) can be used to down-regulate the expression and/or activity of target polypeptides associated with lung/respiratory disorders and malignancies, such as stimulating and activating peptide factors and transmitters, transcription factors, immunoglobulins and antibodies, antibody receptors, cytokines and chemokines, endogenously produced specific and non-specific enzymes, binding proteins, adhesion molecules and their receptors, cytokines and chemokine receptors, adenosine receptors, bradykinin receptors, central nervous system (CNS) and peripheral nervous and non-nervous system receptors, CNS and peripheral nervous and non-nervous system peptide transmitters, defensins, growth factors, vasoactive peptides and receptors, binding proteins and malignancy associated proteins. The antisense oligonucleotides may be used in this way to treat disorders including respiratory obstruction (especially pulmonary obstruction

RESULT 13
 AAAA13338
 IID AAAA13338 standard; cDNA; 816 BP.
 XX
 XX AAAA13338;
 XX
 XX
 XX DT 25-JUL-2000 (first entry)
 XX
 XX Human interleukin-5 (IL-5) nucleotide sequence.
 XX
 XX
 XX Human; interleukin-5; IL-5; inflammatory disease; asthma; eczema;
 KW antisenese oligonucleotide; allergic rhinitis; inflammatory skin disease;
 KW allergic conjunctivitis; inhibitor; ss.
 XX
 XX Homo sapiens.
 OS
 XX
 XX US6048726-A.
 XX
 XX 11-APR-2000.
 PD
 XX
 XX PF 15-MAY-1998; 98US-00079839.
 XX
 XX PF 15-MAY-1998; 98US-00079839.
 XX
 XX (WELT/) WELTMAN J K.
 PA (KARI/) KARIM A S.
 PP
 XX
 XX WELTMAN JK, Karim AS;
 PI
 XX
 XX MPI; 2000-302784/26.
 XX
 XX
 XX PPT Oligonucleotide comprising non-natural internucleoside linkage, useful
 PPT for inhibiting interleukin-5 expression and treating inflammatory
 PPT diseases, asthma, allergic rhinitis, allergic conjunctivitis.
 XX
 XX
 XX Disclosure: Col 3-4; ilpp; English.

This sequence represents the human interleukin-5 (IL-5) encoding nucleotide sequence. Interleukin-5 is involved in eosinophilic inflammation and inflammatory disorders. The present invention relates to an IL-5 antisense oligonucleotide (see AAL1337) which inhibits the expression of IL-5. The antisense oligonucleotide has at least one non-natural internucleoside linkage. The oligonucleotide is able to inhibit IL-5 secretion in a dose dependent manner, and is useful for inhibiting IL-5 expression and therefore treating inflammatory diseases, asthma, allergic rhinitis, allergic conjunctivitis and inflammatory skin diseases such as eczema.

Sequence 816 BP; 277 A; 137 C; 164 G; 238 T; 0 U; 0 Other;
Query Match 69.0%; Score 277.2; DB 3; Length 816;
Best Local Similarity 80.6%; Pred. No. 8.4e-73;
Matches 324; Conservative 0; Mismatches 78; Indels 0; Gaps 0;

QY	1	ATGGAAGTCTTCGAATTGAGTTTGCTAGCTCTTGGGCTGCCATGTTTCTGCCTTT	60
Db	45	ATGAGATGCTTCTGCATTTGAGTTTGCTAGCTCTTGGAGCTGCCTAGTGATGCCATC	104
QY	61	GCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACTCAT	120
Db	105	CCACAGAAATTCACCAAGTGCAATTGGTGAAGAGACCTTGGCACTGCTTCTACTCAT	164
QY	121	CGAACTTGGCTGATAGGCGATGGGAACCTGATGATTCCTACTCCTGAAATAATAAATCAC	180
Db	165	CGAACTCTGCTGATAGCCAAATGAGACTCTGAGGATTCCTGTTCTGTACATAAAAAATCAC	224
QY	181	CAACTGTGCNTTAAGAAGTTTTCAGGGTATAGACACATGAAGAACCAAACTGCCAC	240
Db	225	CAACTGTGCACCTGAAGAAATCTTTTCAGGGAAATAGGCACCTGGAGACTCAAACTGTGGA	284
QY	241	GGGAGGCTGTGGATAAACTATCCAAAACTGCTCTTAATAAAGAACACATAGAGCGC	300
Db	285	GGGGCTACTGTGGAAAGACTATCAAAACTGTGCTTAAATGAAGAAATACATTGACGGC	344

OM nucleic - nucleic search, using sw model

Run on: August 30, 2004, 20:51:08 ; Search time 35.8667 Seconds
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Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA:*

1: /cgn2_6/ptodata/2/ina/5A_COMB.seq.*
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3: /cgn2_6/ptodata/2/ina/6A_COMB.seq.*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq.*
5: /cgn2_6/ptodata/2/ina/pctus_COMB.seq.*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	402	100.0	402	4	US-09-322-409-83
2	402	100.0	402	4	US-09-322-409-84
3	402	100.0	402	4	US-09-451-527-83
4	402	100.0	402	4	US-09-451-527-84
5	402	100.0	610	4	US-09-322-409-80
6	402	100.0	610	4	US-09-322-409-82
7	402	100.0	610	4	US-09-451-527-80
8	402	100.0	610	4	US-09-451-527-82
9	398.8	99.2	405	4	US-09-371-615A-1
10	345	85.8	345	4	US-09-322-409-85
11	345	85.8	345	4	US-09-322-409-87
12	345	85.8	345	4	US-09-322-409-87
13	345	85.8	345	4	US-09-451-527-85
14	277.2	69.0	816	3	US-09-079-839-2
15	275.6	68.6	816	4	US-09-023-655-1236
16	206.4	51.3	1534	3	US-09-629-643A-4
17	206.4	51.3	1534	3	US-09-155-884-4
18	206.2	51.3	377	4	US-09-180-864-1
19	99.4	24.7	3230	3	US-09-280-799-78
20	99.4	24.7	3230	6	5324640-1
21	90.6	22.5	6727	3	US-08-629-643A-5
22	90.6	22.5	6727	3	US-09-280-799-1
23	90.6	22.5	6727	3	US-09-155-884-5
24	40.2	10.0	47	1	US-08-466-852-2
25	38	9.5	7218	1	US-08-232-463-14
26	34.4	8.6	4843	3	US-08-986-485-1
27	33.4	8.3	22846	2	US-08-469-461-3

28 33.4 8.3 22846 3 US-07-890-609-3 Sequence 3, Appli
c 29 32.4 8.1 2797 4 US-09-453-702B-244 Sequence 244, App
c 30 31.8 7.9 832 4 US-09-621-976-2813 Sequence 2813, Ap
c 31 31.8 7.9 1902 4 US-09-220-132-74 Sequence 74, Appl
c 32 31.6 7.9 927 4 US-09-134-001C-150 Sequence 150, App
c 33 31.6 7.9 1642 4 US-08-737-698B-24 Sequence 24, Appl
c 34 31.6 7.9 1642 4 US-09-737-626A-24 Sequence 24, Appl
c 35 31.6 7.9 9626 4 US-09-150-867-2 Sequence 2, Appli
c 36 31.6 7.9 174493 4 US-09-804-471A-3 Sequence 3, Appli
c 37 31.6 7.9 174493 4 US-10-238-709-3 Sequence 3, Appli
c 38 31.6 7.9 1664976 4 US-08-916-421B-1 Sequence 1, Appli
c 39 31.4 7.8 1497 4 US-09-220-132-94 Sequence 94, Appli
c 40 31.4 7.8 21338 4 US-08-961-527-20 Sequence 20, Appl
c 41 31.2 7.8 505 4 US-09-621-976-15639 Sequence 15639, A
c 42 31.2 7.8 1664976 4 US-08-916-421B-1 Sequence 1, Appli
c 43 31 7.7 222 4 US-09-543-681A-1166 Sequence 1166, Ap
c 44 31 7.7 3434 4 US-09-388-743-9 Sequence 9, Appli
c 45 30.8 7.7 1842 4 US-09-328-352-2806 Sequence 2806, Ap

ALIGNMENTS

RESULT 1

US-09-322-409-83 ; Sequence 83, Application US/09322409
; Patent No. 6471957
; GENERAL INFORMATION:
; APPLICANT: Sim, Gek-kee
; APPLICANT: Yang, Shumin
; APPLICANT: Dreitz, Matthew J.
; APPLICANT: Wonderting, Ramani S.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; FILE REFERENCE: IM-2-C1
; CURRENT APPLICATION NUMBER: US/09/322,409
; CURRENT FILING DATE: 1999-05-28
; EARLIER APPLICATION NUMBER: 60/087,306
; EARLIER FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 154
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 83
; LENGTH: 402
; TYPE: DNA
; ORGANISM: Canis familiaris
US-09-322-409-83

Query Match 100.0%; Score 402; DB 4; Length 402;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGATGCTTCTGAATTTGAGTTTGTAGCTCTTGGGGCTGCTATGTTTCTGCTTT 60
DB 1 ATGAGATGCTTCTGAATTTGAGTTTGTAGCTCTTGGGGCTGCTATGTTTCTGCTTT 60
QY 61 GCTGTAGAAAATCCCATGAATAGACTGTGGCAGAGACCTTGACACTGCTCTCCACTCAT 120
DB 61 GCTGTAGAAAATCCCATGAATAGACTGTGGCAGAGACCTTGACACTGCTCTCCACTCAT 120
QY 121 CGAAGTGGCTGATAGGCGATCGGACCTGATGATCTTCTACTCTGAAATATAATCAT 180
DB 121 CGAAGTGGCTGATAGGCGATCGGACCTGATGATCTTCTACTCTGAAATATAATCAT 180
QY 181 CCACTGTGATTAAGAAAGTCTTTTTCAGGGTATAGACACATTAAGAAACCAAACTGCCAC 240
DB 181 CCACTGTGATTAAGAAAGTCTTTTTCAGGGTATAGACACATTAAGAAACCAAACTGCCAC 240
QY 241 GGGAGGCTGTGATTAATCTTCCAAAACCTTGTCTTTTAAATAAGAACACATAGAGCG 300
DB 241 GGGAGGCTGTGATTAATCTTCCAAAACCTTGTCTTTTAAATAAGAACACATAGAGCG 300
QY 301 CAAATAAAGGTGTGTCAGGAGAAAGATGAGAGTGCACAAAGTTCCTAGACTACCTGCAA 360

Db 301 CAAAAAAGGTTGTCAGGAGAAAGATGGAGAGTGACAAAGTTCTTAGACTACCTGCAA 360
QY 361 GTATTTCTTGTTGTAATAAACACCGAGTGGACACCGGAAAGT 402
Db 361 GTATTTCTTGTTGTAATAAACACCGAGTGGACACCGGAAAGT 402

RESULT 2

US-09-322-409-84/c
; Sequence 84, Application US/09322409
; Patent No. 6471957
; GENERAL INFORMATION:
; APPLICANT: Sim, Gek-kee
; APPLICANT: Yang, Shumin
; APPLICANT: Dreitz, Matthew J.
; APPLICANT: Wonderling, Ramani S.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; FILE REFERENCE: IM-2-C1
; CURRENT APPLICATION NUMBER: US/09/322,409
; EARLIER FILING DATE: 1999-05-28
; EARLIER APPLICATION NUMBER: 60/087,306
; NUMBER OF SEQ ID NOS: 154
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 84
; LENGTH: 402
; TYPE: DNA
; ORGANISM: Canis familiaris
US-09-322-409-84

Query Match 100.0%; Score 402; DB 4; Length 402;
Best Local Similarity 100.0%; Pred. No. 5,9e-123;
Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGATGCTTCTGAAATTTGAGTTTGTCTAGCTCTTGGGCTGCCTATGTTTCTGCTTT 60
Db 402 ATGAGATGCTTCTGAAATTTGAGTTTGTCTAGCTCTTGGGCTGCCTATGTTTCTGCTTT 60
QY 61 GCTGTAGAAAATCCCATGAATAGACTGCTGGCAGAGACCTTGACACTGCTCTCCACTCAT 120
Db 342 GCTGTAGAAAATCCCATGAATAGACTGCTGGCAGAGACCTTGACACTGCTCTCCACTCAT 120
QY 121 CGAATCTGGCTGATAGCGGATGGGAACCTGATGATTTCTCTCTCTCTCTCTCTCTCTCT 180
Db 282 CGAATCTGGCTGATAGCGGATGGGAACCTGATGATTTCTCTCTCTCTCTCTCTCTCTCT 180
QY 181 CAATCTGTCATTAAGAAGTTTTCAGGGTATAGACATTTGAAGAACCAAACTGCCAC 240
Db 222 CAATCTGTCATTAAGAAGTTTTCAGGGTATAGACATTTGAAGAACCAAACTGCCAC 240
QY 241 GGGAGGCTGTGGATAAATATTCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 300
Db 162 GGGAGGCTGTGGATAAATATTCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 300
QY 301 CAAAAAAGGTTGTCAGGAGAAAGATGGAGAGTGACAAAGTTCTTAGACTACCTGCAA 360
Db 102 CAAAAAAGGTTGTCAGGAGAAAGATGGAGAGTGACAAAGTTCTTAGACTACCTGCAA 43
QY 361 GTATTTCTTGTTGTAATAAACACCGAGTGGACACCGGAAAGT 402
Db 42 GTATTTCTTGTTGTAATAAACACCGAGTGGACACCGGAAAGT 1

RESULT 3

US-09-451-527-83
; Sequence 83, Application US/09451527
; Patent No. 6482403
; GENERAL INFORMATION:
; APPLICANT: Sim, Gek-kee
; APPLICANT: Yang, Shumin
; APPLICANT: Dreitz, Matthew J.
; APPLICANT: Wonderling, Ramani S.

; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; FILE REFERENCE: IM-2-C2
; CURRENT APPLICATION NUMBER: US/09/451,527
; EARLIER FILING DATE: 1999-12-01
; EARLIER APPLICATION NUMBER: 09/322,409
; EARLIER FILING DATE: 1999-05-28
; EARLIER APPLICATION NUMBER: 60/087,306
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 83
; LENGTH: 402
; TYPE: DNA
; ORGANISM: Canis familiaris
US-09-451-527-83

Query Match 100.0%; Score 402; DB 4; Length 402;
Best Local Similarity 100.0%; Pred. No. 5,9e-123;
Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGATGCTTCTGAAATTTGAGTTTGTCTAGCTCTTGGGCTGCCTATGTTTCTGCTTT 60
Db 1 ATGAGATGCTTCTGAAATTTGAGTTTGTCTAGCTCTTGGGCTGCCTATGTTTCTGCTTT 60
QY 61 GCTGTAGAAAATCCCATGAATAGACTGCTGGCAGAGACCTTGACACTGCTCTCCACTCAT 120
Db 61 GCTGTAGAAAATCCCATGAATAGACTGCTGGCAGAGACCTTGACACTGCTCTCCACTCAT 120
QY 121 CGAATCTGGCTGATAGCGGATGGGAACCTGATGATTTCTCTCTCTCTCTCTCTCTCTCT 180
Db 121 CGAATCTGGCTGATAGCGGATGGGAACCTGATGATTTCTCTCTCTCTCTCTCTCTCTCT 180
QY 181 CAATCTGTCATTAAGAAGTTTTCAGGGTATAGACATTTGAAGAACCAAACTGCCAC 240
Db 181 CAATCTGTCATTAAGAAGTTTTCAGGGTATAGACATTTGAAGAACCAAACTGCCAC 240
QY 241 GGGAGGCTGTGGATAAATATTCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 300
Db 241 GGGAGGCTGTGGATAAATATTCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 300
QY 301 CAAAAAAGGTTGTCAGGAGAAAGATGGAGAGTGACAAAGTTCTTAGACTACCTGCAA 360
Db 301 CAAAAAAGGTTGTCAGGAGAAAGATGGAGAGTGACAAAGTTCTTAGACTACCTGCAA 360
QY 361 GTATTTCTTGTTGTAATAAACACCGAGTGGACACCGGAAAGT 402
Db 361 GTATTTCTTGTTGTAATAAACACCGAGTGGACACCGGAAAGT 402

RESULT 4

US-09-451-527-84/c
; Sequence 84, Application US/09451527
; Patent No. 6482403
; GENERAL INFORMATION:
; APPLICANT: Sim, Gek-kee
; APPLICANT: Yang, Shumin
; APPLICANT: Dreitz, Matthew J.
; APPLICANT: Wonderling, Ramani S.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; FILE REFERENCE: IM-2-C2
; CURRENT APPLICATION NUMBER: US/09/451,527
; EARLIER FILING DATE: 1999-12-01
; EARLIER APPLICATION NUMBER: 09/322,409
; EARLIER FILING DATE: 1999-05-28
; EARLIER APPLICATION NUMBER: 60/087,306
; EARLIER FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 84
; LENGTH: 402
; TYPE: DNA

```
; ORGANISM: Canis familiaris
US-09-451-527-84

Query Match      100.0%; Score 402; DB 4; Length 610;
Best Local Similarity 100.0%; Pred. No. 5.9e-123;
Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGAATGCTTCTGAATTTGAGTTTGTCTAGCTCTTGGGCTGCGCTATGTTTCTGCTTT 60
DB 402 ATGAGAATGCTTCTGAATTTGAGTTTGTCTAGCTCTTGGGCTGCGCTATGTTTCTGCTTT 343

QY 61 GCTGTAGAAATCCCATGATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACTCAT 120
DB 342 GCTGTAGAAATCCCATGATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACTCAT 283

QY 121 CGAACTTGGCTGATAGCGGATGGAACTTCCAGGTATAGACACATTGAAGAACCAAACTGCCAC 180
DB 282 CGAACTTGGCTGATAGCGGATGGAACTTCCAGGTATAGACACATTGAAGAACCAAACTGCCAC 223

QY 181 CAACCTGTGCATTAAGAAAGTTTTCAGGGTATAGACACATTGAAGAACCAAACTGCCAC 240
DB 222 CAACCTGTGCATTAAGAAAGTTTTCAGGGTATAGACACATTGAAGAACCAAACTGCCAC 163

QY 241 GGGGAGGCTGTGGAATACTTATCCAAACTTGTCTTTAATAAAGAACACATAGAGCGC 300
DB 162 GGGGAGGCTGTGGAATACTTATCCAAACTTGTCTTTAATAAAGAACACATAGAGCGC 103

QY 301 CAAAAAAGGTTGTCAGGAGAAAGATGGAGAGTGACAAAGTTCTTAGACTACCTGCAA 360
DB 102 CAAAAAAGGTTGTCAGGAGAAAGATGGAGAGTGACAAAGTTCTTAGACTACCTGCAA 43

QY 361 GTATTTCTTGGTGAATAAATTAACACCGAGTGGACACCGGAAAGT 402
DB 42 GTATTTCTTGGTGAATAAATTAACACCGAGTGGACACCGGAAAGT 1

RESULT 5
US-09-322-409-80
; Sequence 80, Application US/09322409
; Patent No. 6471957
; GENERAL INFORMATION:
; APPLICANT: Sim, Gek-kee
; APPLICANT: Yang, Shumin
; APPLICANT: Dreitz, Matthew J.
; APPLICANT: Wonderling, Ramani S.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; FILE REFERENCE: IM-2-CI
; CURRENT APPLICATION NUMBER: US/09/322,409
; CURRENT FILING DATE: 1999-05-28
; EARLIER FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 154
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 80
; LENGTH: 610
; TYPE: DNA
; ORGANISM: Canis familiaris
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (29)..(430)
US-09-322-409-80

Query Match      100.0%; Score 402; DB 4; Length 610;
Best Local Similarity 100.0%; Pred. No. 7.3e-123;
Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGAATGCTTCTGAATTTGAGTTTGTCTAGCTCTTGGGCTGCGCTATGTTTCTGCTTT 60
DB 29 ATGAGAATGCTTCTGAATTTGAGTTTGTCTAGCTCTTGGGCTGCGCTATGTTTCTGCTTT 88

QY 61 GCTGTAGAAATCCCATGATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACTCAT 120

US-09-322-409-82
; Sequence 82, Application US/09322409
; Patent No. 6471957
; GENERAL INFORMATION:
; APPLICANT: Sim, Gek-kee
; APPLICANT: Yang, Shumin
; APPLICANT: Dreitz, Matthew J.
; APPLICANT: Wonderling, Ramani S.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; FILE REFERENCE: IM-2-CI
; CURRENT APPLICATION NUMBER: US/09/322,409
; CURRENT FILING DATE: 1999-05-28
; EARLIER FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 154
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 82
; LENGTH: 610
; TYPE: DNA
; ORGANISM: Canis familiaris
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (29)..(430)
US-09-322-409-82

Query Match      100.0%; Score 402; DB 4; Length 610;
Best Local Similarity 100.0%; Pred. No. 7.3e-123;
Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGAATGCTTCTGAATTTGAGTTTGTCTAGCTCTTGGGCTGCGCTATGTTTCTGCTTT 60
DB 582 ATGAGAATGCTTCTGAATTTGAGTTTGTCTAGCTCTTGGGCTGCGCTATGTTTCTGCTTT 523

QY 61 GCTGTAGAAATCCCATGATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACTCAT 120
DB 522 GCTGTAGAAATCCCATGATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACTCAT 463

QY 121 CGAACTTGGCTGATAGCGGATGGAACTTCCAGGTATAGACACATTGAAGAACCAAACTGCCAC 180
DB 462 CGAACTTGGCTGATAGCGGATGGAACTTCCAGGTATAGACACATTGAAGAACCAAACTGCCAC 403

QY 181 CAACCTGTGCATTAAGAAAGTTTTCAGGGTATAGACACATTGAAGAACCAAACTGCCAC 240
DB 402 CAACCTGTGCATTAAGAAAGTTTTCAGGGTATAGACACATTGAAGAACCAAACTGCCAC 343

QY 241 GGGGAGGCTGTGGAATACTTATCCAAACTTGTCTTTAATAAAGAACACATAGAGCGC 300
DB 342 GGGGAGGCTGTGGAATACTTATCCAAACTTGTCTTTAATAAAGAACACATAGAGCGC 283

QY 301 CAAAAAAGGTTGTCAGGAGAAAGATGGAGAGTGACAAAGTTCTTAGACTACCTGCAA 360
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Db 282 CAAAAAAGGTGTGCGAGGAAGATGGAGAGTGACAAAGTTCCTAGACTACCTGCAA 223
 QY 361 GTATTCTTGGTGTAAATAAACACCGAGTGGACACCGGAAAGT 402
 Db 222 GTATTCTTGGTGTAAATAAACACCGAGTGGACACCGGAAAGT 181

RESULT 7

US-09-451-527-80
 ; Sequence 80, Application US/09451527
 ; Patent No. 6482403
 ; GENERAL INFORMATION:
 ; APPLICANT: Sim, Gek-Kee
 ; APPLICANT: Yang, Shumin
 ; APPLICANT: Dreitz, Matthew J.
 ; APPLICANT: Wonderling, Ramani S.
 ; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
 ; FILE REFERENCE: IM-2-C2
 ; CURRENT APPLICATION NUMBER: US/09/451,527
 ; EARLIER FILING DATE: 1999-12-01
 ; EARLIER APPLICATION NUMBER: 09/322,409
 ; EARLIER FILING DATE: 1999-05-28
 ; EARLIER APPLICATION NUMBER: 60/087,306
 ; EARLIER FILING DATE: 1998-05-29
 ; NUMBER OF SEQ ID NOS: 174
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 80
 ; LENGTH: 610
 ; TYPE: DNA
 ; ORGANISM: Canis familiaris
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (29)...(430)
 US-09-451-527-80

Query Match 100.0%; Score 402; DB 4; Length 610;
 Best Local Similarity 100.0%; Pred. No. 7.3e-123;
 Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ATGAGATGCTTCGAAATTTGAGTTTGCTAGCTCTGGGGCTGCCTATGTTTCTGCGCTTT 60
 Db 29 ATGAGATGCTTCGAAATTTGAGTTTGCTAGCTCTGGGGCTGCCTATGTTTCTGCGCTTT 68
 QY 61 GCTGTAGAAAATCCCATGAATAGACTGTGGCAGAGACCTTGACACTGCTCTCCACTCAT 120
 Db 89 GCTGTAGAAAATCCCATGAATAGACTGTGGCAGAGACCTTGACACTGCTCTCCACTCAT 148
 QY 121 CGAACTTGGCTGATAGCGGATGGAACTGATTCCTACTCTGAAATAAATAATCAC 180
 Db 149 CGAACTTGGCTGATAGCGGATGGAACTGATTCCTACTCTGAAATAAATAATCAC 208
 QY 181 CAACGTGCAATTAAGAAAGTTTTCAGGGTATAGACATTTGAAGAACCAAACTGCCAC 240
 Db 209 CAACGTGCAATTAAGAAAGTTTTCAGGGTATAGACATTTGAAGAACCAAACTGCCAC 268
 QY 241 GGGAGGCTGTGGATAAACTATTCCAAACTCTCTTTTAAATAAAGAACACATAGAGCGC 300
 Db 269 GGGAGGCTGTGGATAAACTATTCCAAACTCTCTTTTAAATAAAGAACACATAGAGCGC 328
 QY 301 CAAAAAAGGTGTGCGAGGAAGATGGAGAGTGACAAAGTTCCTAGACTACCTGCAA 360
 Db 329 CAAAAAAGGTGTGCGAGGAAGATGGAGAGTGACAAAGTTCCTAGACTACCTGCAA 388
 QY 361 GTATTCTTGGTGTAAATAAACACCGAGTGGACACCGGAAAGT 402
 Db 389 GTATTCTTGGTGTAAATAAACACCGAGTGGACACCGGAAAGT 430

RESULT 8

US-09-451-527-82/c
 ; Sequence 82, Application US/09451527
 ; Patent No. 6482403

; GENERAL INFORMATION:
 ; APPLICANT: Sim, Gek-Kee
 ; APPLICANT: Yang, Shumin
 ; APPLICANT: Dreitz, Matthew J.
 ; APPLICANT: Wonderling, Ramani S.
 ; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
 ; FILE REFERENCE: IM-2-C2
 ; CURRENT APPLICATION NUMBER: US/09/451,527
 ; EARLIER FILING DATE: 1999-12-01
 ; EARLIER APPLICATION NUMBER: 09/322,409
 ; EARLIER FILING DATE: 1999-05-28
 ; EARLIER APPLICATION NUMBER: 60/087,306
 ; EARLIER FILING DATE: 1998-05-29
 ; NUMBER OF SEQ ID NOS: 174
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 82
 ; LENGTH: 610
 ; TYPE: DNA
 ; ORGANISM: Canis familiaris
 US-09-451-527-82

Query Match 100.0%; Score 402; DB 4; Length 610;
 Best Local Similarity 100.0%; Pred. No. 7.3e-123;
 Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGATGCTTCGAAATTTGAGTTTGCTAGCTCTGGGGCTGCCTATGTTTCTGCGCTTT 60
 Db 582 ATGAGATGCTTCGAAATTTGAGTTTGCTAGCTCTGGGGCTGCCTATGTTTCTGCGCTTT 523
 QY 61 GCTGTAGAAAATCCCATGAATAGACTGTGGCAGAGACCTTGACACTGCTCTCCACTCAT 120
 Db 522 GCTGTAGAAAATCCCATGAATAGACTGTGGCAGAGACCTTGACACTGCTCTCCACTCAT 463
 QY 121 CGAACTTGGCTGATAGCGGATGGAACTGATTCCTACTCTGAAATAAATAATCAC 180
 Db 462 CGAACTTGGCTGATAGCGGATGGAACTGATTCCTACTCTGAAATAAATAATCAC 403
 QY 181 CAACGTGCAATTAAGAAAGTTTTCAGGGTATAGACATTTGAAGAACCAAACTGCCAC 240
 Db 402 CAACGTGCAATTAAGAAAGTTTTCAGGGTATAGACATTTGAAGAACCAAACTGCCAC 343
 QY 241 GGGAGGCTGTGGATAAACTATTCCAAACTCTCTTTTAAATAAAGAACACATAGAGCGC 300
 Db 342 GGGAGGCTGTGGATAAACTATTCCAAACTCTCTTTTAAATAAAGAACACATAGAGCGC 283
 QY 301 CAAAAAAGGTGTGCGAGGAAGATGGAGAGTGACAAAGTTCCTAGACTACCTGCAA 360
 Db 282 CAAAAAAGGTGTGCGAGGAAGATGGAGAGTGACAAAGTTCCTAGACTACCTGCAA 223
 QY 361 GTATTCTTGGTGTAAATAAACACCGAGTGGACACCGGAAAGT 402
 Db 222 GTATTCTTGGTGTAAATAAACACCGAGTGGACACCGGAAAGT 181

RESULT 9

US-09-371-615A-1
 ; Sequence 1, Application US/09371615A
 ; Patent No. 6537781
 ; GENERAL INFORMATION:
 ; APPLICANT: IDEXX LABORATORIES
 ; TITLE OF INVENTION: METHODS AND COMPOSITIONS CONCERNING
 ; FILE REFERENCE: 03604001700US00
 ; CURRENT APPLICATION NUMBER: US/09/371,615A
 ; CURRENT FILING DATE: 1999-08-10
 ; NUMBER OF SEQ ID NOS: 8
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 1
 ; LENGTH: 405
 ; TYPE: DNA
 ; ORGANISM: Canis familiaris
 US-09-371-615A-1

Query Match 99.2%; Score 398.8; DB 4; Length 405;
Best Local Similarity 99.5%; Pred. No. 6.7e-122;
Matches 400; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGAGAATGCTTCTGAATTTGAGTTTGTAGCTCTTGGGCTGCTTATGTTCTGCTTT 60
DB 1 ATGAGAATGCTTCTGAATTTGAGTTTGTAGCTCTTGGGCTGCTTATGTTCTGCTTT 60

QY 61 GCTGTAGAAATCCCATGATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACTCAT 120
DB 61 GCTGTAGAAATCCCATGATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACTCAT 120

QY 121 CGAACTTGGCTGATAGCGATGGGAACCTGATGATTTCTTACTCTCTGAAAAATAAAATCAC 180
DB 121 CGAACTTGGCTGATAGCGATGGGAACCTGATGATTTCTTACTCTCTGAAAAATAAAATCAC 180

QY 181 CAACCTGTGCTTAAAGAAAGTTTTCAGGGTATAGACATTTGAGAACCAAACTGCCAC 240
DB 181 CAACCTGTGCTTAAAGAAAGTTTTCAGGGTATAGACATTTGAGAACCAAACTGCCAC 240

QY 241 GGGGAGCTCTGATAAATCTATCCAAAACCTTCTTTTAAATAAAGAACACATAGAGCGC 300
DB 241 GGGGAGCTCTGATAAATCTATCCAAAACCTTCTTTTAAATAAAGAACACATAGAGCGC 300

QY 301 CAAAAAAGGCTGAGAGAAAGATGAGAGTGACAAAGTTCTTAGACTACCTGCAA 360
DB 301 CAAAAAAGGCTGAGAGAAAGATGAGAGTGACAAAGTTCTTAGACTACCTGCAA 360

QY 361 GTATTTCTTGGTGTATTAACACCGAGTGGACACCGGAAAGT 402
DB 361 GTATTTCTTGGTGTATTAACACCGAGTGGACATGGAAGT 402

RESULT 10
US-09-322-409-85
; Sequence 85, Application US/09322409
; Patent No. 6471957
; GENERAL INFORMATION:
; APPLICANT: Sim, Gek-Kee
; APPLICANT: Yang, Shumin
; APPLICANT: Dreitz, Matthew J.
; APPLICANT: Wonderling, Ramani S.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; FILE REFERENCE: IM-2-Cl
; CURRENT APPLICATION NUMBER: US/09/322,409
; CURRENT FILING DATE: 1999-05-28
; EARLIER FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 154
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 85
; LENGTH: 345
; TYPE: DNA
; ORGANISM: Canis familiaris

Query Match 85.8%; Score 345; DB 4; Length 345;
Best Local Similarity 100.0%; Pred. No. 3.5e-104;
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 58 TTTGCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACT 117
DB 1 TTTGCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACT 60

QY 118 CATCGAACTTGGCTGATAGCGGATGGAACTGATGATTTCTTACTCTGAAAAATAAAAT 177
DB 61 CATCGAACTTGGCTGATAGCGGATGGAACTGATGATTTCTTACTCTGAAAAATAAAAT 120

QY 178 CACCAACTGTGCATTAAGAAGTTTTCAGGGTATAGACATTTGAAGAACCAAACTGCC 237
DB 121 CACCAACTGTGCATTAAGAAGTTTTCAGGGTATAGACATTTGAAGAACCAAACTGCC 180

QY 238 CACGGGGAGGCTGTGGATAAACTATTCAAAACCTTGTCTTTTAAATAAAGAACACATAGAG 297
DB 181 CACGGGGAGGCTGTGGATAAACTATTCAAAACCTTGTCTTTTAAATAAAGAACACATAGAG 240

QY 298 CGCCAAAAAAGGCTGTGCAGGAGAAAGATGAGAGTGACAAAGTTCTTAGACTACCTG 357
DB 241 CGCCAAAAAAGGCTGTGCAGGAGAAAGATGAGAGTGACAAAGTTCTTAGACTACCTG 300

QY 358 CAAGTATTTCTTGGTGTATTAACACCGAGTGGACACCGGAAAGT 402
DB 301 CAAGTATTTCTTGGTGTATTAACACCGAGTGGACACCGGAAAGT 345

RESULT 11
US-09-322-409-87/c
; Sequence 87, Application US/09322409
; Patent No. 6471957
; GENERAL INFORMATION:
; APPLICANT: Sim, Gek-Kee
; APPLICANT: Yang, Shumin
; APPLICANT: Dreitz, Matthew J.
; APPLICANT: Wonderling, Ramani S.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; FILE REFERENCE: IM-2-Cl
; CURRENT APPLICATION NUMBER: US/09/322,409
; CURRENT FILING DATE: 1999-05-28
; EARLIER FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 154
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 87
; LENGTH: 345
; TYPE: DNA
; ORGANISM: Canis familiaris

Query Match 85.8%; Score 345; DB 4; Length 345;
Best Local Similarity 100.0%; Pred. No. 3.5e-104;
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 58 TTTGCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACT 117
DB 345 TTTGCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACT 286

QY 118 CATCGAACTTGGCTGATAGCGGATGGAACTGATGATTTCTTACTCTGAAAAATAAAAT 177
DB 285 CATCGAACTTGGCTGATAGCGGATGGAACTGATGATTTCTTACTCTGAAAAATAAAAT 226

QY 178 CACCAACTGTGCATTAAGAAGTTTTCAGGGTATAGACATTTGAAGAACCAAACTGCC 237
DB 225 CACCAACTGTGCATTAAGAAGTTTTCAGGGTATAGACATTTGAAGAACCAAACTGCC 166

QY 238 CACGGGGAGGCTGTGGATAAACTATTCAAAACCTTGTCTTTTAAATAAAGAACACATAGAG 297
DB 165 CACGGGGAGGCTGTGGATAAACTATTCAAAACCTTGTCTTTTAAATAAAGAACACATAGAG 106

QY 298 CGCCAAAAAAGGCTGTGCAGGAGAAAGATGAGAGTGACAAAGTTCTTAGACTACCTG 357
DB 105 CGCCAAAAAAGGCTGTGCAGGAGAAAGATGAGAGTGACAAAGTTCTTAGACTACCTG 46

QY 358 CAAGTATTTCTTGGTGTATTAACACCGAGTGGACACCGGAAAGT 402
DB 45 CAAGTATTTCTTGGTGTATTAACACCGAGTGGACACCGGAAAGT 1

RESULT 12
US-09-451-527-85
; Sequence 85, Application US/09451527

Patent No. 6482403
 GENERAL INFORMATION:
 APPLICANT: Sim, Gek-Kee
 APPLICANT: Yang, Shumin
 APPLICANT: Dreitz, Matthew J.
 APPLICANT: Wonderling, Ramani S.
 TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
 TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF
 FILE REFERENCE: IM-2-C2
 CURRENT APPLICATION NUMBER: US/09/451,527
 CURRENT FILING DATE: 1999-12-01
 EARLIER APPLICATION NUMBER: 09/322,409
 EARLIER FILING DATE: 1999-05-28
 EARLIER APPLICATION NUMBER: 60/087,306
 EARLIER FILING DATE: 1998-05-29
 NUMBER OF SEQ ID NOS: 174
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 85
 LENGTH: 345
 TYPE: DNA
 ORGANISM: Canis familiaris
 NAME/KEY: CDS
 LOCATION: (1)..(345)
 US-09-451-527-85

Query Match 85.8%; Score 345; DB 4; Length 345;
 Best Local Similarity 100.0%; Pred. No. 3.5e-104;
 Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 58 TTTCGTGTAGAAAATCCCATGAAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACT 117
 DB 1 TTTCGTGTAGAAAATCCCATGAAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACT 60
 QY 118 CATCGAATCTGGCTGATAGGGGATGGGAACCTGATGATTCCTACTCTCTGAAAAATAAAAT 177
 DB 61 CATCGAATCTGGCTGATAGGGGATGGGAACCTGATGATTCCTACTCTCTGAAAAATAAAAT 120
 QY 178 CACCAACTGTGCATTAAGAAGTTTTTCAGGGTATAGACATTTGAAGAACCAACTGCC 237
 DB 121 CACCAACTGTGCATTAAGAAGTTTTTCAGGGTATAGACATTTGAAGAACCAACTGCC 180
 QY 238 CACGGGAGGCTGTGGATAAATCTATTCCTCAAACTTGTCTTTAATAAAGAACACATAGAG 297
 DB 181 CACGGGAGGCTGTGGATAAATCTATTCCTCAAACTTGTCTTTAATAAAGAACACATAGAG 240
 QY 298 CGCCAAAAAAGGCTGCAGAGAAAGATGGAGAGTGCACAACTTCTAGACTACCTG 357
 DB 241 CGCCAAAAAAGGCTGCAGAGAAAGATGGAGAGTGCACAACTTCTAGACTACCTG 300
 QY 358 CAAGTATTTCTTGGTGTAAATAAACACCGAGTGCACCCGGAAGT 402
 DB 301 CAAGTATTTCTTGGTGTAAATAAACACCGAGTGCACCCGGAAGT 345

RESULT 13
 US-09-451-527-87/c
 Sequence 87, Application US/09451527
 Patent No. 6482403
 GENERAL INFORMATION:
 APPLICANT: Sim, Gek-Kee
 APPLICANT: Yang, Shumin
 APPLICANT: Dreitz, Matthew J.
 APPLICANT: Wonderling, Ramani S.
 TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
 TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF
 FILE REFERENCE: IM-2-C2
 CURRENT APPLICATION NUMBER: US/09/451,527
 CURRENT FILING DATE: 1999-12-01
 EARLIER APPLICATION NUMBER: 09/322,409
 EARLIER FILING DATE: 1999-05-28
 EARLIER APPLICATION NUMBER: 60/087,306
 EARLIER FILING DATE: 1998-05-29

NUMBER OF SEQ ID NOS: 174
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 87
 LENGTH: 345
 TYPE: DNA
 ORGANISM: Canis familiaris
 US-09-451-527-87

Query Match 85.8%; Score 345; DB 4; Length 345;
 Best Local Similarity 100.0%; Pred. No. 3.5e-104;
 Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 58 TTTCGTGTAGAAAATCCCATGAAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACT 117
 DB 345 TTTCGTGTAGAAAATCCCATGAAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACT 286
 QY 118 CATCGAATCTGGCTGATAGGGGATGGGAACCTGATGATTCCTACTCTCTGAAAAATAAAAT 177
 DB 285 CATCGAATCTGGCTGATAGGGGATGGGAACCTGATGATTCCTACTCTCTGAAAAATAAAAT 226
 QY 178 CACCAACTGTGCATTAAGAAGTTTTTCAGGGTATAGACATTTGAAGAACCAACTGCC 237
 DB 225 CACCAACTGTGCATTAAGAAGTTTTTCAGGGTATAGACATTTGAAGAACCAACTGCC 166
 QY 238 CACGGGAGGCTGTGGATAAATCTATTCCTCAAACTTGTCTTTAATAAAGAACACATAGAG 297
 DB 165 CACGGGAGGCTGTGGATAAATCTATTCCTCAAACTTGTCTTTAATAAAGAACACATAGAG 106
 QY 298 CGCCAAAAAAGGCTGCAGAGAAAGATGGAGAGTGCACAACTTCTAGACTACCTG 357
 DB 105 CGCCAAAAAAGGCTGCAGAGAAAGATGGAGAGTGCACAACTTCTAGACTACCTG 46
 QY 358 CAAGTATTTCTTGGTGTAAATAAACACCGAGTGCACCCGGAAGT 402
 DB 45 CAAGTATTTCTTGGTGTAAATAAACACCGAGTGCACCCGGAAGT 1

RESULT 14
 US-09-079-839-2
 Sequence 2, Application US/09079839
 Patent No. 6048726
 GENERAL INFORMATION:
 APPLICANT: Wellman, Joel K.
 APPLICANT: Karim, Aftab S.
 TITLE OF INVENTION: INHIBITION OF EOSINOPHILIC INFLAMMATION
 FILE REFERENCE: 09998/002001
 CURRENT APPLICATION NUMBER: US/09/079,839
 CURRENT FILING DATE: 1998-05-15
 NUMBER OF SEQ ID NOS: 2
 SOFTWARE: FastSeq for Windows Version 3.0
 SEQ ID NO 2
 LENGTH: 816
 TYPE: DNA
 ORGANISM: Homo sapiens
 US-09-079-839-2

Query Match 69.0%; Score 277.2; DB 3; Length 816;
 Best Local Similarity 80.6%; Pred. No. 1.3e-81;
 Matches 324; Conservative 0; Mismatches 78; Indels 0; Gaps 0;
 QY 1 ATGAGATGCTTCTGGAATTTGAGTTTCTAGCTCTTGGGGCTGCCTATGTTTCTGCTTT 60
 DB 45 ATGAGATGCTTCTGCAATTTGAGTTTCTAGCTCTTGGAGCTGCCTACGCTGATGCCATC 104
 QY 61 GCTGTAGAAAATCCCATGAAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACTCAT 120
 DB 105 CCCACAGAAATCCCAAGTGCATTTGGTGAAGAGACCTTGGCACTGCTTCTACTCAT 164
 QY 121 CGAACTTGGCTGATAGCGGATGGAACTGATGATTCCTACTCTGAAAAATAAAATCAC 180
 DB 165 CGAACTTGGCTGATAGCGCAATGAGACTCTGAGGATTCCTGTTCTGTGTACATAAAATCAC 224
 QY 181 CAAGTGTGCATTAAGAAGTTTTTCAGGGTATAGACATTTGAAGAACCAACTGCCAC 240

Db 225 CAACCTGTGACTCAAGAAATCTTTAGGGAATAGGCACACTGGAGAGTCAAACTGTGCAA 284
QY 241 GGGAGGCTGTGATAAACTATTCCAAAACCTGTCTTTTAATAAAGAACACATAGAGCGC 300
Db 285 GCGGCTACTGTGAAAGACTATTCAAAAACCTGTCTTTAATAAAGAAATACATTGACGCGC 344
QY 301 CAAAAAAAGGTGTCAGAGAAAGATGGAGAGTGCACAAAGTTCTTAGACTACCTGCAA 360
Db 345 CAAAAAAAGGTGTCAGAGAAAGATGGAGAGTGCACAAAGTTCTTAGACTACCTGCAA 404
QY 361 GTATTTCTTGCTGTAAATAAACCCGAGTGGACACCGGAAAGT 402
Db 405 GAGTTTCTTGCTGTAAATAAACCCGAGTGGACACCGGAAAGT 446

RESULT 15

US-09-023-655-1236
; Sequence 1236, Application US/09023655
; Patent No. 6607879
; GENERAL INFORMATION:
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: Susan G. Stuart
; APPLICANT: Jeffrey J. Sellhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
; TITLE OF INVENTION: EXPRESSION
; NUMBER OF SEQUENCES: 1508
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/023,655
; FILING DATE: HERewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0001 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1236:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 816 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: 9288305
US-09-023-655-1236

Query Match 68.6%; Score 275.6; DB 4; Length 816;
Best Local Similarity 80.3%; Pred. NO. 4.4e-81;
Matches 323; Conservative 0; Mismatches 79; Indels 0; Gaps 0;

QY 1 ATGAGAAATGCTTCTGAATTCGATGCTTGGGCTGCTAGCTTGGGCTGCTATGTTCTGCTTT 60
Db 45 ATGAGGATGCTTCTGCAATTCGATGCTTGGGCTGCTAGCTTGGGCTGCTATGTTCTGCTTT 104

QY 61 GCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACCTTGTGACACTGCTCTCCACTCAT 120
Db 105 CCCACAGAAATTTCCCAAGTGCATTGGTGAAGAGAGACCTTGGCACTGCTTCTTACTCAT 164
QY 121 CGAACTTGGCTGATAGCGGATGGAACTGATGATTCCTACTCTCTGAAATATAAAATCAC 180
Db 165 CGAACTTGGCTGATAGCGGATGGAACTGATGATTCCTACTCTCTGAAATATAAAATCAC 224
QY 181 CAACCTGTGCATTAAAGAAAGTTTTTCAGGGTATAGACACATTTGAAGAACCAAACTGCCCCAC 240
Db 225 CAACCTGTGCATTAAAGAAAGTTTTTCAGGGTATAGACACATTTGAAGAACCAAACTGCCCCAC 284
QY 241 GGGAGGCTGTGGATAAACTATTCCAAAACCTGTCTTTTAATAAAGAACACATAGAGCGC 300
Db 285 GGGGCTACTGTGAAAGACTATTGAAAACCTTGTCTTTAATAAAGAAATACATTGACGCGC 344
QY 301 CAAAAAAAGGTGTCAGAGAAAGATGGAGAGTGCACAAAGTTCTTAGACTACCTGCAA 360
Db 345 CAAAAAAAGGTGTCAGAGAAAGATGGAGAGTGCACAAAGTTCTTAGACTACCTGCAA 404
QY 361 GTATTTCTTGCTGTAAATAAACCCGAGTGGACACCGGAAAGT 402
Db 405 GAGTTTCTTGCTGTAAATAAACCCGAGTGGACACCGGAAAGT 446

Search completed: August 31, 2004, 06:34:46
Job time : 37.8667 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 30, 2004, 21:24:28 ; Search time 1350.53 Seconds
(without alignments)
8888.782 Million cell updates/sec

Title: US-10-787-382-7
Perfect score: 402
Sequence: 1 atgagaatcttctgaattt.....ccgagtggaacacggaaagt 402

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:

1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_est1:*
10: gb_est2:*
11: gb_hic:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_lam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_phg:*
27: em_gss_vrt:*
28: gb_gss1:*
29: gb_gss2:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	277.2	69.0	405	29	AY412020 Homo sapi
2	277.2	69.0	456	14	CD559532
C 3	277.2	69.0	456	14	CD559686
C 4	277.2	69.0	470	14	CD559687

5	277.2	69.0	492	14	CD559533
6	273.2	68.0	405	29	AY412021
7	266.8	66.4	467	14	CD559688
C 8	266.8	66.4	478	14	CD559534
9	266.2	66.2	463	14	CD559535
C 10	266.2	66.2	473	14	CD559689
11	266.2	66.2	489	14	CD559536
C 12	264.6	65.8	467	14	CD559690
C 13	261.6	65.1	477	14	CD559608
14	192.6	47.9	399	29	AY412022
15	131.8	32.8	622	29	CE311159
C 16	78	19.4	503	13	EQ598873
17	42.4	10.5	1025	13	EX441235
18	40.6	10.1	522	12	BI670794
19	40	10.0	317	14	CD087271
20	39.8	9.9	535	28	AZ370501
21	39.2	9.8	603	12	BJ328562
22	39.2	9.8	619	12	BJ328648
23	39.2	9.8	905	29	CNS00D59
24	38.8	9.7	1201	13	EX397166
25	38.6	9.6	1359	12	BG543026
26	38.2	9.5	667	29	CE510121
27	38.2	9.5	797	29	CC567321
28	38	9.5	432	9	AA560540
29	38	9.5	494	14	CE094467
30	38	9.5	623	28	AQ576964
31	38	9.5	666	28	AQ326668
C 32	38	9.5	1011	29	CNS00JRI
33	37.8	9.4	584	13	BQ526053
34	37.8	9.4	671	13	BX707130
35	37.8	9.4	684	13	BX758408
36	37.8	9.4	715	13	EX773473
37	37.8	9.4	724	13	EX773491
38	37.8	9.4	783	14	CF343019
39	37.8	9.4	892	13	EX776535
C 40	37.6	9.4	699	28	AQ781738
41	37.6	9.4	964	14	CD048643
C 42	37.6	9.4	1026	13	EX461051
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44	37.4	9.3	457	12	BI379332
45	37.4	9.3	695	28	BZ019774

ALIGNMENTS

RESULT 1

AY412020

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

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AUTHORS

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JOURNAL

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REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

REFERENCE

AUTHORS

AY412020 Homo sapiens IL5 gene, VIRTUAL TRANSCRIPT, partial sequence,
Genomic survey sequence.

AY412020.1 GI:39767985

GSS.

Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarawal, A.,

Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,

Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,

Adams, M.D. and Cargill, M.

Inferring nonneutral evolution from human-chimp-mouse orthologous

gene trios

Science 302 (5652), 1960-1963 (2003)

14671302

2 (bases 1 to 405)

Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarawal, A.,

Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,

Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,

Adams, M.D. and Cargill, M.

Direct Submission

linear GSS 16-DEC-2003

AY412020.1

AY412020.1

AY412020.1

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AY412020.1

JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
 COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment.

FEATURES Location/Qualifiers
 source 1..405

gene /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
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 /gene="IL5"
 /locus_tag="HCM4418"

ORIGIN

Query Match 69.0%; Score 277.2; DB 29; Length 405;
 Best Local Similarity 80.6%; Pred. No. 2.3e-58;
 Matches 324; Conservative 0; Mismatches 78; Indels 0; Gaps 0;

QY 1 ATGAGATGCTTCTGAATTTGAGTTTGTCTAGCTCTTGGGCTGCTATGTTTCTGCTTT 60
 Db 1 ATGAGATGCTTCTGCAATTTGAGTTTGTCTAGCTCTTGGGCTGCTATGTTTCTGCTTT 60

QY 61 GCTGTAGAAATCCATGATAGACTGGTGGCAGACCTTGACATGCTCTCCATCAT 120
 Db 61 CCCACAGAAATTCCTCAAGTGCATTTGGTGAAGAGACCTTGGCAGCTTCTTCTCAT 120

QY 121 CGAACTTGGCTGATAGCGATGGAACTGATGATCTCTCTGAAATAAAATCAC 180
 Db 121 CGAACTTGGCTGATAGCGATGGAACTGATGATCTCTCTGAAATAAAATCAC 180

QY 181 CAATGTGCATTAAGAAAGTTTTCAGGGTATGACACATTTGAAGACCAATCGCCAC 240
 Db 181 CAATGTGCATTAAGAAAGTTTTCAGGGTATGACACATTTGAAGACCAATCGCCAC 240

QY 241 GGGGAGCTGGGATAAATCTTCCAAACTTGTCTTAAATAAGACACATAGAGCC 300
 Db 241 GGGGAGCTGGGATAAATCTTCCAAACTTGTCTTAAATAAGACACATAGAGCC 300

QY 301 CAAAAAAGAGTGTGAGGAGAAAGATGGAGAGTGCAAAAGTTCTCTAGACTACCTGCAA 360
 Db 301 CAAAAAAGAGTGTGAGGAGAAAGATGGAGAGTGCAAAAGTTCTCTAGACTACCTGCAA 360

QY 361 GTATTTCTTGTGTAATAACACCGAGTGGACCCGGAAGT 402
 Db 361 GAGTTTCTTGTGTAATAACACCGAGTGGATAATAGAAAGT 402

RESULT 2
 CD559532 456 bp mRNA linear EST 11-JUN-2003
 LOCUS
 DEFINITION AGENCOURT_14497057 NIH_MGC_195 Homo sapiens cDNA clone
 IMAGE:6971772 5', mRNA sequence.

ACCESSION CD559532
 VERSION CD559532.1 GI:31585600
 KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 456)

NH-MGC http://mgc.nci.nih.gov/.

Tissue Procurement: Narayan Bhat

CDNA Library preparation: Bhat Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov

Plate: IRBK1 row: g column: 11

High quality sequence stop: 456.

FEATURES

Location/Qualifiers

source 1..456

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:6971772"

/tissue_type="mixed"

/lab_host="DH5A (T1 phage-resistant)"

/clone_lib="NIH_MGC_195"

/note="Vector: PDNR-Dual; Site 1: loxP-Sali; Site 2:

loxP-HindIII; Clones from this library have been PCR-amplified using gene-specific primers to contain the complete open reading frame (based on known gene sequences available from NCBI's RefSeq). Template for PCR is CDNA derived from either pooled cytoplasmic polyA RNA from 30 cells lines or pooled total RNA from 10 different tissues (from BD Biosciences/Clontech and Washington University). PCR products are directionally cloned into the loxP sites of the PDNR-dual vector. Library constructed by Dr. Narayan Bhat, Earl Bere III and Hongling Liao (Gene Expression Laboratory, Research Technology Program, SAIC Frederick, NCI-Frederick, Frederick, MD 21702). For information on which gene each clone represents, please visit our anonymous ftp site at ftp://image.llnl.gov/image/rearrayed_plates/IRBK.presv.dat a Note: this is a NIH_MGC Library."

ORIGIN

Query Match 69.0%; Score 277.2; DB 14; Length 456;
 Best Local Similarity 80.6%; Pred. No. 2.3e-58;
 Matches 324; Conservative 0; Mismatches 78; Indels 0; Gaps 0;

QY 1 ATGAGATGCTTCTGAATTTGAGTTTGTCTAGCTCTTGGGCTGCTATGTTTCTGCTTT 60
 Db 22 ATGAGATGCTTCTGCAATTTGAGTTTGTCTAGCTCTTGGGCTGCTATGTTTCTGCTTT 81

QY 61 GCTGTAGAAATCCATGATAGACTGGTGGCAGACCTTGACATGCTCTCCATCAT 120
 Db 82 CCCACAGAAATTCCTCAAGTGCATTTGGTGAAGAGACCTTGGCAGCTTCTTCTCAT 141

QY 121 CGAACTTGGCTGATAGCGATGGAACTGATGATCTCTACTCTCTGAAAAATAAAATCAC 180
 Db 142 CGAACTTGGCTGATAGCGATGGAACTGATGATCTCTCTCTGAAAAATAAAATCAC 201

QY 181 CAATGTGCATTAAGAAAGTTTTCAGGGTATGACACATTTGAAGACCAATCGCCAC 240
 Db 202 CAATGTGCATTAAGAAAGTTTTCAGGGTATGACACATTTGAAGACCAATCGCCAC 261

QY 241 GGGGAGCTGTGATAAATCTTCCAAACTTGTCTTAAATAAGACACATAGAGCCG 300
 Db 262 GGGGAGCTGTGATAAATCTTCCAAACTTGTCTTAAATAAGACACATAGAGCCG 321

QY 301 CAAAAAAGAGTGTGAGGAGAAAGATGGAGAGTGCAAAAGTTCTCTAGACTACCTGCAA 360
 Db 322 CAAAAAAGAGTGTGAGGAGAAAGATGGAGAGTGCAAAAGTTCTCTAGACTACCTGCAA 381

QY 361 GTATTTCTTGTGTAATAACACCGAGTGGACCCGGAAGT 402
 Db 382 GAGTTTCTTGTGTAATAACACCGAGTGGATAATAGAAAGT 423

RESULT 3

CD559686/c

LOCUS

DEFINITION AGENCOURT_14497093 NIH_MGC_195 Homo sapiens cDNA clone

IMAGE:6971772 3', mRNA sequence.

ACCESSION CD559686

VERSION CD559686.1 GI:31585754

KEYWORDS EST.

SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 456)
 NIH-MGC http://mgc.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 CONTACT: Daniela S. Gerhard, Ph.D.
 Office of Cancer Genomics
 National Cancer Institute / NIH
 Bldg. 31 Rm10A07 Bethesda, MD 20892
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Narayan Bhat
 cDNA Library Preparation: Bhat Laboratory
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: IRBK1 row: g column: 11
 High quality sequence stop: 456.
 Location/Qualifiers
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 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:6971772"
 /tissue_type="mixed"
 /lab_host="DH5A (T1 phage-resistant)"
 /clone_lib="NIH MGC 195"
 /note="Vector: pDNR-Dual; Site 1: loxP-Sall; Site 2:
 loxP-HindIII; Clones from this library have been
 PCR-amplified using gene-specific primers to contain the
 complete open reading frame (based on known gene sequences
 available from NCBI's RefSeq). Template for PCR is cDNA
 derived from either pooled cytoplasmic polyA RNA from 30
 cells lines or pooled total RNA from 10 different tissues
 (from BD Biosciences/Clontech and Washington University).
 PCR products are directionally cloned into the loxP sites
 of the pDNR-Dual vector. Library constructed by Dr.
 Narayan Bhat, Earl Bere III and Hongling Liao (Gene
 Expression Laboratory, Research Technology Program, SAIC
 Frederick, NCI-Frederick, Frederick, MD 21702). For
 information on which gene each clone represents, please
 visit our anonymous ftp site at
 ftp://image.llnl.gov/image/rearrayed_plates/IRBK.presv.dat
 a Note: this is a NIH_MGC Library."

ORIGIN

Query Match 69.0%; Score 277.2; DB 14; Length 456;
 Best Local Similarity 80.6%; Pred. No. 2.3e-58;
 Matches 324; Conservative 0; Mismatches 78; Indels 0; Gaps 0;
 QY 1 ATGAGATGCTTCTGAATTGAGTTTGTCTAGCTCTTGGGCTGCTTGTCTGCTTTT 60
 DB 433 ATGAGGATGCTTCTGCAATTCAGTTTGTCTAGCTCTTGGAGTCTGCTGATGCCATC 374
 QY 61 GCTGTAGAAATCCCATGAATAGACTGTGGCAGACCTTGACACTGCTCTCCACTCAT 120
 DB 373 CCCACAGAAATCCCAAGTGCATTTGGTGAAGAGACCTTGGACATGCTTCTACTCAT 314
 QY 121 CGAACTTGGCTGATAGGCGATGGGAACCTGTATGATTTCTACTCTGTAATAAATAATCAC 180
 DB 313 CGAACTTGGCTGATAGCAATGAGACTCTGAGGATTCCTGTTCTGTACATAAATAATCAC 254
 QY 181 CAACTGTGCATTAAGAAGTTTTTCAGGGTATAGACATGTGAGACCAACCACTGCCAC 240
 DB 253 CAACTGTGCATGAAGAATCTTTTCAGGGATAGGCACCTGGAGATCAAACTGTGCAA 194
 QY 241 GGGGAGGCTGTGGATAAATACTATTCAAAACCTTGTCTTTTAATAAAGAACACATAGCGGC 300
 DB 193 GGGGTACTGTGGAAGACTATTCAAAAACCTTGTCTTTTAATAAAGAACATACATTGACGCC 134

QY 301 CAAAAAAAAGGTGTGAGGAGAAAGATGGAGAGTGACAAAGTTCTTAGACTACTGCAA 360
 DB 133 CAAAAAAAAGGTGTGAGGAGAAAGATGGAGAGTGACAAAGTTCTTAGACTACTGCAA 74
 QY 361 GTATTCTTGTGTAAATAAACACCCAGTGGACACCGGAAAGT 402
 DB 73 GAGTTCTTGTGTAAATAAACACCCAGTGGATATAGAAAGT 32
 RESULT 4
 CD559687/c
 LOCUS AGENCOURT 14497029 NIH MGC 195 Homo sapiens cDNA clone
 DEFINITION IMAGE:6971771 5', mRNA sequence.
 ACCESSION CD559687
 VERSION CD559687.2 GI:38453484
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 470)
 NIH-MGC http://mgc.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 CONTACT: Daniela S. Gerhard, Ph.D.
 Office of Cancer Genomics
 National Cancer Institute / NIH
 Bldg. 31 Rm10A07 Bethesda, MD 20892
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Narayan Bhat
 cDNA Library Preparation: Bhat Laboratory
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: IRBK1 row: g column: 10
 High quality sequence start: 14
 High quality sequence stop: 470.
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 /organism="Homo sapiens"
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 /db_xref="taxon:9606"
 /clone="IMAGE:6971771"
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 /clone_lib="NIH MGC 195"
 /note="Vector: pDNR-Dual; Site 1: loxP-Sall; Site 2:
 loxP-HindIII; Clones from this library have been
 PCR-amplified using gene-specific primers to contain the
 complete open reading frame (based on known gene sequences
 available from NCBI's RefSeq). Template for PCR is cDNA
 derived from either pooled cytoplasmic polyA RNA from 30
 cells lines or pooled total RNA from 10 different tissues
 (from BD Biosciences/Clontech and Washington University).
 PCR products are directionally cloned into the loxP sites
 of the pDNR-Dual vector. Library constructed by Dr.
 Narayan Bhat, Earl Bere III and Hongling Liao (Gene
 Expression Laboratory, Research Technology Program, SAIC
 Frederick, NCI-Frederick, Frederick, MD 21702). For
 information on which gene each clone represents, please
 visit our anonymous ftp site at
 ftp://image.llnl.gov/image/rearrayed_plates/IRBK.presv.dat
 a Note: this is a NIH_MGC Library."

ORIGIN

Query Match 69.0%; Score 277.2; DB 14; Length 470;
 Best Local Similarity 80.6%; Pred. No. 2.3e-58;
 Matches 324; Conservative 0; Mismatches 78; Indels 0; Gaps 0;

[illegible]

RESULT 5	CD3559533	492 bp	mrna	linear	EST 26-NOV-2003
LOCUS	CD3559533				
DEFINITION	AGENCOURT 14496993 NIH MGC 195 Homo sapiens cDNA clone				
	IMAGE:6917771 5', mRNA sequence.				
ACCESSION	CD3559533				
VERSION	CD3559533.2	GI:38558947			
KEYWORDS	EST.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.				
REFERENCE	1 (bases 1 to 492)				
AUTHORS	NIH-MGC http://mgc.nci.nih.gov/ .				
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)				
JOURNAL	Unpublished (1999)				
COMMENT	On Jun 10, 2003 this sequence version replaced gi:31585601.				

Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-x@mail.nih.gov
Tissue Procurement: Narayan Bhat
CDNA Library Preparation: Bhat Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: JEBK1 Row: 9 Column: 10
High quality sequence start: 14
High quality sequence stop: 492.

PCR-amplified using gene-specific primers to contain the complete open reading frame (based on known gene sequences available from NCBI's RefSeq). Template for PCR is cDNA derived from either pooled cytoplasmic polyA RNA from 30 cells lines or pooled total RNA from 10 different tissues (from BD Biosciences/Clontech and Washington University). PCR products are directionally cloned into the loxp sites of the pGNR-dual vector. Library constructed by Dr. Narayan Bhat, Earl Bere III and Hongling Liao (Gene Expression Laboratory, Research Technology Program, SAIC Frederick, NCI-Frederick, Frederick, MD 21702). For information on which gene each clone represents, please visit our anonymous ftp site at ftp://image.llnl.gov/image/rearrayed_plates/IRSK.presv.dat. A Note: this is a NIH MGC Library."

ORIGIN

Query Match 69.0%; Score 277.2; DB 14; Length 492;
Best Local Similarity 80.6%; Pred. No. 2.3e-58;
Matches 324; Conservative 0; Mismatches 79; Indels 0; Gaps 0;

1	ATGAGATGCTTCTGAAATTTGATTTGCTTAGCTCTTGGGGCTGCCTATATGTTTCTGCCTTT	60
56	ATGGAGATGCTTCTGCAATTTGAGTTTCTAGCTCTTGGAGCTGCCCTACGTATATGCCATC	115
61	GCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACCTTGCACATGCTCTCCACTCAT	120
116	CCCAAGAAAATCCCAAGTGCATTTGGTGAAGAGACCTTGGCAGCTGTTTCTACTCAT	175
121	CGAACTTGGCTGATAGCGGATGGGAACCTGATGATTTCTTACTCTCGAAATAAAAAATCAC	180
176	CGAACTCTGTGTATAGCCATGAGACTCTGAGGATTTCTGTTCCTGTACATATAAAATCAC	235
181	CAACTGTGCATTAAGAAGTTTTTTCAGGGTATAGACACATTTGAAGAACCAAACTGCCAC	240
236	CAACTGTGCATGAAGAAAATCTTTCAGGGAATAGGCACACTGGAGAGTCAAACTGTGCAA	295
241	GGGGAGCTCTGGATAAACAATATCCAAAATCTGCTCTTTTAATAAAGAACACATAGAGGC	300
296	GGGGGTACTGTGGAAGACATATTCAAAAACTTTGTCTTAAATAGAAATACATTCACCGCC	355
301	CAAAAAAAAAGGTGTGCAGGAGAAAAGATGGAGAGTGACAAAGTTCCTAGACTACCTGCAA	360
356	CAAAAAAAAAGTGTGGAGAAAGAACGCGGAGNGTAAACCAATTCCTAGACTACCTGCAA	415
361	GTATTTCTTGGTGTATATAACACCGAGTGGACACCGGAAAAGT	402
416	GAGTTTCTTGGTGTATAGCAACCGGAGTGGATTAATAGAAGT	457

AY412021
LOCUS
DEFINITION
405 bp DNA linear GSS 16-DEC-2003
Pan troglodytes IL5 gene, VIRTUAL TRANSCRIPT, partial sequence,
genomic survey sequence.
ACCESSION
AY412021
VERSION
AY412021.1 GI:39767986
KEYWORDS
GSS.

SOURCE	ORGANISM	TITLE	JOURNAL	PUBLISHED	REFERENCE
Pan troglodytes (chimpanzee)	Pan troglodytes		gene trios		
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.			Science 302 (5652), 1960-1963 (2003)	14671302	
1 (bases 1 to 405)					2 (bases 1 to 405)
Clodd, A.G., Glandowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Perriera, S., Wang, G., Zheng, X.H., White, T.J., Sainsky, J.J., Adams, M.D. and Cargill, M.		Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios			

FEATURES	SOURCE
1. High Accuracy: The model achieves a high accuracy rate, consistently performing well across various datasets and tasks.	1. High Accuracy: The model achieves a high accuracy rate, consistently performing well across various datasets and tasks.
2. Scalability: The model is designed to handle large-scale data and complex tasks, making it suitable for enterprise-level applications.	2. Scalability: The model is designed to handle large-scale data and complex tasks, making it suitable for enterprise-level applications.
3. Interpretability: The model provides clear and understandable explanations for its predictions, enhancing transparency and trust.	3. Interpretability: The model provides clear and understandable explanations for its predictions, enhancing transparency and trust.
4. Robustness: The model is highly robust to noise and outliers, ensuring reliable performance in real-world scenarios.	4. Robustness: The model is highly robust to noise and outliers, ensuring reliable performance in real-world scenarios.
5. Efficiency: The model is optimized for fast processing and low resource consumption, making it ideal for resource-constrained environments.	5. Efficiency: The model is optimized for fast processing and low resource consumption, making it ideal for resource-constrained environments.

TITLE
JOURNAL
COMMENTS

Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Adams, M.D. and Cargill, M.
Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering
them based on alignment.

FEATURES	Location/Qualifiers
source	1. .405

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/locus_tag="HCN4418"

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dq

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db

1 ATGACGAATCAACTTCCTGATTTGACATTTGCTAGCTGTTGGAGTGCCTACGGTAGTGCAATC 60

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[illegible][illegible]

100
 121
 102

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181 CAACCTGTGCACTAAAGGAGTCTTTCTCAGGGTATAGACACATTTGAGAGAACCCACACAGCCAC 240

D_b 181 CAACNNNGCACTGAAGAAATCTTTTCAGGGAAATAGGCACACTGGAGAGAGICAAAACIGTGGCAA Z40
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Db 241 GGGGGTACTGTGGAAAGACTATTCCAAAACCTTGCCTTAATAAAGAAATACATTGGANGGC 300

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Db 361 GACTTTCTTGGTGTAAATGAACACCGAGTGGATAATAGAAAGT 402

RESULT 7

CD59688/c	CD59688	467 bp	mRNA	linear	EST 19-NOV-2003
LOCUS					

DEFINITION AGENCOURT_14496964 NIH_MGC_195 Homo sapiens cDNA clone IMAGE:6971770 5', mRNA sequence.

CD559688
ACCESSION
CD559688.2
VERSION
GI:38453486

KEYWORDS
SOURCE
EST.
Homo sapiens (human)

ORGANISM	Homo sapiens	Craniata: Vertebrata: Euteleostomi; Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi;
Source	NCBI	NCBI

DIFFERENCE 1 (bases 1 to 467)

1 (cases 1 to 107)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health. Mammalian Gene Collection (MGC)

UNPUBLISHED
ON THE 10 2003 THIS SEQUENCE VERSION ROLAND AT 31585756.

COMMENT
On Jun 10, 2003 this sequence version replaced gar300000.
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics

Office of Cancer Genomics
National Cancer Institute / NIH
Building 31, Room 107 Bethesda, MD 20892

Bldg. 31 RM10A07 Bethesda, MD 20832
Email: cgapbs@mail.nih.gov

LOCUS CD59534 478 bp mRNA linear EST 26-NOV-2003
 DEFINITION AGENCOURT_14496928 NIH_MGC_195 Homo sapiens cDNA clone
 IMAGE:6971770 5', mRNA sequence.
 ACCESSION CD59534
 VERSION CD59534.2 GI:38558949
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 478)
 AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT On Jun 10, 2003 this sequence version replaced gi:31585602.
 Contact: Daniela S. Gerhard, Ph.D.
 Office of Cancer Genomics
 National Cancer Institute / NIH
 Bldg. 31 Rm10A07 Bethesda, MD 20892
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Narayan Bhat
 cDNA Library Preparation: Bhat Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: IRBK1 row: 9 column: 09
 High quality sequence start: 3
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 /lab_host="DH5A (T1 phage-resistant)"
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 loxp-HindIII; Clones from this library have been
 PCR-amplified using gene-specific primers to contain the
 complete open reading frame (based on known gene sequences
 available from NCBI's RefSeq). Template for PCR is cDNA
 derived from either pooled cytoplasmic polyA RNA from 30
 cells lines or pooled total RNA from 10 different tissues
 (from BD Biosciences/Clontech and Washington University).
 PCR products are directionally cloned into the loxp sites
 of the pDNR-Dual vector. Library constructed by Dr.
 Narayan Bhat, Earl Bere III and Hongling Liao (Gene
 Expression Laboratory, Research Technology Program, SAIC
 Frederick, NCI-Frederick, Frederick, MD 21702). For
 information on which gene each clone represents, please
 visit our anonymous ftp site at
ftp://image.llnl.gov/image/rearrayed_plates/IRBK.presv.dat
 a Note: this is a NIH_MGC Library."

ORIGIN

Query Match 66.4%; Score 266.8; DB 14; Length 478;
 Best Local Similarity 80.6%; Pred. No. 8.9e-56;
 Matches 324; Conservative 0; Mismatches 77; Indels 1; Gaps 1;
 1 ATGAGATGCTTCTGAAATTGAGTTTGGCTTTGGGGCTGCCATGTTTCTGCTTT 60
 45 ATGAGATGCTTCTGAAATTGAGTTTGGCTTTGGGGCTGCCATGTTTCTGCTTT 104
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 105 CCCACAGAAATCCCAAGTGCATGGTGAAGAGACCTTGGCACTGTTCTACTCAT 164
 121 CGAACTTGCTGTAGCGATGGACCTGATGATTTCTTACTCTGAAATAAATACAC 180
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181 CAACTGTGCTTAAAGAAAGTCTTTTTCAGGCTATAGACATTTGAAGAAACCAAACTCCAC 240
 225 CAACTGTGCTTAAAGAAAGTCTTTTTCAGGCTATAGACATTTGAAGAAACCAAACTCCAC 284
 241 GGGAGGCTGTGCTGATAAAGTCTTTTTCAGGCTATAGACATTTGAAGAAACCAAACTCCAC 300
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 404 GAGTTTCTTGTGCTGATAAAGTCTTTTTCAGGCTATAGACATTTGAAGAAACCAAACTCCAC 445

CD59535 463 bp mRNA linear EST 26-NOV-2003
 AGENCOURT_14496865 NIH_MGC_195 Homo sapiens cDNA clone
 IMAGE:6971769 5', mRNA sequence.
 ACCESSION CD59535
 VERSION CD59535.2 GI:38558950
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 463)
 AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT On Jun 10, 2003 this sequence version replaced gi:31585603.
 Contact: Daniela S. Gerhard, Ph.D.
 Office of Cancer Genomics
 National Cancer Institute / NIH
 Bldg. 31 Rm10A07 Bethesda, MD 20892
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Narayan Bhat
 cDNA Library Preparation: Bhat Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: IRBK1 row: 9 column: 08
 High quality sequence stop: 463.
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 /note="Vector: pDNR-Dual; Site 1: loxp-Sall; Site 2:
 loxp-HindIII; Clones from this library have been
 PCR-amplified using gene-specific primers to contain the
 complete open reading frame (based on known gene sequences
 available from NCBI's RefSeq). Template for PCR is cDNA
 derived from either pooled cytoplasmic polyA RNA from 30
 cells lines or pooled total RNA from 10 different tissues
 (from BD Biosciences/Clontech and Washington University).
 PCR products are directionally cloned into the loxp sites
 of the pDNR-Dual vector. Library constructed by Dr.
 Narayan Bhat, Earl Bere III and Hongling Liao (Gene
 Expression Laboratory, Research Technology Program, SAIC
 Frederick, NCI-Frederick, Frederick, MD 21702). For
 information on which gene each clone represents, please
 visit our anonymous ftp site at
ftp://image.llnl.gov/image/rearrayed_plates/IRBK.presv.dat
 a Note: this is a NIH_MGC Library."

FEATURES

source

ftp://image.llnl.gov/image/rearranged_plates/IRBK.presv.dat
a Note: this is a NIH_MGC Library."

ORIGIN

Query Match 66.2%; Score 266.2; DB 14; Length 463;
Best Local Similarity 80.4%; Pred. No. 1.2e-55;
Matches 324; Conservative 0; Mismatches 78; Indels 1; Gaps 1;

QY 1 ATGAGAATGCTTCTGAATTTAGTTTGTAGCTTCTGGGGTGGCTTATGTTCTGCGCTTT 60
DB 28 ATGAGGATGCTTCTGCAATTTGCTAGCTTCTGGAGCTGCTTACGTGTATGCCATC 87

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DB 88 CCACAGAAATCCCAAGTGCATTTGGTGAAGAGACCTTGGCACTGCTTCTACTCAT 147

QY 121 CGAACTTGGCTGATAGCGGATGGAACTCTGATGATTTCTTACTCTCTGAAATATAAATCAC 180
DB 148 CGAACTTGGCTGATAGCGGATGGAACTCTGATGATTTCTTACTCTCTGAAATATAAATCAC 207

QY 181 CAACCTGTCATTAAGAGAGTTTTCAGGGTATAGACACATTTGAAGAACCAAACTGCCAC 240
DB 208 CAACCTGTCATTAAGAGAGTTTTCAGGGTATAGACACATTTGAAGAACCAAACTGCCAC 267

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DB 268 GGGGACTGTGGAAGACTATTCAAAACTTGTCTTATAAAGAAATACATGACGGC 327

QY 301 C-AAAAAAGGTGTGAGAGAAAGATGGAGAGTGACAAAGTTCCTAGACTACCTGCA 359
DB 328 CAAAAAAGGTGTGAGAGAAAGATGGAGAGTGACAAAGTTCCTAGACTACCTGCA 387

QY 360 AGTATTTCTTGGTGTATTAACACCGAGTGGACACCGGAAAGT 402
DB 388 AGTATTTCTTGGTGTATTAACACCGAGTGGATATAGAAAGT 430

RESULT 10
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LOCUS CD559689 473 bp mRNA linear EST 19-NOV-2003
DEFINITION AGENCOURT_14496801 NIH_MGC_195 Homo sapiens cDNA clone
IMAGE:6971769 5', mRNA sequence.
CD559689
VERSION CD559689.2 GI:38453487
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 473)
NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT On Jun 10, 2003 this sequence version replaced gi:31585757.
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: Narayan Bhat
CDNA Library Preparation: Bhat Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: IRBK1 row: g column: 08
High quality sequence start: 16
High quality sequence stop: 473.
Location/Qualifiers
1..473
/organism="Homo sapiens"
/mol_type="mRNA"

FEATURES
source

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

/db_xref="taxon:9606"
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/note="vector: PDNR-Dual; Site 1: loxP-Sall; Site_2:
loxP-HindIII; Clones from this library have been
PCR-amplified using gene-specific primers to contain the
complete open reading frame (based on known gene sequences
available from NCB1's RefSeq). Template for PCR is cDNA
derived from either pooled cytoplasmic polyA RNA from 30
cells lines or pooled total RNA from 10 different tissues
(from BD Biosciences/Clontech and Washington University).
PCR products are directionally cloned into the loxP sites
of the PDNR-Dual vector. Library constructed by Dr.
Narayan Bhat, Earl Bere III and Hongling Liao (Gene
Expression Laboratory, Research Technology Program, SAIC
Frederick, NCI-Frederick, Frederick, MD 21702). For
information on which gene each clone represents, please
visit our anonymous ftp site at
ftp://image.llnl.gov/image/rearranged_plates/IRBK.presv.dat
a Note: this is a NIH_MGC Library."

ORIGIN

Query Match 66.2%; Score 266.2; DB 14; Length 473;
Best Local Similarity 80.4%; Pred. No. 1.2e-55;
Matches 324; Conservative 0; Mismatches 78; Indels 1; Gaps 1;

QY 1 ATGCAATGCTTCTGCAATTTGCTAGCTTCTGGGGTGGCTATGTTCTGCTTT 60
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QY 61 GCTGTAGAAATCCCATGATAGCTGGTGGCAGAGCTTGACACTCTCTCCACTCAT 120
DB 389 CCCACAGAAATCCCAAGTGCATTTGGTGAAGAGACCTTGGCACTGCTTCTACTCAT 330

QY 121 CGAACTTGGCTGATAGCGGATGGAACTCTGATGATTTCTTCTGAAAAATAAATCAC 180
DB 329 CGAACTTGGCTGATAGCGGATGGAACTCTGATGATTTCTTCTGATACATAAATCAC 270

QY 181 CAACCTGTCATTAAGAGAGTTTTCAGGGTATAGACACATTTGAAGAACCAAACTGCCAC 240
DB 269 CAACCTGTCATTAAGAGAGTTTTCAGGGTATAGACACATTTGAAGAACCAAACTGCCAC 210

QY 241 GGGGAGGCTGTGATAAATCTATCCAAACTTGTCTTTAATAAAGAACACATAGAGCGC 300
DB 209 GGGGGTACTGTGGAAGACTATTCAAAACTTGTCTTAAAGAAATACATGACCGC 150

QY 301 C-AAAAAAGGTGTGAGAGAAAGATGGAGAGTGACAAAGTTCCTAGACTACCTGCA 359
DB 149 CAAAAAAGGTGTGAGAGAAAGATGGAGAGTGACAAAGTTCCTAGACTACCTGCA 90

QY 360 AGTATTTCTTGGTGTATTAACACCGAGTGGACACCGGAAAGT 402
DB 89 AGAGTTTCTTGGTGTATTAACACCGAGTGGATATAGAAAGT 47

RESULT 11
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LOCUS CD559536 489 bp mRNA linear EST 26-NOV-2003
DEFINITION AGENCOURT_14496804 NIH_MGC_195 Homo sapiens cDNA clone
IMAGE:6971768 5', mRNA sequence.
CD559536
VERSION CD559536.2 GI:38558953
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 489)
NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)

COMMENT

On Jun 10, 2003 this sequence version replaced gi:31585604.

Contact: Daniela S. Gerhard, Ph.D.

Office of Cancer Genomics

National Cancer Institute / NIH

Bldg. 31 Rm10A07 Bethesda, MD 20892

Email: cgapbs-remail.nih.gov

Tissue Procurement: Narayan Bhat

cDNA Library Preparation: Bhat Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: IRBK1 row: g column: 07

High quality sequence start: 17

High quality sequence stop: 489.

FEATURES

source

1..489

/organism="Homo sapiens"

/mol_type="mRNA"

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/clones="IMAGE:6971768"

/tissue_type="mixed"

/lab_host="DH5A (T1 phage-resistant)"

/clone_lib="NIH_MGC_195"

/note="Vector: pDNR-Dual; Site 1: loxP-Sali; Site 2: loxP-HindIII; Clones from this library have been PCR-amplified using gene-specific primers to contain the complete open reading frame (based on known gene sequences available from NCBI's RefSeq). Template for PCR is cDNA derived from either pooled cytoplasmic polyA RNA from 30 cells lines or pooled total RNA from 10 different tissues (from BD Biosciences/Clontech and Washington University). PCR products are directionally cloned into the loxP sites of the pDNR-Dual vector. Library constructed by Dr. Narayan Bhat, Earl Bere III and Hongling Liao (Gene Expression Laboratory, Research Technology Program, SAIC Frederick, NCI-Frederick, Frederick, MD 21702). For information on which gene each clone represents, please visit our anonymous ftp site at

ftp://image.llnl.gov/image/rearrayed_plates/IRBK.presv.dat

ORIGIN

Query Match 66.28; Score 266.2; DB 14; Length 489;

Best Local Similarity 80.4%; Pred. No. 1.2e-55;

Matches 324; Conservative 0; Mismatches 78; Indels 1; Gaps 1;

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Qy 1 ATGAGAAATGCTTCTGAATTTGAGTTTGCTAGCTCTTGGGCTCGCTATGTTCTGCTTT 60
Db 54 ATGAGGATGCTTCTGCAATTTGAGTTTGCTAGCTCTTGGAGCTGCTACGTGATGCATC 113
Qy 61 GCTGTAGAAATCCATGAATAGACTGGTGGGAGACCTTGACACTGCTTCCATCAT 120
Db 114 CCCACAGAAATCCACAGTCAATGGTGGAAAGAGACCTTGCACTGCTTCTACTCAT 173
Qy 121 CGAATCTGGCTGATAGCGGATGGAACTCTGATCTTCTACTCTCTGAAATAAATATCAC 180
Db 174 CGAATCTGGCTGATAGCGGATGGAACTCTGATCTTCTACTCTCTGAAATAAATATCAC 233
Qy 181 CAATCTGGCTGATAGCGGATGGAACTCTGATCTTCTACTCTCTGAAATAAATATCAC 240
Db 234 CAATCTGGCTGATAGCGGATGGAACTCTGATCTTCTACTCTCTGAAATAAATATCAC 293
Qy 241 GGGGAGCTGCTGATAGCGGATGGAACTCTGATCTTCTACTCTCTGAAATAAATATCAC 300
Db 294 GGGGAGCTGCTGATAGCGGATGGAACTCTGATCTTCTACTCTCTGAAATAAATATCAC 353
Qy 301 C-AAAAAAGGTGTCAGGAGAAAGATGGAGAGTGACAAAAGTTCCTAGACTACTGCA 359
Db 354 CAAAAAAGGTGTCAGGAGAAAGATGGAGAGTGACAAAAGTTCCTAGACTACTGCA 413
Qy 360 AGTATTCTTGGTGTATTAACACCGAGTGGACCCGGAGT 402

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Db

414 AGAGTTCTTGGTGTATTAACACCGAGTGGATATAGAAAGT 456

RESULT 12

CD559690/c

LOCUS

DEFINITION

AGENCOURT.14496838 NIH_MGC_195 Homo sapiens cDNA clone

IMAGE:6971768 5', mRNA sequence.

ACCESSION

CD559690

VERSION

CD559690.2 GI:38453490

KEYWORDS

SOURCE

ORGANISM

Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 467)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

On Jun 10, 2003 this sequence version replaced gi:31585758.

Contact: Daniela S. Gerhard, Ph.D.

Office of Cancer Genomics

National Cancer Institute / NIH

Bldg. 31 Rm10A07 Bethesda, MD 20892

Email: cgapbs-remail.nih.gov

Tissue Procurement: Narayan Bhat

cDNA Library Preparation: Bhat Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: IRBK1 row: g column: 07

High quality sequence stop: 467.

Location/Qualifiers

1..467

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clones="IMAGE:6971768"

/tissue_type="mixed"

/lab_host="DH5A (T1 phage-resistant)"

/clone_lib="NIH_MGC_195"

/note="Vector: pDNR-Dual; Site 1: loxP-Sali; Site 2:

loxP-HindIII; Clones from this library have been

PCR-amplified using gene-specific primers to contain the

complete open reading frame (based on known gene sequences

available from NCBI's RefSeq). Template for PCR is cDNA

derived from either pooled cytoplasmic polyA RNA from 30

cells lines or pooled total RNA from 10 different tissues

(from BD Biosciences/Clontech and Washington University).

PCR products are directionally cloned into the loxP sites

of the pDNR-Dual vector. Library constructed by Dr.

Narayan Bhat, Earl Bere III and Hongling Liao (Gene

Expression Laboratory, Research Technology Program, SAIC

Frederick, NCI-Frederick, Frederick, MD 21702). For

information on which gene each clone represents, please

visit our anonymous ftp site at

ftp://image.llnl.gov/image/rearrayed_plates/IRBK.presv.dat

a Note: this is a NIH_MGC Library."

ORIGIN

Query Match 65.88; Score 264.6; DB 14; Length 467;

Best Local Similarity 80.1%; Pred. No. 3.1e-55;

Matches 323; Conservative 0; Mismatches 79; Indels 1; Gaps 1;

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Qy 61 GCTGTAGAAATCCATGAATAGACTGGTGGGAGACCTTGACACTGCTTCCATCAT 120

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 121 CGAATCTGGTGTATGAGCGATGGAACTGATGATTCCTTACTCTCTGAAATATAAATCAC 180
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 323 CGAATCTGCTGATAGCCAAATGAGACTTTGAGGATTCCTGCTCTGATATAAATCAC 264
 Db
 181 CAATCTGTGCTATTAAGAAGTTTTTCAGGGTATAGACATTTGAAGAACCAAACTGCCAC 240
 Qy
 263 CAATCTGTGCTACTGAAGAAATCTTCAGGGAATAGGCACACTGGAGAGTCAAACTGTGCAA 204
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 143 CAAAAAAGAAAGTGTGAGGAGAAAGACGAGAGTAAACCAATTCCTAGACTACCTGCA 84
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 DEFINITION
 AGENCOURT 14496997 NIH MGC 195 Homo sapiens cdna clone
 IMAGE:6971867 5', mRNA sequence.
 CD559608
 ACCESSION
 CD559608.2 GI:38558942
 VERSION
 EST.
 KEYWORDS
 SOURCE
 ORGANISM
 Homo sapiens (human)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 NIH-MGC http://mgi.nci.nih.gov/
 1 (bases 1 to 477)
 AUTHORS
 TITLE
 JOURNAL
 COMMENT
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 On Jun 10, 2003 this sequence version replaced gi:31585676.
 Contact: Daniela S. Gerhard, Ph.D.
 Office of Cancer Genomics
 National Cancer Institute / NIH
 Bldg. 31 Rm10A07 Bethesda, MD 20892
 Email: cgaps-@email.nih.gov
 Tissue Procurement: Narayan Bhat
 cDNA Library Preparation: Bhat Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov

Plate: IRBK2 row: 9 column: 10
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 High quality sequence stop: 353.
 Location/Qualifiers
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 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:6971867"
 /tissue_type="mixed"
 /lab_host="DH5A (T1 phage-resistant)"
 /clone_lib="NIH MGC 195"
 /note="Vector: pDNR-Dual; Site 1: loxP-Sali; Site 2:
 loxP-HindIII; Clones from this library have been
 PCR-amplified using gene-specific primers to contain the
 complete open reading frame (based on known gene sequences
 available from NCBI's RefSeq). Template for PCR is cDNA
 derived from either pooled cytoplasmic polyA RNA from 30
 cells lines or pooled total RNA from 10 different tissues
 (from BD Biosciences/Clontech and Washington University).
 PCR products are directionally cloned into the loxP sites

FEATURES

source
 1..477
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:6971867"
 /tissue_type="mixed"
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 /clone_lib="NIH MGC 195"
 /note="Vector: pDNR-Dual; Site 1: loxP-Sali; Site 2:
 loxP-HindIII; Clones from this library have been
 PCR-amplified using gene-specific primers to contain the
 complete open reading frame (based on known gene sequences
 available from NCBI's RefSeq). Template for PCR is cDNA
 derived from either pooled cytoplasmic polyA RNA from 30
 cells lines or pooled total RNA from 10 different tissues
 (from BD Biosciences/Clontech and Washington University).
 PCR products are directionally cloned into the loxP sites

of the pDNR-Dual vector. Library constructed by Dr.
 Narayan Bhat, Earl Bere III and Hongling Liao (Gene
 Expression Laboratory, Research Technology Program, SAIC
 Frederick, NCI-Frederick, Frederick, MD 21702). For
 information on which gene each clone represents, please
 visit our anonymous ftp site at
 ftp://image.llnl.gov/image/rearrayed_plates/IRBK.presv.dat
 a Note: this is a NIH_MGC Library."

ORIGIN

Query Match 65.1%; Score 261.6; DB 14; Length 477;
 Best Local Similarity 78.8%; Pred. No. 1.7e-54;
 Matches 312; Conservative 0; Mismatches 84; Indels 0; Gaps 0;
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 Qy 67 GAAATCCCATGATAGACTGTGCGCAGACCTTGACACTGCTCTCCACTCATCGAACT 126
 Db 107 GAAATTTCCCAAGTGCATTTGGTGAAGAGACCTTGGCAGCTGCTTTCTACTGCTGAACT 166
 Qy 127 TGGCTGATAGGCGATGGGAACCTGATTCCTTACTCTCTGAAAAATAAAAAATCACAAC 186
 Db 167 CTGCTGATAGCAATGAGACTCTGAGGATTCCTGTTCTGTACATAAAATCACAAC 226
 Qy 187 TGCATTAAGAAGTTTTCAGGCTATAGACATTTGAAGACCAAACTGCCCGGGGAG 246
 Db 227 TGCACCTGAAGAAATCTTTTCAGGGAATATGCACATCGGAGTCAAACTGTCAAGGGGGT 286
 Qy 247 GCTGTGGATAAATATTCCAAAACCTGCTTTAATAAAGAACACATAGACGCGCAAAA 306
 Db 287 ACTGTGGAAGACATTTCAAAAACCTGCTTTAATAAAGAAATACATTTGACGCGCAAAA 346
 Qy 307 AAAAGGTGTGAGGAGAAAGATGGAGAGTGCAGAAATTCCTAGACTACCTGCAAGTATT 366
 Db 347 AAAAAGCGGTAGAGAAAGACGAGAGTAAACCAATTCCTAAACTACCTGCAAGGTTT 406
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RESULT 14

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 LOCUS
 DEFINITION
 Mus musculus ILS gene, VIRTUAL TRANSCRIPT, partial sequence,
 genomic survey sequence.
 AY412022

ACCESSION

AY412022

VERSION

AY412022.1 GI:39767987

KEYWORDS

GSS.

SOURCE

Mus musculus (house mouse)

ORGANISM

Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus; Mus.

REFERENCE

1 (bases 1 to 399)

AUTHORS

Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarawal, A.,
 Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
 Ferreria, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
 Adams, M.D. and Cargill, M.

TITLE

Inferred nonneutral evolution from human-chimp-mouse orthologous
 gene trios

JOURNAL

Science 302 (5652), 1960-1963 (2003)

PUBMED

14671302

REFERENCE

2 (bases 1 to 399)

AUTHORS

Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarawal, A.,
 Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
 Ferreria, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
 Adams, M.D. and Cargill, M.

TITLE

Direct Submission
 Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
 Rockville, MD 20850, USA
 This sequence was made by sequencing genomic exons and ordering

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FEATURES
  source
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Qy 184 CTGTGCAATTAAGAAGTTTTCAGGTATAGACACATGAGACCAACTGCCACGGG 243
Db 178 CTATGCAATGGAGAAATCTTTCAGGGCTAGACATAGTGAAGAAATCAAACTGTCGTGG 237

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Qy 304 AAATAAGGTGTGAGAGAGAAAGATGGAGATGACAAAGTTCTTAGACTACCTGCAAGTA 363
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Qy 364 TTCTTGTGTGTAATAACCGAGTGGACACCGGAAAG 401
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RESULT 15
CE331159
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DEFINITION
  tigr-gss-dog-1700033986568 Dog Library Canis familiaris genomic,
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ACCESSION
  CE331159
VERSION
  CE331159.1 GI:36147469
KEYWORDS
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SOURCE
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  Canis familiaris
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
  1. (bases 1 to 622)
  Kirkness,E.F., Batina,V., Halpern,A.L., Levy,S., Remington,K.,
  Rusch,D.B., Deicher,A.L., Pop,M., Wang,W., Fraser,C.M. and
  Venter,J.C.
  The dog genome: survey sequencing and comparative analysis
  Science 301 (5641), 1898-1903 (2003)
  22875432
  14512627
  Contact: Kirkness EF
  The Institute for Genomic Research
  Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
  Rockville, MD 20850, USA
  Tel: 301-838-0200
  Fax: 301-838-0208
  Email: ekirknes@tigr.org
  Class: shotgun.
  Location/Qualifiers

FEATURES
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  Matches 136; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 171 TAAAAATCACCACCTGTGCTGATTAAGAAGTTTTCAGGGTATAGACACATTGAAGAACA 230
Db 35 TATTTAGCACCACCTGTGCTGATTAAGAAGTTTTCAGGGTATAGACACATTGAAGAACA 94

Qy 231 AACTGCCCCACGGGAGGCTGTGGATAAATACTATTCCTTCTTCTTCTTCTTCTTCTTCTT 290
Db 95 AACTGCCCCACGGGAGGCTGTGGATAAATACTATTCCTTCTTCTTCTTCTTCTTCTTCTT 154

Qy 291 CATAGAGCGCCCAAAAAAAGGT 313
Db 155 CATAGAGCGCCCAAAAAAAGT 177

Search completed: August 31, 2004, 13:00:13
Job time : 1352.53 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model
Run on: August 31, 2004, 01:25:57 ; Search time 237.867 Seconds
(without alignments)
8317.320 Million cell updates/sec

Title: US-10-787-382-7
Perfect score: 402
Sequence: 1 atgagaatgtcttgaattt.....ccgagtgacacgcggaagt 402

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 3237270 seqs, 2460713050 residues

Total number of hits satisfying chosen parameters: 6474540

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : Published Applications NA:*
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 - 2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq.*
 - 3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq.*
 - 4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq.*
 - 5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq.*
 - 6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq.*
 - 7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq.*
 - 8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq.*
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 - 19: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	402	100.0	402	9	US-09-755-633-7
2	402	100.0	402	9	US-09-755-633-8
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4	402	100.0	402	15	US-10-218-654-84
5	402	100.0	402	15	US-10-262-439-83
6	402	100.0	402	15	US-10-262-439-84
7	402	100.0	610	9	US-09-755-633-4
8	402	100.0	610	9	US-09-755-633-6
9	402	100.0	610	15	US-10-218-654-80
10	402	100.0	610	15	US-10-218-654-82
11	402	100.0	610	15	US-10-262-439-80
12	402	100.0	610	15	US-10-262-439-82
13	345	85.8	345	9	US-09-755-633-9
14	345	85.8	345	9	US-09-755-633-11

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16	345	85.8	345	15	US-10-218-654-87	Sequence 87, Appl
17	345	85.8	345	15	US-10-262-439-85	Sequence 85, Appl
18	345	85.8	345	15	US-10-262-439-87	Sequence 87, Appl
19	277.2	69.0	816	16	US-10-191-997-90	Sequence 90, Appl
20	275.6	68.6	816	17	US-10-641-643-1236	Sequence 1236, Ap
21	275.6	68.6	858	15	US-10-295-074-8	Sequence 8, Appl
22	275.6	68.6	858	15	US-10-295-074-10	Sequence 10, Appl
23	259	64.4	571	9	US-09-755-633-21	Sequence 21, Appl
24	231.4	57.6	864	15	US-10-235-074-12	Sequence 12, Appl
25	231.4	57.6	864	15	US-10-235-074-14	Sequence 14, Appl
26	145.8	36.3	1658	9	US-09-755-633-18	Sequence 18, Appl
27	144.2	35.9	1658	9	US-09-755-633-19	Sequence 19, Appl
28	99.4	24.7	3230	9	US-09-800-629A-78	Sequence 78, Appl
29	99.4	24.7	3230	17	US-10-679-532-78	Sequence 78, Appl
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32	67.2	16.7	5397	15	US-10-311-455-1018	Sequence 1018, Ap
33	65.6	16.3	5397	15	US-10-311-455-1017	Sequence 1017, Ap
34	42.6	10.6	65	10	US-09-908-975-2631	Sequence 2631, Ap
35	42	10.4	367378	15	US-10-312-841-2	Sequence 2, Appl
36	40.6	10.1	60	10	US-09-908-975-11360	Sequence 11360, A
37	37.2	9.3	694	13	US-10-424-599-27005	Sequence 27005, A
38	36	9.0	8634	15	US-10-311-455-1030	Sequence 1030, Ap
39	35.8	8.9	1049	13	US-10-424-599-41750	Sequence 41750, A
40	35.8	8.9	6129	15	US-10-240-485-136	Sequence 136, App
41	35.6	8.9	17280	13	US-10-221-714A-498	Sequence 498, App
42	35.4	8.8	530	13	US-10-424-599-3699	Sequence 3699, Ap
43	35.4	8.8	710	17	US-10-437-963-69757	Sequence 69757, A
44	35.4	8.8	175077	13	US-10-087-192-1168	Sequence 1168, Ap
45	35.2	8.8	488	13	US-10-027-632-39049	Sequence 39049, A

ALIGNMENTS

RESULT 1

US-09-755-633-7
; Sequence 7, Application US/09755633
; Patent No. US20020127200A1
; GENERAL INFORMATION:
; APPLICANT: Yang, Shumin
; APPLICANT: McCall, Catherine A.
; APPLICANT: Weber, Eric R.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; FILE REFERENCE: IN-2-CL-C1
; CURRENT APPLICATION NUMBER: US/09/755,633
; PRIOR FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: 09/322,409
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/087,306
; PRIOR FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 402
; TYPE: DNA
; ORGANISM: Canis familiaris
US-09-755-633-7

Query Match 100.0%; Score 402; DB 9; Length 402;
Best Local Similarity 100.0%; Pred. No. 5.7e-117;
Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGAGAAATGCTTCTCAATTTGAGTTGCTAGCTCTGGGGTGCCTATGTTTCGCCCTTT 60
Db 1 ATGAGAAATGCTTCTCAATTTGAGTTGCTAGCTCTGGGGTGCCTATGTTTCGCCCTTT 60
QY 61 GCTGTAGAAATCCCATGATGAGCTGGCAGAGACTTGACACTCTCTCCACTCAT 120
Db 61 GCTGTAGAAATCCCATGATGAGCTGGCAGAGACTTGACACTCTCTCCACTCAT 120

121 CGAATTGGCTGATAGCGGATGGGAACCTGATGATTCCTACTCTGAAATATAAATAC 180
121 CGAATTGGCTGATAGCGGATGGGAACCTGATGATTCCTACTCTGAAATATAAATAC 180
181 CAATGTGCATTAAGAAGTATTTTTCAGGGTATAGACACATTTGAAGAACCAAACTGCCAC 240
181 CAATGTGCATTAAGAAGTATTTTTCAGGGTATAGACACATTTGAAGAACCAAACTGCCAC 240
241 GGGAGGCTGGTAACTATTCCTAACTTCTTTTATAAAGAACACATAGAGCC 300
241 GGGAGGCTGGTAACTATTCCTAACTTCTTTTATAAAGAACACATAGAGCC 300
301 CAAAAAAGGCTGTCAGGAGAAAGATGGAGAGTGACAAAGTCTCTAGACTACCTGCAA 360
301 CAAAAAAGGCTGTCAGGAGAAAGATGGAGAGTGACAAAGTCTCTAGACTACCTGCAA 360
361 GTATTTCTGGTGTATTAACACCGAGTGACACCGGAAAGT 402
361 GTATTTCTGGTGTATTAACACCGAGTGACACCGGAAAGT 402

RESULT 2

US-09-755-633-8/c
; Sequence 8, Application US/09755633
; Patent No. US2002012700A1
; GENERAL INFORMATION:
; APPLICANT: Yang, Shumin
; APPLICANT: McCall, Catherine A.
; APPLICANT: Weber, Eric R.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; FILE REFERENCE: IM-2-C1-C1
; CURRENT APPLICATION NUMBER: US/09755,633
; CURRENT FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: 09/322,409
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/087,306
; PRIOR FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 8
; LENGTH: 402
; TYPE: DNA
; ORGANISM: Canis familiaris
US-09-755-633-8

Query Match 100.0%; Score 402; DB 9; Length 402;
Best Local Similarity 100.0%; Pred. No. 5.7e-117;
Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGGAATGCTTCTGAATTTGAGTTTCTAGCTCTGGGCTGCTATGTTCTGCTTT 60
DB 402 ATGGAATGCTTCTGAATTTGAGTTTCTAGCTCTGGGCTGCTATGTTCTGCTTT 343
QY 61 GCTGTAGAAATCCATGAATAGACTGGTGGAGAGACCTTGACACTGCTCTCACTCAT 120
DB 342 GCTGTAGAAATCCATGAATAGACTGGTGGAGAGACCTTGACACTGCTCTCACTCAT 283
QY 121 CGAATCTGGCTGATAGCGGATGGGAACCTGATGATTCCTCTGAAATATAAATAC 180
DB 282 CGAATCTGGCTGATAGCGGATGGGAACCTGATGATTCCTCTGAAATATAAATAC 223
QY 181 CAATGTGCATTAAGAAGTATTTTTCAGGGTATAGACACATTTGAAGAACCAAACTGCCAC 240
DB 222 CAATGTGCATTAAGAAGTATTTTTCAGGGTATAGACACATTTGAAGAACCAAACTGCCAC 163
QY 241 GGGAGGCTGGTAACTATTCCTAACTTCTTTTATAAAGAACACATAGAGCC 300
DB 162 GGGAGGCTGGTAACTATTCCTAACTTCTTTTATAAAGAACACATAGAGCC 103
QY 301 CAAAAAAGGCTGTCAGGAGAAAGATGGAGAGTGACAAAGTCTCTAGACTACCTGCAA 360
DB 102 CAAAAAAGGCTGTCAGGAGAAAGATGGAGAGTGACAAAGTCTCTAGACTACCTGCAA 43

QY 361 GTATTTCTGGTGTATTAACACCGAGTGACACCGGAAAGT 402
DB 42 GTATTTCTGGTGTATTAACACCGAGTGACACCGGAAAGT 1

RESULT 3

US-10-218-654-83
; Sequence 83, Application US/10218654
; Publication No. US20030099609A1
; GENERAL INFORMATION:
; APPLICANT: Sim, Gek-Kee
; APPLICANT: Yang, Shumin
; APPLICANT: Dreitz, Matthew J.
; APPLICANT: Wonderling, Ramani S.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; FILE REFERENCE: IM-2-C1
; CURRENT APPLICATION NUMBER: US/10/218,654
; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: US/09/322,409
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/087,306
; PRIOR FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 154
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 83
; LENGTH: 402
; TYPE: DNA
; ORGANISM: Canis familiaris
US-10-218-654-83

Query Match 100.0%; Score 402; DB 15; Length 402;
Best Local Similarity 100.0%; Pred. No. 5.7e-117;
Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGGAATGCTTCTGAATTTGAGTTTCTAGCTCTGGGCTGCTATGTTCTGCTTT 60
DB 1 ATGGAATGCTTCTGAATTTGAGTTTCTAGCTCTGGGCTGCTATGTTCTGCTTT 60
QY 61 GCTGTAGAAATCCATGAATAGACTGGTGGAGAGACCTTGACACTGCTCTCACTCAT 120
DB 61 GCTGTAGAAATCCATGAATAGACTGGTGGAGAGACCTTGACACTGCTCTCACTCAT 120
QY 121 CGAATCTGGCTGATAGCGGATGGGAACCTGATGATTCCTACTCTGAAATATAAATAC 180
DB 121 CGAATCTGGCTGATAGCGGATGGGAACCTGATGATTCCTACTCTGAAATATAAATAC 180
QY 181 CAATGTGCATTAAGAAGTATTTTTCAGGGTATAGACACATTTGAAGAACCAAACTGCCAC 240
DB 181 CAATGTGCATTAAGAAGTATTTTTCAGGGTATAGACACATTTGAAGAACCAAACTGCCAC 240
QY 241 GGGAGGCTGGTAACTATTCCTAACTTCTTTTATAAAGAACACATAGAGCC 300
DB 241 GGGAGGCTGGTAACTATTCCTAACTTCTTTTATAAAGAACACATAGAGCC 300
QY 301 CAAAAAAGGCTGTCAGGAGAAAGATGGAGAGTGACAAAGTCTCTAGACTACCTGCAA 360
DB 301 CAAAAAAGGCTGTCAGGAGAAAGATGGAGAGTGACAAAGTCTCTAGACTACCTGCAA 360
QY 361 GTATTTCTGGTGTATTAACACCGAGTGACACCGGAAAGT 402
DB 361 GTATTTCTGGTGTATTAACACCGAGTGACACCGGAAAGT 402

RESULT 4

US-10-218-654-84/c
; Sequence 84, Application US/10218654
; Publication No. US20030099609A1
; GENERAL INFORMATION:
; APPLICANT: Sim, Gek-Kee
; APPLICANT: Yang, Shumin
; APPLICANT: Dreitz, Matthew J.

; APPLICANT: Wonderling, Ramani S.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; FILE OF INVENTION: ACID MOLECULES, AND USES THEREOF
; FILE REFERENCE: IM-2-C1
; CURRENT APPLICATION NUMBER: US/10/218,654
; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: US/09/322,409
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/087,306
; PRIOR FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 154
; SOFTWARE: PatentIn ver. 2.0
; SEQ ID NO 84
; LENGTH: 402
; TYPE: DNA
; ORGANISM: Canis familiaris
US-10-218-654-84

Query Match 100.0%; Score 402; DB 15; Length 402;
Best Local Similarity 100.0%; Pred. No. 5.7e-117;
Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGATGCTCTGGAATTTGAGTTTCTAGCTCTTGGGCTGCCTATGTTCTGCTTT 60
DB 402 ATGAGATGCTCTGGAATTTGAGTTTCTAGCTCTTGGGCTGCCTATGTTCTGCTTT 343
QY 61 GCTGTAGAAAATCCCATGAATAGACTGGTGGCAGACCTTGACATGCTCTCCACTCAT 120
DB 342 GCTGTAGAAAATCCCATGAATAGACTGGTGGCAGACCTTGACATGCTCTCCACTCAT 283
QY 121 CGAATCTGGCTGATAGCGATGGAACTGATGATCTTCTACTCTGAAATAAAATCAC 180
DB 282 CGAATCTGGCTGATAGCGATGGAACTGATGATCTTCTACTCTGAAATAAAATCAC 223
QY 181 CAATCTGTGCTATTAAGAAAGTTTTTCAGGGTATAGACACATTTGAAGAACCAACTGCCAC 240
DB 222 CAATCTGTGCTATTAAGAAAGTTTTTCAGGGTATAGACACATTTGAAGAACCAACTGCCAC 163
QY 241 GGGGAGCTGTGATTAACCTATTCCAAAATCTTCTTTTAAATAAAGACACATAGAGCGC 300
DB 162 GGGGAGCTGTGATTAACCTATTCCAAAATCTTCTTTTAAATAAAGACACATAGAGCGC 103
QY 301 CAAAAAAGAGTGTGCAGAGAAAGATGAGAGTGACAAAGTTCTTAGACTACCTGCA 360
DB 102 CAAAAAAGAGTGTGCAGAGAAAGATGAGAGTGACAAAGTTCTTAGACTACCTGCA 43
QY 361 GTATTTCTTGGTGAATAAACCAGAGTGGACACCGGAAAGT 402
DB 42 GTATTTCTTGGTGAATAAACCAGAGTGGACACCGGAAAGT 1

RESULT 5
US-10-262-439-83
; Sequence 83, Application US/10262439
; Publication No. US20030143196A1
; GENERAL INFORMATION:
; APPLICANT: Sim, Gek-Ke
; APPLICANT: Yang, Shumin
; APPLICANT: Dreitz, Matthew J.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; FILE OF INVENTION: ACID MOLECULES, AND USES THEREOF
; FILE REFERENCE: IM-2-C2
; CURRENT APPLICATION NUMBER: US/10/262,439
; CURRENT FILING DATE: 2002-09-30
; PRIOR APPLICATION NUMBER: US/09/451,527
; PRIOR FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: 09/322,409
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/087,306
; PRIOR FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: PatentIn ver. 2.0

; SEQ ID NO 83
; LENGTH: 402
; TYPE: DNA
; ORGANISM: Canis familiaris
US-10-262-439-83

Query Match 100.0%; Score 402; DB 15; Length 402;
Best Local Similarity 100.0%; Pred. No. 5.7e-117;
Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGATGCTCTGGAATTTGAGTTTCTAGCTCTTGGGCTGCCTATGTTCTGCTTT 60
DB 1 ATGAGATGCTCTGGAATTTGAGTTTCTAGCTCTTGGGCTGCCTATGTTCTGCTTT 60
QY 61 GCTGTAGAAAATCCCATGAATAGACTGGTGGCAGACCTTGACATGCTCTCCACTCAT 120
DB 61 GCTGTAGAAAATCCCATGAATAGACTGGTGGCAGACCTTGACATGCTCTCCACTCAT 120
QY 121 CGAATCTGGCTGATAGCGATGGAACTGATGATCTTCTACTCTGAAATAAAATCAC 180
DB 121 CGAATCTGGCTGATAGCGATGGAACTGATGATCTTCTACTCTGAAATAAAATCAC 180
QY 181 CAATCTGTGCTATTAAGAAAGTTTTTCAGGGTATAGACACATTTGAAGAACCAACTGCCAC 240
DB 181 CAATCTGTGCTATTAAGAAAGTTTTTCAGGGTATAGACACATTTGAAGAACCAACTGCCAC 240
QY 241 GGGGAGCTGTGGAATAAATACTATTCCAAAATCTTCTTTTAAATAAAGACACATAGAGCGC 300
DB 241 GGGGAGCTGTGGAATAAATACTATTCCAAAATCTTCTTTTAAATAAAGACACATAGAGCGC 300
QY 301 CAAAAAAGAGTGTGCAGAGAAAGATGAGAGTGACAAAGTTCTTAGACTACCTGCA 360
DB 301 CAAAAAAGAGTGTGCAGAGAAAGATGAGAGTGACAAAGTTCTTAGACTACCTGCA 360
QY 361 GTATTTCTTGGTGAATAAACCAGAGTGGACACCGGAAAGT 402
DB 361 GTATTTCTTGGTGAATAAACCAGAGTGGACACCGGAAAGT 402

RESULT 6
US-10-262-439-84/c
; Sequence 84, Application US/10262439
; Publication No. US20030143196A1
; GENERAL INFORMATION:
; APPLICANT: Sim, Gek-Ke
; APPLICANT: Yang, Shumin
; APPLICANT: Dreitz, Matthew J.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; FILE OF INVENTION: ACID MOLECULES, AND USES THEREOF
; FILE REFERENCE: IM-2-C2
; CURRENT APPLICATION NUMBER: US/10/262,439
; CURRENT FILING DATE: 2002-09-30
; PRIOR APPLICATION NUMBER: US/09/451,527
; PRIOR FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: 09/322,409
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/087,306
; PRIOR FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: PatentIn ver. 2.0
; SEQ ID NO 84
; LENGTH: 402
; TYPE: DNA
; ORGANISM: Canis familiaris
US-10-262-439-84

Query Match 100.0%; Score 402; DB 15; Length 402;
Best Local Similarity 100.0%; Pred. No. 5.7e-117;
Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGATGCTCTGGAATTTGAGTTTCTAGCTCTTGGGCTGCCTATGTTCTGCTTT 60

Db 402 ATGAGATGCTTCTGAATTTGAGTTTCTAGCTCTTGGGCTGCCTATGTTTCTGCCTTT 343
Qy 61 GCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTTCCACTCAT 120
Db 342 GCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTTCCACTCAT 283
Qy 121 CGAATCTGGCTGTAGAGCGATGGGACCTGATGATTCCTACTCCTGAAATATAAATCAC 180
Db 282 CGAATCTGGCTGTAGAGCGATGGGACCTGATGATTCCTACTCCTGAAATATAAATCAC 223
Qy 181 CAATCTGTCATTAAGAAGTTTTTTCAGGGTATAGACACATTTGAAGAACCAAACTGCCAC 240
Db 222 CAATCTGTCATTAAGAAGTTTTTTCAGGGTATAGACACATTTGAAGAACCAAACTGCCAC 163
Qy 241 GGGAGGCTGTGGATAAATCTTCCAAAATCTGTTTATAAAGAACACATAGAGCGC 300
Db 162 GGGAGGCTGTGGATAAATCTTCCAAAATCTGTTTATAAAGAACACATAGAGCGC 103
Qy 301 CAAAAAAAAGGTGTGCAGGAGAAAGATGGAGAGTGACAAAGTTCTTAGACTACCTGCAA 360
Db 102 CAAAAAAAAGGTGTGCAGGAGAAAGATGGAGAGTGACAAAGTTCTTAGACTACCTGCAA 43
Qy 361 GTATTTCTTGGTGTAAATAAACACCGAGTGGACACCGGAAAGT 402
Db 42 GTATTTCTTGGTGTAAATAAACACCGAGTGGACACCGGAAAGT 1

RESULT 7

US-09-755-633-4
; Sequence 4, Application US/09755633
; Patent No. US20020127200A1
; GENERAL INFORMATION:
; APPLICANT: Yang, Shumin
; APPLICANT: McCall, Catherine A.
; APPLICANT: Weber, Eric R.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; FILE REFERENCE: IM-2-C1-C1
; CURRENT APPLICATION NUMBER: US/09/755,633
; PRIOR FILING DATE: 2001-01-05
; PRIOR FILING DATE: 1999-05-28
; PRIOR FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 610
; TYPE: DNA
; ORGANISM: Canis familiaris
; NAME/KEY: CDS
; LOCATION: (29) .. (430)
US-09-755-633-4

Query Match 100.0%; Score 402; DB 9; Length 610;
Best Local Similarity 100.0%; Pred. No. 7.2e-117;
Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGAGATGCTTCTGAATTTGAGTTTCTAGCTCTTGGGCTGCCTATGTTTCTGCCTTT 60
Db 29 ATGAGATGCTTCTGAATTTGAGTTTCTAGCTCTTGGGCTGCCTATGTTTCTGCCTTT 88
Qy 61 GCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTTCCACTCAT 120
Db 89 GCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTTCCACTCAT 148
Qy 121 CGAATCTGGCTGTAGAGCGATGGGACCTGATGATTCCTACTCCTGAAATATAAATCAC 180
Db 149 CGAATCTGGCTGTAGAGCGATGGGACCTGATGATTCCTACTCCTGAAATATAAATCAC 208
Qy 181 CAATCTGTCATTAAGAAGTTTTTTCAGGGTATAGACACATTTGAAGAACCAAACTGCCAC 240

Db 209 CAATCTGTCATTAAGAAGTTTTTTCAGGGTATAGACACATTTGAAGAACCAAACTGCCAC 268
Qy 241 GGGAGGCTGTGGATAAATCTTCCAAAATCTGTTTATAAAGAACACATAGAGCGC 300
Db 269 GGGAGGCTGTGGATAAATCTTCCAAAATCTGTTTATAAAGAACACATAGAGCGC 328
Qy 301 CAAAAAAAAGGTGTGCAGGAGAAAGATGGAGAGTGACAAAGTTCTTAGACTACCTGCAA 360
Db 329 CAAAAAAAAGGTGTGCAGGAGAAAGATGGAGAGTGACAAAGTTCTTAGACTACCTGCAA 388
Qy 361 GTATTTCTTGGTGTAAATAAACACCGAGTGGACACCGGAAAGT 402
Db 389 GTATTTCTTGGTGTAAATAAACACCGAGTGGACACCGGAAAGT 430

RESULT 8

US-09-755-633-6/c
; Sequence 6, Application US/09755633
; Patent No. US20020127200A1
; GENERAL INFORMATION:
; APPLICANT: Yang, Shumin
; APPLICANT: McCall, Catherine A.
; APPLICANT: Weber, Eric R.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; FILE REFERENCE: IM-2-C1-C1
; CURRENT APPLICATION NUMBER: US/09/755,633
; PRIOR FILING DATE: 2001-01-05
; PRIOR FILING DATE: 1999-05-28
; PRIOR FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 610
; TYPE: DNA
; ORGANISM: Canis familiaris
US-09-755-633-6

Query Match 100.0%; Score 402; DB 9; Length 610;
Best Local Similarity 100.0%; Pred. No. 7.2e-117;
Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGAGATGCTTCTGAATTTGAGTTTCTAGCTCTTGGGCTGCCTATGTTTCTGCCTTT 60
Db 582 ATGAGATGCTTCTGAATTTGAGTTTCTAGCTCTTGGGCTGCCTATGTTTCTGCCTTT 523
Qy 61 GCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTTCCACTCAT 120
Db 522 GCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTTCCACTCAT 463
Qy 121 CGAATCTGGCTGTAGAGCGATGGGACCTGATGATTCCTACTCCTGAAATATAAATCAC 180
Db 462 CGAATCTGGCTGTAGAGCGATGGGACCTGATGATTCCTACTCCTGAAATATAAATCAC 403
Qy 181 CAATCTGTCATTAAGAAGTTTTTTCAGGGTATAGACACATTTGAAGAACCAAACTGCCAC 240
Db 402 CAATCTGTCATTAAGAAGTTTTTTCAGGGTATAGACACATTTGAAGAACCAAACTGCCAC 343
Qy 241 GGGAGGCTGTGGATAAATCTTCCAAAATCTGTTTATAAAGAACACATAGAGCGC 300
Db 342 GGGAGGCTGTGGATAAATCTTCCAAAATCTGTTTATAAAGAACACATAGAGCGC 283
Qy 301 CAAAAAAAAGGTGTGCAGGAGAAAGATGGAGAGTGACAAAGTTCTTAGACTACCTGCAA 360
Db 282 CAAAAAAAAGGTGTGCAGGAGAAAGATGGAGAGTGACAAAGTTCTTAGACTACCTGCAA 223
Qy 361 GTATTTCTTGGTGTAAATAAACACCGAGTGGACACCGGAAAGT 402
Db 222 GTATTTCTTGGTGTAAATAAACACCGAGTGGACACCGGAAAGT 181

FILE REFERENCE: IM-2-C1
CURRENT APPLICATION NUMBER: US/10/218,654
SEQUENCE 80, Application US/10218654
Publication No. US20030099609A1
GENERAL INFORMATION:
APPLICANT: Yang, Shumin
APPLICANT: Dreitz, Matthew J.
APPLICANT: Wonderling, Ramani S.
TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
FILE REFERENCE: IM-2-C1
CURRENT APPLICATION NUMBER: US/10/218,654
PRIORITY FILING DATE: 2002-08-13
PRIORITY FILING DATE: 1999-05-28
PRIORITY FILING DATE: 60/087,306
NUMBER OF SEQ ID NOS: 154
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 80
LENGTH: 610
TYPE: DNA
ORGANISM: Canis familiaris
US-10-218-654-82

Query Match 100.0%; Score 402; DB 15; Length 610;
Best Local Similarity 100.0%; Pred. No. 7.2e-117;
Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGAATGCTTCTGAATTTGAGTTTGTAGCTCTTGGGGCTGCTATGTTTCTGCTTTT 60
DB 582 ATGAGAATGCTTCTGAATTTGAGTTTGTAGCTCTTGGGGCTGCTATGTTTCTGCTTTT 523
QY 61 GCTGTAGAAAATCCCATGAATAGTGGTGCAGAGACCTTGACACTCTCTCCACTCAT 120
DB 522 GCTGTAGAAAATCCCATGAATAGTGGTGCAGAGACCTTGACACTCTCTCCACTCAT 463
QY 121 CGAACTTGGCTGATAGGGGATGGGAACCTGATGTTCTTCTCTGAAAAATAAAATCAC 180
DB 462 CGAACTTGGCTGATAGGGGATGGGAACCTGATGTTCTTCTCTGAAAAATAAAATCAC 403
QY 181 CAACCTGTGCTTAAAGAGATTTTTCAGGGTATAGACACTTGAAGAACCAACCTGCCAC 240
DB 402 CAACCTGTGCTTAAAGAGATTTTTCAGGGTATAGACACTTGAAGAACCAACCTGCCAC 343
QY 241 GGGGAGGCTGTGGATAAACTATTCCAAAACCTTGTCTTTAAATAAAGAACACATAGAGCG 300
DB 342 GGGGAGGCTGTGGATAAACTATTCCAAAACCTTGTCTTTAAATAAAGAACACATAGAGCG 283
QY 301 CAAAAAAGAGTGTGCAGGAGAAAGATGGAGAGTGACAAAGTCTCTAGACTACCTGCAA 360
DB 282 CAAAAAAGAGTGTGCAGGAGAAAGATGGAGAGTGACAAAGTCTCTAGACTACCTGCAA 223
QY 361 GTATTCTTGGTGTAAATAAACACCGAGTGGACCGGAAAGT 402
DB 222 GTATTCTTGGTGTAAATAAACACCGAGTGGACCGGAAAGT 181

RESULT 11
US-10-262-439-80
Sequence 80, Application US/10262439
Publication No. US20030143196A1
GENERAL INFORMATION:
APPLICANT: Sim, Gek-Ke
APPLICANT: Yang, Shumin
APPLICANT: Dreitz, Matthew J.
APPLICANT: Wonderling, Ramani S.
TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
FILE REFERENCE: IM-2-C2
CURRENT APPLICATION NUMBER: US/10/262,439
PRIORITY FILING DATE: 2002-09-30
PRIORITY FILING DATE: 1999-12-01
PRIORITY FILING DATE: 09/322,409
PRIORITY FILING DATE: 1999-05-28
PRIORITY FILING DATE: 60/087,306
NUMBER OF SEQ ID NOS: 174
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 80
LENGTH: 610
TYPE: DNA

RESULT 9
US-10-218-654-80
Sequence 80, Application US/10218654
Publication No. US20030099609A1
GENERAL INFORMATION:
APPLICANT: Yang, Shumin
APPLICANT: Dreitz, Matthew J.
APPLICANT: Wonderling, Ramani S.
TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
FILE REFERENCE: IM-2-C1
CURRENT APPLICATION NUMBER: US/10/218,654
PRIORITY FILING DATE: 2002-08-13
PRIORITY FILING DATE: 1999-05-28
PRIORITY FILING DATE: 60/087,306
NUMBER OF SEQ ID NOS: 154
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 80
LENGTH: 610
TYPE: DNA
ORGANISM: Canis familiaris
US-10-218-654-80

Query Match 100.0%; Score 402; DB 15; Length 610;
Best Local Similarity 100.0%; Pred. No. 7.2e-117;
Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGAATGCTTCTGAATTTGAGTTTGTAGCTCTTGGGGCTGCTATGTTTCTGCTTTT 60
DB 29 ATGAGAATGCTTCTGAATTTGAGTTTGTAGCTCTTGGGGCTGCTATGTTTCTGCTTTT 88
QY 61 GCTGTAGAAAATCCCATGAATAGTGGTGCAGAGACCTTGACACTCTCTCCACTCAT 120
DB 89 GCTGTAGAAAATCCCATGAATAGTGGTGCAGAGACCTTGACACTCTCTCCACTCAT 148
QY 121 CGAACTTGGCTGATAGGGGATGGGAACCTGATGTTCTTCTCTGAAAAATAAAATCAC 180
DB 149 CGAACTTGGCTGATAGGGGATGGGAACCTGATGTTCTTCTCTGAAAAATAAAATCAC 208
QY 181 CAACCTGTGCTTAAAGAGATTTTTCAGGGTATAGACACTTGAAGAACCAACCTGCCAC 240
DB 209 CAACCTGTGCTTAAAGAGATTTTTCAGGGTATAGACACTTGAAGAACCAACCTGCCAC 268
QY 241 GGGGAGGCTGTGGATAAACTATTCCAAAACCTTGTCTTTAAATAAAGAACACATAGAGCG 300
DB 269 GGGGAGGCTGTGGATAAACTATTCCAAAACCTTGTCTTTAAATAAAGAACACATAGAGCG 328
QY 301 CAAAAAAGAGTGTGCAGGAGAAAGATGGAGAGTGACAAAGTCTCTAGACTACCTGCAA 360
DB 329 CAAAAAAGAGTGTGCAGGAGAAAGATGGAGAGTGACAAAGTCTCTAGACTACCTGCAA 388
QY 361 GTATTCTTGGTGTAAATAAACACCGAGTGGACCGGAAAGT 402
DB 369 GTATTCTTGGTGTAAATAAACACCGAGTGGACCGGAAAGT 430

RESULT 10
US-10-218-654-82/c
Sequence 82, Application US/10218654
Publication No. US20030099609A1
GENERAL INFORMATION:
APPLICANT: Sim, Gek-Ke
APPLICANT: Yang, Shumin
APPLICANT: Dreitz, Matthew J.
APPLICANT: Wonderling, Ramani S.
TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
FILE REFERENCE: IM-2-C1
CURRENT APPLICATION NUMBER: US/10/218,654
PRIORITY FILING DATE: 2002-08-13
PRIORITY FILING DATE: 1999-05-28
PRIORITY FILING DATE: 60/087,306
NUMBER OF SEQ ID NOS: 154
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 80
LENGTH: 610
TYPE: DNA
ORGANISM: Canis familiaris
US-10-218-654-82

ORGANISM: Canis familiaris
FEATURE:
NAME/KEY: CDS
LOCATION: (29) .. (430)
US-10-262-439-80

Query Match
Best Local Similarity 100.0%; Score 402; DB 15; Length 610;
Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGATGCTTCGAATTTGAGTTTGTAGTTTGGGGCTGCTATGTTTCTGCTTT 523
DB 29 ATGAGATGCTTCGAATTTGAGTTTGTAGTTTGGGGCTGCTATGTTTCTGCTTT 120
QY 61 GCTGTAGAAAATCCCATGAATAGACTGTGGCAGAGACCTTTGACACTGCTCCACTCAT 120
DB 89 GCTGTAGAAAATCCCATGAATAGACTGTGGCAGAGACCTTTGACACTGCTCCACTCAT 148
QY 121 CGAATCTGGCTGATAGCGATGGGAACCTGATGATTCCTACTCTGAAAATAAAAAATCAC 180
DB 149 CGAATCTGGCTGATAGCGATGGGAACCTGATGATTCCTACTCTGAAAATAAAAAATCAC 208
QY 181 CAATCTGTCATTAAAGAGTTTTCAGGGTATAGACATTTGAAGACCAAACTGCCAC 240
DB 209 CAATCTGTCATTAAAGAGTTTTCAGGGTATAGACATTTGAAGACCAAACTGCCAC 268
QY 241 GGGGAGGCTGTGGATAAATCTTCCAAAACCTTGTCTTTTAAATAAAGAACACATAGAGCGC 300
DB 269 GGGGAGGCTGTGGATAAATCTTCCAAAACCTTGTCTTTTAAATAAAGAACACATAGAGCGC 328
QY 301 CAAAAAAGAGTGTGAGGAGAAAGATGGAGAGTGACAAAGTTCTTAGACTCTGCA 360
DB 329 CAAAAAAGAGTGTGAGGAGAAAGATGGAGAGTGACAAAGTTCTTAGACTCTGCA 388
QY 361 GTATTCTTGTGTGTAATAAACACCGAGTGGACACCGGAAAGT 402
DB 389 GTATTCTTGTGTGTAATAAACACCGAGTGGACACCGGAAAGT 430

RESULT 12
US-10-262-439-82/c
Sequence 82, Application US/10262439
Publication No. US20030143196A1
GENERAL INFORMATION:
APPLICANT: Sim, Gek-kee
APPLICANT: Yang, Shumin
APPLICANT: Dreitz, Matthew J.
APPLICANT: Wonderling, Ramani S.
TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
FILE REFERENCE: IM-2-C2
CURRENT APPLICATION NUMBER: US/10/262,439
CURRENT FILING DATE: 2002-09-30
PRIOR APPLICATION NUMBER: US/09/451,527
PRIOR FILING DATE: 1999-12-01
PRIOR APPLICATION NUMBER: 09/322,409
PRIOR FILING DATE: 1999-05-28
PRIOR APPLICATION NUMBER: 60/087,306
PRIOR FILING DATE: 1998-05-29
NUMBER OF SEQ ID NOS: 174
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 82
LENGTH: 610
TYPE: DNA
ORGANISM: Canis familiaris
US-10-262-439-82

Query Match
Best Local Similarity 100.0%; Score 402; DB 15; Length 610;
Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 582 ATGAGATGCTTCGAATTTGAGTTTGTAGTTTGGGGCTGCTATGTTTCTGCTTT 523
QY 61 GCTGTAGAAAATCCCATGAATAGACTGTGGCAGAGACCTTTGACACTGCTCCACTCAT 120
DB 522 GCTGTAGAAAATCCCATGAATAGACTGTGGCAGAGACCTTTGACACTGCTCCACTCAT 463
QY 121 CGAATCTGGCTGATAGCGATGGGAACCTGATGATTCCTACTCTGAAAATAAAAAATCAC 180
DB 462 CGAATCTGGCTGATAGCGATGGGAACCTGATGATTCCTACTCTGAAAATAAAAAATCAC 403
QY 181 CAATCTGTCATTAAAGAGTTTTCAGGGTATAGACATTTGAAGACCAAACTGCCAC 240
DB 402 CAATCTGTCATTAAAGAGTTTTCAGGGTATAGACATTTGAAGACCAAACTGCCAC 343
QY 241 GGGGAGGCTGTGGATAAATCTTCCAAAACCTTGTCTTTTAAATAAAGAACACATAGAGCGC 300
DB 342 GGGGAGGCTGTGGATAAATCTTCCAAAACCTTGTCTTTTAAATAAAGAACACATAGAGCGC 283
QY 301 CAAAAAAGAGTGTGAGGAGAAAGATGGAGAGTGACAAAGTTCTTAGACTCTGCA 360
DB 282 CAAAAAAGAGTGTGAGGAGAAAGATGGAGAGTGACAAAGTTCTTAGACTCTGCA 223
QY 361 GTATTCTTGTGTGTAATAAACACCGAGTGGACACCGGAAAGT 402
DB 222 GTATTCTTGTGTGTAATAAACACCGAGTGGACACCGGAAAGT 181

RESULT 13

US-09-755-633-9
Sequence 9, Application US/09755633
Patent No. US20020127200A1
GENERAL INFORMATION:
APPLICANT: Yang, Shumin
APPLICANT: McGill, Catherine A.
APPLICANT: Weber, Eric R.
TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
FILE REFERENCE: IM-2-C1-C1
CURRENT APPLICATION NUMBER: US/09/755,633
CURRENT FILING DATE: 2001-01-05
PRIOR APPLICATION NUMBER: 09/322,409
PRIOR FILING DATE: 1999-05-28
PRIOR APPLICATION NUMBER: 60/087,306
PRIOR FILING DATE: 1998-05-29
NUMBER OF SEQ ID NOS: 21
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 9
LENGTH: 345
TYPE: DNA
ORGANISM: Canis familiaris
FEATURE:
NAME/KEY: CDS
LOCATION: (1) .. (345)
US-09-755-633-9

Query Match
Best Local Similarity 100.0%; Score 345; DB 9; Length 345;
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 TTTGCTGTAGAAAATCCCATGAATAGACTGTGGCAGAGACCTTTGACACTGCTCCACT 60
QY 118 CATCGAACTTGGCTGATAGCGATGGGAACCTGATGATTCCTACTCTGAAAATAAAAAAT 177
DB 61 CATCGAACTTGGCTGATAGCGATGGGAACCTGATGATTCCTACTCTGAAAATAAAAAAT 120
QY 178 CACCAACTGTGCATTAAGAGTTTTCAGGGTATAGACATTTGAAGACCAAACTGCC 237
DB 121 CACCAACTGTGCATTAAGAGTTTTCAGGGTATAGACATTTGAAGACCAAACTGCC 180
QY 238 CACGGGAGGCTGTGATAAATCTTCCAAAACCTTGTCTTTTAAATAAAGAACACATAGAG 297

Db 181 CACGGGAGGCTGTGATTAACCTATTCCTAACTTCTTTTAAATAAAGAACACATAGAG 240
Qy 298 CGCAAAAAAAGGTGTGAGAGAAAGATGAGAGTGCACAAAGTTCTTAGACTACCTG 357
Db 241 CGCAAAAAAAGGTGTGAGAGAAAGATGAGAGTGCACAAAGTTCTTAGACTACCTG 300
Qy 358 CAAGTATTTCTTGGTGTATTAACACCGAGTGGACACCGGAAAGT 402
Db 301 CAAGTATTTCTTGGTGTATTAACACCGAGTGGACACCGGAAAGT 345

RESULT 14

US-09-755-633-11/c
; Sequence 11, Application US/09755633
; Patent No. US20020127200A1
; GENERAL INFORMATION:
; APPLICANT: Yang, Shumin
; APPLICANT: McCall, Catherine A.
; APPLICANT: Weber, Eric R.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; FILE REFERENCE: IM-2-CI-C1
; CURRENT APPLICATION NUMBER: US/09/755,633
; PRIOR FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: 09/322,409
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/087,306
; PRIOR FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 345
; TYPE: DNA
; ORGANISM: Canis familiaris
US-09-755-633-11

Query Match 85.8%; Score 345; DB 9; Length 345;
Best Local Similarity 100.0%; Pred. No. 6.6e-99;
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 58 TTTGCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACT 117
Db 345 TTTGCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACT 286
Qy 118 CATCGAACTTGGCTGTAGAGCGATGGGAACCTGATGATTCCTACTCTCTGAAAAATAAAAT 177
Db 285 CATCGAACTTGGCTGTAGAGCGATGGGAACCTGATGATTCCTACTCTCTGAAAAATAAAAT 226
Qy 178 CACCAACTGTGCATTAAGAAGTTTTCAGGGTATAGACACATTTGAAGAACCAAACTGCC 237
Db 225 CACCAACTGTGCATTAAGAAGTTTTCAGGGTATAGACACATTTGAAGAACCAAACTGCC 166
Qy 238 CACGGGAGGCTGTGGATAAATTCCTAACTTCCAAAACCTGTCTTTAATAAAGAACACATAGAG 297
Db 165 CACGGGAGGCTGTGGATAAATTCCTAACTTCCAAAACCTGTCTTTAATAAAGAACACATAGAG 106
Qy 298 CGCAAAAAAAGGTGTGAGAGAAAGATGAGAGTGCACAAAGTTCTTAGACTACCTG 357
Db 105 CGCAAAAAAAGGTGTGAGAGAAAGATGAGAGTGCACAAAGTTCTTAGACTACCTG 46
Qy 358 CAAGTATTTCTTGGTGTATTAACACCGAGTGGACACCGGAAAGT 402
Db 45 CAAGTATTTCTTGGTGTATTAACACCGAGTGGACACCGGAAAGT 1

RESULT 15

US-10-218-654-85
; Sequence 85, Application US/10218654
; Publication No. US20030099609A1
; GENERAL INFORMATION:
; APPLICANT: Sim, Gek-Kee
; APPLICANT: Yang, Shumin
; APPLICANT: Dreitz, Matthew J.

; APPLICANT: Wonderling, Ramani S.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; FILE REFERENCE: IM-2-C1
; CURRENT APPLICATION NUMBER: US/10/218,654
; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: US/09/322,409
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/087,306
; PRIOR FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 154
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 85
; LENGTH: 345
; TYPE: DNA
; ORGANISM: Canis familiaris
; NAME/KEY: CDS
; LOCATION: (1)...(345)
US-10-218-654-85

Query Match 85.8%; Score 345; DB 15; Length 345;
Best Local Similarity 100.0%; Pred. No. 6.6e-99;
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 58 TTTGCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACT 117
Db 1 TTTGCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACT 60
Qy 118 CATCGAACTTGGCTGTAGAGCGATGGGAACCTGATGATTCCTACTCTCTGAAAAATAAAAT 177
Db 61 CATCGAACTTGGCTGTAGAGCGATGGGAACCTGATGATTCCTACTCTCTGAAAAATAAAAT 120
Qy 178 CACCAACTGTGCATTAAGAAGTTTTCAGGGTATAGACACATTTGAAGAACCAAACTGCC 237
Db 121 CACCAACTGTGCATTAAGAAGTTTTCAGGGTATAGACACATTTGAAGAACCAAACTGCC 180
Qy 238 CACGGGAGGCTGTGGATAAATTCCTAACTTCCAAAACCTGTCTTTAATAAAGAACACATAGAG 297
Db 181 CACGGGAGGCTGTGGATAAATTCCTAACTTCCAAAACCTGTCTTTAATAAAGAACACATAGAG 240
Qy 298 CGCAAAAAAAGGTGTGAGAGAAAGATGAGAGTGCACAAAGTTCTTAGACTACCTG 357
Db 241 CGCAAAAAAAGGTGTGAGAGAAAGATGAGAGTGCACAAAGTTCTTAGACTACCTG 300
Qy 358 CAAGTATTTCTTGGTGTATTAACACCGAGTGGACACCGGAAAGT 402
Db 301 CAAGTATTTCTTGGTGTATTAACACCGAGTGGACACCGGAAAGT 345

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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Perfect score: 610
Sequence: 1 caaggaacactgaacatt.....acagatgaataatttgag 610

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues
Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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31: em_htg_inv.*
32: em_htg_other.*
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34: em_htg_pln.*
35: em_htg_rod.*
36: em_htg_mam.*
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41: em_htgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	610	100.0	610	4	AF331919	AF331919 Canis fam
2	610	100.0	610	6	AR241536	AR241536 Sequence
3	610	100.0	610	6	AR241537	AR241537 Sequence
4	610	100.0	610	6	AR254492	AR254492 Sequence
5	610	100.0	610	6	AR254493	AR254493 Sequence
6	610	100.0	610	6	BD211558	BD211558 Canine an
7	610	100.0	610	6	BD211559	BD211559 Canine an
8	405.8	66.5	838	4	AF025436	AF025436 Felis cat
9	402	65.9	402	6	AR241538	AR241538 Sequence
10	402	65.9	402	6	AR241539	AR241539 Sequence
11	402	65.9	402	6	AR254494	AR254494 Sequence
12	402	65.9	402	6	AR254495	AR254495 Sequence
13	402	65.9	402	6	BD211560	BD211560 Canine an
14	402	65.9	402	6	BD211561	BD211561 Canine an
15	401.8	65.9	405	6	AR300436	AR300436 Sequence
16	401.8	65.9	405	6	AX083939	AX083939 Sequence
17	379	62.1	816	6	E01639	E01639 cDNA encodi
18	379	62.1	816	6	E13591	E13591 cDNA encodi
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22	364.4	59.7	520	4	OU35038	OU35038 Ovis aries
23	357.4	58.6	529	4	SSC133452	AJ133452 Sus scrof
24	345	56.6	345	6	AR241540	AR241540 Sequence
25	345	56.6	345	6	AR241541	AR241541 Sequence
26	345	56.6	345	6	AR254496	AR254496 Sequence
27	345	56.6	345	6	AR254497	AR254497 Sequence
28	345	56.6	345	6	BD211562	BD211562 Canine an
29	345	56.6	345	6	BD211563	BD211563 Canine an
30	341	55.9	405	4	AF068770	AF068770 Felis cat
31	337.8	55.4	405	4	ECU91947	U91947 Equus cabal
32	329.8	54.1	356	4	AF091133	AF091133 Canis fam
33	329.8	54.1	405	4	BTINIL5U5	Z67872 B.taurus mR
34	326.6	53.5	405	4	SSC010088	AJ010088 Sus scrof
35	281.2	46.1	354	4	AF051372	AF051372 Felis cat
36	280.2	45.9	405	9	AF294756	AF294756 Salmir's
37	276.6	45.3	858	6	AX766521	AX766521 Sequence
38	275.6	45.2	858	6	AX766523	AX766523 Sequence
39	275.4	45.1	405	9	CEYIN5A	L26033 Cercopithec
40	273.8	44.9	405	9	MMU19848	U19848 Macaca mula
41	267.4	43.8	564	10	CPU34588	U34588 Cavia porce
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44	243.4	39.9	421	12	SYN1L5A	M33949 Synthetic h
45	232.4	38.1	864	6	AX766527	AX766527 Sequence

ALIGNMENTS

RESULT 1
AF331919
LOCUS AF331919
DEFINITION Canis familiaris interleukin-5 mRNA, complete cds.
ACCESSION AF331919
VERSION AF331919.1 GI:15919180
KEYWORDS
SOURCE Canis familiaris (dog)
ORGANISM Canis familiaris
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE 1 (bases 1 to 610)
AUTHORS Yang,S., Sellins,K.S., Weber,E. and McCall,C.
TITLE Canine interleukin-5; molecular characterization of the gene and
expression of biologically active recombinant protein

J. Interferon Cytokine Res. 21 (6), 361-367 (2001)
 21334408
 MEDLINE
 PUBMED
 11440633
 REFERENCE
 2 (bases 1 to 610)
 Yung, S.
 TITLE
 Direct Submission
 JOURNAL
 Submitted (22-DEC-2000) Immunology, Heeska Corporation, 1613
 Prospect Parkway, Ft Collins, CO 80525, USA
 FEATURES
 Location/Qualifiers
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 /note="IL-5"
 /codon_start=1
 /product="interleukin-5"
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 /translations="MSRLNLSLALGAAYVSAFAVENPMRLVAVETLLSLSTHRTWL
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 433..610
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 Query Match 100.0%; Score 610; DB 4; Length 610;
 Best Local Similarity 100.0%; Pred. No. 4.4e-154;
 Matches 610; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 DB 1 CAAGGCAAACTGAACTTCAGAGCTATGAGAACTCTCTCAATTTGAGTTGCTAGC 60
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 QY 421 ACCGGAAGTTGAGAACAAACCGGCTTATTTAGTGAAGATTTTGGAGAGAAATGGTTT 480
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 DB 541 TTCAGACAAAGTAAATATTTTCAGGCATCCTACTACTTTATCATTTCACACAGATGAAA 600
 QY 601 TATATTGGAG 610
 DB 601 TATATTGGAG 610

RESULT 2
 AR241536
 LOCUS
 DEFINITION
 Sequence 80 from patent US 6471957.
 AR241536
 ACCESSION
 AR241536.1 GI:27287245
 VERSION
 KEYWORDS
 SOURCE
 Unknown.
 ORGANISM
 Unclassified.
 REFERENCE
 1 (bases 1 to 610)
 AUTHORS
 Sim, G.-K., Yang, S., Dreitz, M. J. and Wonderling, R. S.
 TITLE
 Canine IL-4 immunoregulatory proteins and uses thereof
 JOURNAL
 Patent: US 6471957-A 80 29-OCT-2002;
 FEATURES
 Location/Qualifiers
 source
 1..610
 /organism="unknown"
 /mol_type="genomic DNA"
 Query Match 100.0%; Score 610; DB 6; Length 610;
 Best Local Similarity 100.0%; Pred. No. 4.4e-154;
 Matches 610; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CAAGGCAAACTGAACTTCAGAGCTATGAGAACTCTCTCAATTTGAGTTGCTAGC 60
 DB 1 CAAGGCAAACTGAACTTCAGAGCTATGAGAACTCTCTCAATTTGAGTTGCTAGC 60
 QY 61 TCTTGGGCTGCCCTATGTTCTGCCCTTGTCTGAGAAATCCCATCAATAGACTGGTGGC 120
 DB 61 TCTTGGGCTGCCCTATGTTCTGCCCTTGTCTGAGAAATCCCATCAATAGACTGGTGGC 120
 QY 121 AGAGACCTTGACACTGCTCTCCACTCATCGAACTTGGCTGATAGGGGATGGAACTGTAT 180
 DB 121 AGAGACCTTGACACTGCTCTCCACTCATCGAACTTGGCTGATAGGGGATGGAACTGTAT 180
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 DB 181 GATTCCTACTCTCGAAATTAATAATCACCACTGTGCAATTAAGAAGTTTTCAGGGTAT 240
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 DB 241 AGACACATTGAAGAACCAAACTGCCACGGGGAGGCTGTGGATAAATACTATTCAAAACCTT 300
 QY 301 GTCTTTTAATAAAGAACACATAGAGCGCCAAAAAAGGTGTGCAGGAGAAAGATGGAG 360
 DB 301 GTCTTTTAATAAAGAACACATAGAGCGCCAAAAAAGGTGTGCAGGAGAAAGATGGAG 360
 QY 361 AGTGACAAAAGTTCCTAGACTACCTGCAAGTATTTCTTGGTGTAAATAAACCAGATGGAC 420
 DB 361 AGTGACAAAAGTTCCTAGACTACCTGCAAGTATTTCTTGGTGTAAATAAACCAGATGGAC 420
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 DB 541 TTCAGACAAAGTAAATATTTTCAGGCATCCTACTACTTTATCATTTCACACAGATGAAA 600
 QY 601 TATATTGGAG 610
 DB 601 TATATTGGAG 610

RESULT 3
 AR241537/c

LOCUS	AR241537	610 bp	DNA	linear	PAT 20-DEC-2002
DEFINITION	Sequence 82 from patent US 6471957.				
ACCESSION	AR241537				
VERSION	AR241537.1	GI:27287246			
KEYWORDS					
SOURCE	Unknown.				
ORGANISM	Unclassified.				
REFERENCE	1 (bases 1 to 610)				
AUTHORS	Sim,G.-K., Yang,S., Dreibl,M.J. and Wonderling,R.S.				
TITLE	Canine IL-4 immunoregulatory proteins and uses thereof				
JOURNAL	Patent: US 6471957-A 82 29-OCT-2002;				
FEATURES	Location/Qualifiers				
source	1..610				
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ORIGIN					
	Query Match	100.0%;	Score 610;	DB 6;	Length 610;
	Best Local Similarity	100.0%;	Pred No. 4.4e-154;		
	Matches 610;	Conservative	0;	Mismatches	0;
	Indels	0;	Gaps	0;	
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Db	610	CAAGGCAAA	CAC	TGAA	CAT
QY	61	TC	TGGGGT	GC	CTA
Db	550	TC	TGGGGT	GC	CTA
QY	121	AGAGAC	CTT	GACA	CT
Db	490	AGAGAC	CTT	GACA	CT
QY	181	GA	TTCT	TACT	CT
Db	430	GA	TTCT	TACT	CT
QY	241	AGAC	CAT	T	GA
Db	370	AGAC	CAT	T	GA
QY	301	GT	CTTT	TA	TA
Db	310	GT	CTTT	TA	TA
QY	361	AG	TGAC	AA	AG
Db	250	AG	TGAC	AA	AG
QY	421	AC	CG	AA	AG
Db	190	AC	CG	AA	AG
QY	481	TT	TGG	CG	AT
Db	130	TT	TGG	CG	AT
QY	541	TT	CAG	AG	CA
Db	70	TT	CAG	AG	CA
QY	601	TAT	ATT	TG	AG
Db	10	TAT	ATT	TG	AG
RESULT 4					
LOCUS	AR254492	610 bp	DNA	linear	PAT 20-DEC-2002
DEFINITION	Sequence 80 from patent US 6482403.				
ACCESSION	AR254492				
VERSION	AR254492.1	GI:27303380			

REFERENCE 1 (bases 1 to 610)
 AUTHORS Sim,G.-K., Yang,S., Dreitz,M.J. and Wonderling,R.S.
 TITLE Caniney IL-13 immunoregulatory proteins and uses thereof
 JOURNAL Patent: US 6482403-A 82 19-NOV-2002;
 FEATURES Location/Qualifiers
 source 1..610
 /organism="unknown"
 /mol_type="genomic DNA"

ORIGIN
 Query Match 100.0%; Score 610; DB 6; Length 610;
 Best Local Similarity 100.0%; Pred. No. 4.4e-154;
 Matches 610; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAAGGCAAACTGAACTTTCAGAGCTATGAGAAATGCTTCTGAAATTTGAGTTGCTAGC 60
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 Db 550 TCTTGGGCGCTGCTATGCTTCTGCTTTGCTGTAGAAATCCCATGAAATAGACTGTTGGC 491
 Qy 121 AGAGACCTTGACACTGCTTCCACTCATGAACTTGGCTGATAGGCGATGGAACTGTAT 180
 Db 490 AGAGACCTTGACACTGCTTCCACTCATGAACTTGGCTGATAGGCGATGGAACTGTAT 431
 Qy 181 GATTCTTACTCTGAAATAAATACCAACTGCTGATTAAGAAAGTTTTCAGGGTAT 240
 Db 430 GATTCTTACTCTGAAATAAATACCAACTGCTGATTAAGAAAGTTTTCAGGGTAT 371
 Qy 241 AGACACATTAAGAAACCAACTGCCACGGGGAGCTGTGATPAATACTATTCAAAACCT 300
 Db 370 AGACACATTAAGAAACCAACTGCCACGGGGAGCTGTGATPAATACTATTCAAAACCT 311
 Qy 301 GTCTTTAATAAAGACACATAGAGCCGCAAAAAAAGGTGTCAGGAGAAAGATGGAG 360
 Db 310 GTCTTTAATAAAGACACATAGAGCCGCAAAAAAAGGTGTCAGGAGAAAGATGGAG 251
 Qy 361 AGTGACAAAGTTCTAGACTACCTGCAAGTATTTCTTGGTGTAAATAACACCGAGTGGAC 420
 Db 250 AGTGACAAAGTTCTAGACTACCTGCAAGTATTTCTTGGTGTAAATAACACCGAGTGGAC 191
 Qy 421 ACCGAAAGTTGAGAACAAACCGGCTTATTTGATGGAAGATTTTGGAGAAAGATGGTTT 480
 Db 190 ACCGAAAGTTGAGAACAAACCGGCTTATTTGATGGAAGATTTTGGAGAAAGATGGTTT 131
 Qy 481 TTTGGCGATGAGATGAGGCGCAACCAAGTAGGAGCTTATGCGCAGTATAACTAGC 540
 Db 130 TTTGGCGATGAGATGAGGCGCAACCAAGTAGGAGCTTATGCGCAGTATAACTAGC 71
 Qy 541 TTCAGACAAAGTAAATATTTTCAGGCATCCTACTACTTATCATCTCACAGATGAAA 600
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 Qy 601 TATATTTGAG 610
 Db 10 TATATTTGAG 1

RESULT 6
 BD211558
 LOCUS
 DEFINITION BD211558 610 bp DNA linear PAT 17-JUL-2003
 Canine and feline immunoregulatory proteins, nucleic acid molecules
 and method of using the same.
 ACCSSION BD211558
 VERSION BD211558.1 GI:33021328
 KEYWORDS JP 2002516104-A/64.
 SOURCE Canis familiaris (dog)
 ORGANISM Canis familiaris
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 REFERENCE 1 (bases 1 to 610)
 AUTHORS Sim,G., Yang,S., Dreitz,M.J. and Wonderling,R.S.

TITLE Canine and feline immunoregulatory proteins, nucleic acid molecules
 and method of using the same
 JOURNAL Patent: JP 2002516104-A 64 04-JUN-2002;
 COMMENT HESKA CORP
 OS Canis familiaris (dog)
 PN JP 2002516104-A/64
 PD 04-JUN-2002
 PF 28-MAY-1999 JP 2000551002
 PR 29-MAY-1998 US 60/087306
 PI GEKKEE SIM,SHUMIN YANG, MATTHEW J DREITZ, RAMANI S WONDERLING PC
 C12N15/09,A61K31/7088,A61K38/21,A61K39/00,A61K39/395,
 PC A61K39/395,
 PC A61K45/00,A61K48/00,A61P37/02,A61P37/04,C07K14/475,C07K14/535,
 PC C07K14/54,
 PC C07K14/56,C07K14/705,C07K16/24,C07K16/28,C12N1/21,C12N5/10, PC
 G01N33/15,
 PC G01N33/50,C12N15/00,A61K37/02,A61K37/66,C12N5/00 CC Canine
 and feline immunoregulatory proteins, nucleic acid CC
 molecules and
 CC method of using the same
 FH Key Location/Qualifiers
 FT CDS (29)...(430).

FEATURES
 source 1..610
 /organism="Canis familiaris"
 /mol_type="genomic DNA"
 /db_xref="taxon:9615"

ORIGIN
 Query Match 100.0%; Score 610; DB 6; Length 610;
 Best Local Similarity 100.0%; Pred. No. 4.4e-154;
 Matches 610; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAAGGCAAACTGAACTTTCAGAGCTATGAGAAATGCTTCTGAAATTTGAGTTGCTAGC 60
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 Qy 61 TCTTGGGCGCTGCTATGCTTCTGCTTTGCTGTAGAAATCCCATGAAATAGACTGTTGGC 120
 Db 61 TCTTGGGCGCTGCTATGCTTCTGCTTTGCTGTAGAAATCCCATGAAATAGACTGTTGGC 120
 Qy 121 AGAGACCTTGACACTGCTTCCACTCATGAACTTGGCTGATAGGCGATGGAACTGTAT 180
 Db 121 AGAGACCTTGACACTGCTTCCACTCATGAACTTGGCTGATAGGCGATGGAACTGTAT 180
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 Db 421 ACCGAAAGTTGAGAACAAACCGGCTTATTTGATGGAAGATTTTGGAGAAAGATGGTTT 480
 Qy 481 TTTGGCGATGAGATGAGGCGCAACCAAGTAGGAGCTTATGCGCAGTATAACTAGC 540
 Db 481 TTTGGCGATGAGATGAGGCGCAACCAAGTAGGAGCTTATGCGCAGTATAACTAGC 540
 Qy 541 TTCAGACAAAGTAAATATTTTCAGGCATCCTACTACTTATCATCTCACAGATGAAA 600
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Db 17 CAAAGCAACACTGAGCATTTGAGAGCCATGAGATGCTTCTGCAATTTGAGTTTGCTAGC 76
QY 61 TCTTGGGCTCGCTATGCTTCTGCTTTGCTGTAGAAAATCCCATGAATAGACTGCTGGC 120
Db 77 TCTTGGGCTCGCTATGCTTCTGCTTTGCTGTACAAAGTCCCATGAAATAGGCTGCTGGC 136
QY 121 AGAGACCTTGACACTGCTTCCACTGATCGAACTTGCTGCTGATAGGCGATGGAACTGAT 180
Db 137 AGAGACCTTGACACTGCTTCCACTGATCGAACTTGCTGCTGATAGGCGATGGAACTGAT 196
QY 181 GATTCCTACTCTGAAATGAAATACCAACTGCTGATTAAGAAAGTTTTCAGGGTAT 240
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QY 241 AGACACATTTGAAGAACCAACTGCTGCTGAGGAGCTGCTGATTAAGAAAGTTTTCAGGGTAT 300
Db 257 AGACACATTTGAAGAACCAACTGCTGCTGAGGAGCTGCTGATTAAGAAAGTTTTCAGGGTAT 316
QY 301 GTCTTTTAAAGAAACACATAGAGCGCCAAAGAAAGTGTGCGAGGAAAGATGGAG 360
Db 317 GTCTTTTAAAGAAACACATAGAGCGCCAAAGAAAGTGTGCGAGGAAAGATGGAG 376
QY 361 AGTGACAAAGTTCTAGACTACCTGCAAGTATTTCTTGGTGTAAATAAACACCGAGTGGAC 420
Db 377 AGTAAAGAAAGTTCTAGACTACCTGCAAGTATTTCTTGGTGTAAATAAACACCTGAGTGGAC 436
QY 421 ACCGAAAGTTGAGAAACCAAGCGCTTATTTGATGGAAGATTTTGGAGAGAA----- 474
Db 437 AATGAAAGTTGAGATGAAAGTGGTATTTGATGGAAGATTTTGGAGAGAA----- 496
QY 475 -TGCTTTTGGGATGAGATGAGGCGCAACCAAGTAGGACCTAATGGCAGTATA 533
Db 497 TGTTATTTTGGCAATGAGATGAGGCGCAAC-----AGGGTCACTGTA 542
QY 534 ACTAAGCTTCAGAGCAAAAGTAAATTTTCCAGGCTCCTACTACTTT 580
Db 543 ATTAAGCTTCAGAGCAAAAGTAAATTTTCCAGGCTCCTACTACTTT 588

RESULT 9
AR241538
LOCUS AR241538 402 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 83 from patent US 6471957.
ACCESSION AR241538
VERSION AR241538.1 GI:27287247
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 402)
AUTHORS Sim,G.-K., Yang,S., Dreitz,M.J. and Wonderling,R.S.
TITLE Canine IL-4 immunoregulatory proteins and uses thereof
JOURNAL Patent: US 6471957-A 83 29-OCT-2002;
FEATURES Location/Qualifiers
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/organism="unknown"
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Query Match 65.9%; Score 402; DB 6; Length 402;
Best Local Similarity 100.0%; Pred. No. 8.2e-98;
Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 29 ATGAGATGCTTCTGAAATTTGAGTTTCTAGCTTTTGGGCTGCTTATGTTTCTGCTTT 88
Db 1 ATGAGATGCTTCTGAAATTTGAGTTTCTAGCTTTTGGGCTGCTTATGTTTCTGCTTT 60
QY 89 GCTGTAGAAATCCCATGATGAGTGGTGGCAGAGACCTTGACACTGCTTCCACTCAT 148
Db 61 GCTGTAGAAATCCCATGATGAGTGGTGGCAGAGACCTTGACACTGCTTCCACTCAT 120

QY 149 CGAACTTGGCTGATAGGCGATGGGAACTGTATGATTTCTTACTCTGAAATATAAATATCAC 208
Db 121 CGAACTTGGCTGATAGGCGATGGGAACTGTATGATTTCTTACTCTGAAATATAAATATCAC 180
QY 209 CAACCTGTGCATTTAAAGAAAGTTTTCAGGCTATAGACACATTTGAAGAACCAAACTGCCAC 268
Db 181 CAACCTGTGCATTTAAAGAAAGTTTTCAGGCTATAGACACATTTGAAGAACCAAACTGCCAC 240
QY 269 GGGAGGCTGTGATTAACCTATTCCAAAACCTTGTCTTTAATAAAGAACACATAGAGCGC 328
Db 241 GGGAGGCTGTGATTAACCTATTCCAAAACCTTGTCTTTAATAAAGAACACATAGAGCGC 300
QY 329 CAAAAAAGAGTGTGAGGAGAAAGATGGAGAGTGAACAAAGTTTCTAGACTACCTGCAA 388
Db 301 CAAAAAAGAGTGTGAGGAGAAAGATGGAGAGTGAACAAAGTTTCTAGACTACCTGCAA 360
QY 389 GTATTTCTTGTGTGTAATAACACCGAGTGGACACCGGAAAGT 430
Db 361 GTATTTCTTGTGTGTAATAACACCGAGTGGACACCGGAAAGT 402

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Best Local Similarity 100.0%; Pred. No. 8.2e-98;
Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 402 ATGAGATGCTTCTGAAATTTGAGTTTCTAGCTTTTGGGCTGCTTATGTTTCTGCTTT 343

QY 89 GCTGTAGAAATCCCATGATGAGTGGTGGCAGAGACCTTGACACTGCTTCCACTCAT 148
Db 342 GCTGTAGAAATCCCATGATGAGTGGTGGCAGAGACCTTGACACTGCTTCCACTCAT 283

QY 149 CGAACTTGGCTGATAGGCGATGGGAACTGTATGATTTCTTACTCTGAAATATAAATATCAC 208
Db 282 CGAACTTGGCTGATAGGCGATGGGAACTGTATGATTTCTTACTCTGAAATATAAATATCAC 223

QY 209 CAACCTGTGCATTTAAAGAAAGTTTTCAGGCTATAGACACATTTGAAGAACCAAACTGCCAC 268
Db 222 CAACCTGTGCATTTAAAGAAAGTTTTCAGGCTATAGACACATTTGAAGAACCAAACTGCCAC 163

QY 269 GGGAGGCTGTGATTAACCTATTCCAAAACCTTGTCTTTAATAAAGAACACATAGAGCGC 328
Db 162 GGGAGGCTGTGATTAACCTATTCCAAAACCTTGTCTTTAATAAAGAACACATAGAGCGC 103

QY 329 CAAAAAAGAGTGTGAGGAGAAAGATGGAGAGTGAACAAAGTTTCTAGACTACCTGCAA 388
Db 102 CAAAAAAGAGTGTGAGGAGAAAGATGGAGAGTGAACAAAGTTTCTAGACTACCTGCAA 43

QY 389 GTATTTCTTGTGTGTAATAACACCGAGTGGACACCGGAAAGT 430
Db 42 GTATTTCTTGTGTGTAATAACACCGAGTGGACACCGGAAAGT 1


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RESULT 11
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LOCUS AR254494 402 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 83 from patent US 6482403.
ACCESSION AR254494
VERSION AR254494.1 GI:27303382
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 402)
AUTHORS Sim,G.-K., Yang,S., Dreitz,M.J. and Wonderling,R.S.
TITLE Canine IL-13 immunoregulatory proteins and uses thereof
JOURNAL Patent: US 6482403-A 83 19-NOV-2002;
FEATURES
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    /mol_type="genomic DNA"
ORIGIN
Query Match 65.9%; Score 402; DB 6; Length 402;
Best Local Similarity 100.0%; Pred. No. 8.2e-98;
Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 29 ATGAGAATGCTTCTGAATTTGAGTTTCTAGCTCTTGGGCTGCTATGTTCTGCTTT 88
DB 1 ATGAGAATGCTTCTGAATTTGAGTTTCTAGCTCTTGGGCTGCTATGTTCTGCTTT 60
QY 89 GCTGTAGAAAATCCCATGAATAGACTGCTGGCAGACCTTGGACACTCTCTCCACTCAT 148
DB 61 GCTGTAGAAAATCCCATGAATAGACTGCTGGCAGACCTTGGACACTCTCTCCACTCAT 120
QY 149 CGAACTGGCTGATAGGCGATGGGAACCTGATGATCTTACTCTGAAAAATAAAATCAC 208
DB 121 CGAACTGGCTGATAGGCGATGGGAACCTGATGATCTTACTCTGAAAAATAAAATCAC 180
QY 209 CAACCTGTCATTAAGAGTTTTCAGGTTATAGACATGAGAGACCTTGGACCTCTCCACTCAT 268
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QY 269 GGGGAGGCTGTGGATAAATCTTCCAAAACCTTGCTTTAATAAAGAACACATAGAGCGC 328
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QY 329 CAAAAAAAAGGTGCGAGGAAGATGGAGATGACAAAGTTCTCTAGACTACCTGCA 388
DB 301 CAAAAAAAAGGTGCGAGGAAGATGGAGATGACAAAGTTCTCTAGACTACCTGCA 360
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DB 361 GTATTTCTTGTGTAATAAACCAGGTGGACACCGGAAAGT 402

RESULT 12
AR254495/c
LOCUS AR254495 402 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 84 from patent US 6482403.
ACCESSION AR254495
VERSION AR254495.1 GI:27303383
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 402)
AUTHORS Sim,G.-K., Yang,S., Dreitz,M.J. and Wonderling,R.S.
TITLE Canine IL-13 immunoregulatory proteins and uses thereof
JOURNAL Patent: US 6482403-A 84 19-NOV-2002;
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    /mol_type="genomic DNA"
ORIGIN
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Query Match 65.9%; Score 402; DB 6; Length 402;
Best Local Similarity 100.0%; Pred. No. 8.2e-98;
Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 29 ATGAGAATGCTTCTGAATTTGAGTTTCTAGCTCTTGGGCTGCTATGTTCTGCTTT 88
DB 402 ATGAGAATGCTTCTGAATTTGAGTTTCTAGCTCTTGGGCTGCTATGTTCTGCTTT 343
QY 89 GCTGTAGAAAATCCCATGAATAGACTGCTGGCAGACCTTGGACACTCTCTCCACTCAT 148
DB 342 GCTGTAGAAAATCCCATGAATAGACTGCTGGCAGACCTTGGACACTCTCTCCACTCAT 283
QY 149 CGAACTGGCTGATAGGCGATGGGAACCTGATGATCTTACTCTGAAAAATAAAATCAC 208
DB 282 CGAACTGGCTGATAGGCGATGGGAACCTGATGATCTTACTCTGAAAAATAAAATCAC 223
QY 209 CAACCTGTCATTAAGAGTTTTCAGGTTATAGACATGAGAGACCTTGGACCTCTCCACTCAT 268
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DB 102 CAAAAAAAAGGTGCGAGGAAGATGGAGATGACAAAGTTCTCTAGACTACCTGCA 43
QY 389 GTATTTCTTGTGTAATAAACCAGGTGGACACCGGAAAGT 430
DB 42 GTATTTCTTGTGTAATAAACCAGGTGGACACCGGAAAGT 1

RESULT 13
BD211560 402 bp DNA linear PAT 17-JUL-2003
LOCUS BD211560
DEFINITION Canine and feline immunoregulatory proteins, nucleic acid molecules and method of using the same.
ACCESSION BD211560
VERSION BD211560.1 GI:33021330
KEYWORDS JP 2002516104-A/66.
SOURCE Canis familiaris (dog)
ORGANISM Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Theria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE 1 (bases 1 to 402)
AUTHORS Sim,G., Yang,S., Dreitz,M.J. and Wonderling,R.S.
TITLE Canine and feline immunoregulatory proteins, nucleic acid molecules and method of using the same
JOURNAL Patent: JP 2002516104-A 66 04-JUN-2002;
COMMENT HESKA CORP
OS Canis familiaris (dog)
PN JP 2002516104-A/66
PD 04-JUN-2002
PF 28-MAY-1999 JP 2000551002
PR 29-MAY-1998 US 60/087306
PI GEKKEE SIM, SHUMIN YANG, MATTHEW J DREITZ, RAMANI S WONDERLING PC C12N15/09, A61K31/7088, A61K38/00, A61K39/00, A61K39/395, PC A61K39/395, PC A61K45/00, A61K48/00, A61P37/02, A61P37/04, C07K14/475, C07K14/535, PC C07K14/54, PC C07K14/56, PC C07K14/705, C07K16/24, C07K16/28, C12N1/21, C12N5/10, PC G01N33/15, PC G01N33/50, C12N15/00, A61K37/02, A61K37/66, C12N5/00 CC Canine and feline immunoregulatory proteins, nucleic acid CC molecules and feline immunoregulatory proteins, nucleic acid CC CC method of using the same
FH Key Location/Qualifiers
FT source 1..402
FT /organism="Canis familiaris (dog)"
FT Location/Qualifiers
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/organism="Canis familiaris"
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ORIGIN
Query Match      65.9%; Score 402; DB 6; Length 402;
Best Local Similarity 100.0%; Pred. No. 8.2e-98;
Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 29 ATGAGAATGCTTCTGAATTTGAGTTTGTAGCTCTTTGGGGCTGCTATGTTTCTGCCTTT 88
DB 1 ATGAGAATGCTTCTGAATTTGAGTTTGTAGCTCTTTGGGGCTGCTATGTTTCTGCCTTT 60

QY 89 GCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACTCAT 148
DB 61 GCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACTCAT 120

QY 149 CGAACTTGGCTGATAGGCGATGGGAACCTGATGATTTCTTCTGAAAATAAAAAATCAC 208
DB 121 CGAACTTGGCTGATAGGCGATGGGAACCTGATGATTTCTTCTGAAAATAAAAAATCAC 180

QY 209 CAACCTGTGCATTAAGAAGTTTTTCAGGGTATAGACATTTGAAGAACCCTGCTGCCAC 268
DB 181 CAACCTGTGCATTAAGAAGTTTTTCAGGGTATAGACATTTGAAGAACCCTGCTGCCAC 240

QY 269 GGGGAGGCTGTGGATAAATTTCCAAAACCTTGTCTTTAATAAAGAACACATAGAGCGC 328
DB 241 GGGGAGGCTGTGGATAAATTTCCAAAACCTTGTCTTTAATAAAGAACACATAGAGCGC 300

QY 329 CAAAAAAAAGGTGTGAGGAGAAAGATGGAGAGTGAACAAAGTTCTTAGACTACCTGCAC 388
DB 301 CAAAAAAAAGGTGTGAGGAGAAAGATGGAGAGTGAACAAAGTTCTTAGACTACCTGCAC 360

QY 389 GTATTTCTTGTGTAAATAAACACCGAGTGGACACCGGAAAGT 430
DB 361 GTATTTCTTGTGTAAATAAACACCGAGTGGACACCGGAAAGT 402

RESULT 14
BD211561/c
LOCUS
DEFINITION
Canine and feline immunoregulatory proteins, nucleic acid molecules
and method of using the same.
ACCESSION
BD211561
VERSION
BD211561.1 GI:33021331
KEYWORDS
JP 2002516104-A/67.
SOURCE
Canis familiaris (dog)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE
1 (bases 1 to 402)
Sim,G., Yang,S., Dreitz,M.J. and Wonderling,R.S.
Canine and feline immunoregulatory proteins, nucleic acid molecules
and method of using the same
Patent: JP 2002516104-A 67 04-JUN-2002;
HESKA CORP
COMMENT
OS Canis familiaris (dog)
PN JP 2002516104-A/67
PD 04-JUN-2002
PF 28-MAY-1999 JP 2000551002
PI GEKKEE SIM, SHUMIN YANG, MATTHEW J DREITZ, RAMANI S WONDERLING PC
C12N15/09 A61K31/7088,A61K38/00,A61K38/21,A61K39/00,A61K39/395,
PC A61K39/395,
PC A61K45/00,A61K48/00,A61P37/02,A61P37/04,C07K14/475,C07K14/535,
PC C07K14/54,
PC C07K14/56,C07K14/705,C07K16/24,C07K16/28,C12N1/21,C12N5/10, PC
GOIN33/15,
PC GOIN33/50,C12N15/00,A61K37/02,A61K37/66,C12N5/00 CC Canine
and feline immunoregulatory proteins, nucleic acid CC
molecules and method of using the same
FH Key
Location/Qualifiers

FT source 1..402
FT /organism="Canis familiaris (dog)",
FEATURES
Location/Qualifiers
1..402
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/db_xref="taxon:9615"

ORIGIN
Query Match      65.9%; Score 402; DB 6; Length 402;
Best Local Similarity 100.0%; Pred. No. 8.2e-98;
Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 29 ATGAGAATGCTTCTGAATTTGAGTTTGTAGCTCTTTGGGGCTGCTATGTTTCTGCCTTT 88
DB 402 ATGAGAATGCTTCTGAATTTGAGTTTGTAGCTCTTTGGGGCTGCTATGTTTCTGCCTTT 343

QY 89 GCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACTCAT 148
DB 342 GCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACTCAT 283

QY 149 CGAACTTGGCTGATAGGCGATGGGAACCTGATGATTTCTTCTGAAAATAAAAAATCAC 208
DB 282 CGAACTTGGCTGATAGGCGATGGGAACCTGATGATTTCTTCTGAAAATAAAAAATCAC 223

QY 209 CAACCTGTGCATTAAGAAGTTTTTCAGGGTATAGACATTTGAAGAACCCTGCTGCCAC 268
DB 222 CAACCTGTGCATTAAGAAGTTTTTCAGGGTATAGACATTTGAAGAACCCTGCTGCCAC 163

QY 269 GGGGAGGCTGTGGATAAATTTCCAAAACCTTGTCTTTAATAAAGAACACATAGAGCGC 328
DB 162 GGGGAGGCTGTGGATAAATTTCCAAAACCTTGTCTTTAATAAAGAACACATAGAGCGC 103

QY 329 CAAAAAAAAGGTGTGAGGAGAAAGATGGAGAGTGAACAAAGTTCTTAGACTACCTGCAC 388
DB 102 CAAAAAAAAGGTGTGAGGAGAAAGATGGAGAGTGAACAAAGTTCTTAGACTACCTGCAC 43

QY 389 GTATTTCTTGTGTAAATAAACACCGAGTGGACACCGGAAAGT 430
DB 42 GTATTTCTTGTGTAAATAAACACCGAGTGGACACCGGAAAGT 1

RESULT 15
AR300436
LOCUS
DEFINITION
Sequence 1 from patent US 6537781.
ACCESSION
AR300436
VERSION
AR300436.1 GI:31687875
KEYWORDS
SOURCE
Unknown.
ORGANISM
Unclassified.
REFERENCE
1 (bases 1 to 405)
AUTHORS
Guo,H., Lawton,R., Mermer,B. and Aiyappa,A.P.
TITLE
Methods and compositions concerning canine interleukin 5
JOURNAL
Patent: US 6537781-A 1 25-MAR-2003;
FEATURES
Location/Qualifiers
1..405
/mol_type="genomic DNA"

ORIGIN
Query Match      65.9%; Score 401.8; DB 6; Length 405;
Best Local Similarity 99.5%; Pred. No. 9.3e-98;
Matches 403; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 29 ATGAGAATGCTTCTGAATTTGAGTTTGTAGCTCTTTGGGGCTGCTATGTTTCTGCCTTT 88
DB 1 ATGAGAATGCTTCTGAATTTGAGTTTGTAGCTCTTTGGGGCTGCTATGTTTCTGCCTTT 60

QY 89 GCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACTCAT 148
DB 61 GCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACTCAT 120

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Qy	149	CGAACTTGGCTGATAGCGATGGGAACCTGATGATTCCTACTCTCTGAAAATAAAATCAC	208
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Qy	209	CAACTGTGCATTAAAGAAGTTTTTCAGGGTATAGACACATTTGAAGAACCAAACTGCCAC	268
Db	181	CAACTGTGCATTAAAGAAGTTTTTCAGGGTATAGACACATTTGAAGAACCAAACTGCCAC	240
Qy	269	GGGAGGCTGTGATAAACTATTCCAAAACCTTCTTTAATAAAGAACACATAGAGCGC	328
Db	241	GGGAGGCTGTGATAAACTATTCCAAAACCTTCTTTAATAAAGAACACATAGAGCGC	300
Qy	329	CAAAAAAAGGTGTCAGGAGAAAGATGGAGAGTGACAAAAGTTCTTAGACTACCTGCAA	388
Db	301	CAAAAAAAGGTGTCAGGAGAAAGATGGAGAGTGACAAAAGTTCTTAGACTACCTGCAA	360
Qy	389	GTATTTCTTGGTGAATAAACACCGAGTGGACACCGGAAAGTTGA	433
Db	361	GTATTTCTTGGTGAATAAACACCGAGTGGACCAATGGAAGTTGA	405

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Job time : 2639.86 secs

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Sheet

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model
Run on: August 30, 2004, 21:24:28 ; Search time 1159.04 Seconds
(without alignments)
8888.782 Million cell updates/sec

Title: US-10-787-382-9
Perfect score: 345
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
Searched: 27513289 seqs, 14931090276 residues
Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:
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2: em_esthum:*
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8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_phg:*
27: em_gss_vrl:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	231.4	67.1	405	29	AY412020	AY412020 Homo sapi
2	231.4	67.1	456	14	CD559532	CD559532 AGENCOURT
C 3	231.4	67.1	456	14	CD559686	CD559686 AGENCOURT
C 4	231.4	67.1	470	14	CD559687	CD559687 AGENCOURT

5	231.4	67.1	492	14	CD559533	CD559533 AGENCOURT
6	227.4	65.9	405	29	AY412021	AY412021 Pan trogl
7	222.4	64.5	477	14	CD559608	CD559608 AGENCOURT
C 8	221	64.1	467	14	CD559688	CD559688 AGENCOURT
9	221	64.1	478	14	CD559534	CD559534 AGENCOURT
10	220.4	63.9	463	14	CD559535	CD559535 AGENCOURT
C 11	220.4	63.9	473	14	CD559689	CD559689 AGENCOURT
12	220.4	63.9	489	14	CD559536	CD559536 AGENCOURT
C 13	218.8	63.4	467	14	CD559690	CD559690 AGENCOURT
14	182.6	52.9	399	29	AY412022	AY412022 Mus muscu
15	131.8	38.2	622	29	CB331159	CB331159 tigr-gss-
C 16	78	22.6	503	13	BQ598873	BQ598873 Mi-P-E4-a
17	42.4	12.3	1025	13	EX441235	EX441235 BX441235
18	40.6	11.8	522	12	BI670794	BI670794 PflST0aa0
19	40	11.6	317	14	CD087271	CD087271 MC1-0036T
20	39.8	11.5	535	28	AZ370501	AZ370501 1M0121K03
21	39.2	11.4	603	12	BJ328562	BJ328562 BJ328562
22	39.2	11.4	619	12	BJ328648	BJ328648 BJ328648
23	39.2	11.4	905	29	CNS00D59	AL060243 Drosophi
24	38.8	11.2	1201	13	EX397166	EX397166 BX397166
25	38.6	11.2	1359	12	BQ543026	BQ543026 602570858
26	38.2	11.1	667	29	CE510121	CE510121 tigr-gss-
27	38.2	11.1	797	29	CC567321	CC567321 CH240_441
28	38	11.0	432	9	AA560540	AA560540 v119f05_r
29	38	11.0	494	14	CB094467	CB094467 h270d02_b
C 30	38	11.0	1011	29	CNS00JRI	AL076645 Drosophi
31	37.8	11.0	584	13	BQ526053	BQ526053 NISC_ro14
32	37.8	11.0	671	13	EX707130	EX707130 BX707130
33	37.8	11.0	684	13	BX758408	BX758408 BX758408
34	37.8	11.0	715	13	BX773473	BX773473 BX773473
35	37.8	11.0	724	13	BX773491	BX773491 BX773491
36	37.8	11.0	783	14	CF343019	CF343019 AGENCOURT
37	37.8	11.0	892	13	BX776535	BX776535 BX776535
C 38	37.6	10.9	699	28	AQ781738	AQ781738 HS_3122_A
39	37.6	10.9	964	14	CD048643	CD048643 AGENCOURT
C 40	37.6	10.9	1026	13	BX461051	BX461051 BX461051
41	37.6	10.9	1201	9	AL550373	AL550373 AL550373
42	37.4	10.8	457	12	B3373332	B3373332 BFLG1_000
43	37.4	10.8	695	28	BZ019774	BZ019774 ced85f04.
C 44	37.4	10.8	965	29	CNS03PGL	AL207966 Tetraodon
C 45	37.2	10.8	330	10	BF091941	BF091941 RC6-TN007

ALIGNMENTS

RESULT 1
AY412020

LOCUS AV412020 405 bp DNA linear GSS 16-DEC-2003
DEFINITION Homo sapiens IL5 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.

ACCESSION AY412020
VERSION AY412020.1 GI:39767985

KEYWORDS GSS.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 405)
AUTHORS Clark,A.G., Gnanowski,S., Nielson,R., Thomas,P., Kejarival,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferrieria,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.

TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302

REFERENCE 2 (bases 1 to 405)

AUTHORS Clark,A.G., Gnanowski,S., Nielson,R., Thomas,P., Kejarival,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferrieria,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
TITLE Direct Submission

JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
 COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment.
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 /mol_type="genomic DNA"
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 Best Local Similarity 80.4%; Pred.No.1e-45;
 Matches 271; Conservative 0; Mismatches 66; Indels 0; Gaps 0;
 QY 9 AGAAAATCCCATGATAGACTGGTGGCAGAGACCTTGACACTGCTCCACTCATCGAAC 68
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 QY 66 AGAAATTCCTCCACAGTGCATTGGTGAAGAGACCTTGGCAGCTGCTTCTACTCATCGAAC 125
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 QY 69 TTGGCTGATAGCGCATGGGAACCTGTATGATCTCTACTCTCTGAAAAATAAAATCACCAACT 128
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 QY 129 GTGCATTAAAGAACTTTTTCAGGGTATAGACATTTGAAGACCAAACTGCCCCACGGGA 198
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 QY 186 GTGCACTGAAGAAATCTTTTCAGGATATAGGCACACTGGGAGTCAAACTGTGCAAGGGGG 245
 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 QY 189 GCGCTGTGATATAACTATTCCAAAACCTTGTCTTTAATAAAGAACACATAGAGCGCCAAA 248
 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 QY 246 TACTGTGAAAGACTATTCAAAACCTTGTCTTTAATAAAGAAATACATTGACGCGCCAAA 305
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 QY 306 AAAAAGTGTCCGAGAAAGAGACGGAGAGTAAACCAATTCCTAGACTACTCTGCAAGGATT 365
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 QY 309 TCTTGCTGTATAAACACCGAGTGGACACCGGAAAGT 345
 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
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 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
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 DEFINITION AGNCOUNT 14497057 NIH MGC_195 Homo sapiens cDNA clone
 IMAGE:691772 5', mRNA sequence.
 CD559532
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM Homo sapiens (human)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE
 AUTHORS NIH-MGC <http://mgi.nci.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Daniela S. Gerhard, Ph.D.
 Office of Cancer Genomics
 National Cancer Institute / NIH
 Bldg. 31 Rm10A07 Bethesda, MD 20892
 Email: cgabps-remail.nih.gov
 Tissue Procurement: Narayan Bhat
 cDNA Library Preparation: Bhat Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: IRBK1 row: g column: 11
 High quality sequence stop: 456.

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DEFINITION	AGENCOURT 14497029 NIH_MGC_195 Homo sapiens cDNA clone				
ACCESSION	IMAGE:6971771 5', mRNA sequence.				
VERSION	CD559687				
KEYWORDS	EST.				
SOURCE	CD559687.2 GI:38453484				
ORGANISM	Homo sapiens (human)				
REFERENCE	Homo sapiens				
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
TITLE	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
JOURNAL	1 (bases 1 to 470)				
COMMENT	NIH-MGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999) On Jun 10, 2003 this sequence version replaced gi:31585755. Contact: Daniela S. Gerhard, Ph.D. Office of Cancer Genomics National Cancer Institute / NIH Bldg. 31 Rm10A07 Bethesda, MD 20892 Email: cgapbs-r@mail.nih.gov Tissue Procurement: Narayan Bhat CDNA Library Preparation: Bhat Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: IRBK1 row: g column: 10 High quality sequence start: 14 High quality sequence stop: 470. Location/Qualifiers				
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ORIGIN	67.1%; Score 231.4; DB 14; Length 456; Query Match Best Local Similarity 80.4%; Pred. No. 9.9e-46; Matches 271; Conservative 0; Mismatches 66; Indels 0; Gaps 0;				
QY	9	AGAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACTCATCGAAC	68		
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QY	189	GGCTGTGGATAAATATTCCAAAACCTTCTTTTAATAAAGAACACATAGAGCCCAAAA	248		
Db	188	TACTGTGGAAGACTATTCAAAAACCTTCTTCTTAATAAAGAAATACATTGACGCCCAAAA	129		
QY	249	AAAAGGTGTGCAGGGAAGATGGAGATGACAAAGTTCTCTAGACTACCTGCAAGTATT	308		
Db	128	AAAAAGTGTGGAAGAAAGACGGAGATTAACCAATTCCTAGACTACCTGCAAGATT	69		
QY	309	TCTTGGTGTATAAACAACCGAGTGGACACCGGAAGT	345		
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RESULT 4	CD559687/c				

QY 189 GGCTGTGGTAACTATTCCTTTTAAATTAAGAACACATAGAGCGCCAAA 248
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 QY 249 AAAAAGTGTGCAGGAGAAAGATGGAGAGTGACAAAGTTCCTAGACTACCTGCAAGTATT 308
 Db 141 AAAAAGTGTGGAGAGAAAGCGAGAGTAACCAATTCCTAGACTACCTGCAAGATT 82
 QY 309 TCTTGGTGTAAATAACACCGAGTGGACACCGGAAAGT 345
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 RESULT 5
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 DEFINITION AGENCOURT 14496993 NIH MGC 195 Homo sapiens cDNA clone
 IMAGE:6971771 5', mRNA sequence.
 ACCESSION CD559533
 VERSION CD559533.2 GI:38558947
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 NIH-MGC <http://mgi.nci.nih.gov/>.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 On Jun 10, 2003 this sequence version replaced gi:31585601.
 Contact: Daniela S. Gerhard, Ph.D.
 Office of Cancer Genomics
 National Cancer Institute / NIH
 Bldg. 31 Rm10A07 Bethesda, MD 20892
 Email: cgabs-remail.nih.gov
 Tissue Procurement: Narayan Bhat
 cDNA Library Preparation: Bhat Laboratory
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
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 PCR-amplified using gene-specific primers to contain the
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 available from NCBI's RefSeq). Template for PCR is cDNA
 derived from either pooled cytoplasmic polyA RNA from 30
 cells lines or pooled total RNA from 10 different tissues
 (from BD Biosciences/Clontech and Washington University).
 PCR products are directionally cloned into the loxp sites
 of the pDNR-Dual vector. Library constructed by Dr.
 Narayan Bhat, Earl Bere III and Hongling Liao (Gene
 Expression Laboratory, Research Technology Program, SAIC
 Frederick, NCI-Frederick, Frederick, MD 21702). For
 information on which gene each clone represents, please
 visit our anonymous ftp site at
ftp://image.llnl.gov/image/rearrayed_plates/IRBK.prsV.dat
 a Note: this is a NIH_MGC Library."

ORIGIN
 Query Match 65.9%; Score 227.4; DB 29; Length 405;
 Best Local Similarity 79.2%; Fred. No. 9.3e-45;

Query Match 67.1%; Score 231.4; DB 14; Length 492;
 Best Local Similarity 80.4%; Fred. No. 9.9e-46;
 Matches 271; Conservative 0; Mismatches 66; Indels 0; Gaps 0;

 QY 9 AGAAATCCCATGATGACCTGGTGGCAGAGACCTTGACACTGTCTCCCACTCATCGAAC 68
 Db 121 AGAAATCCCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 180
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 QY 249 AAAAAGTGTGCAGGAGAAAGATGAGAGTGACAAAGTTCCTAGACTACCTGCAAGTATT 308
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 Db 421 TCTTGGTGTAAATAACACCGAGTGGATAATAGAAAGT 457

 RESULT 6
 AY412021
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 genomic survey sequence.
 ACCESSION AY412021
 VERSION AY412021.1 GI:39767985
 KEYWORDS GSS.
 SOURCE Pan troglodytes (chimpanzee)
 ORGANISM Pan troglodytes
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
 1 (bases 1 to 405)
 Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,
 Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
 Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
 Adams, M.D. and Cargill, M.
 Inferring nonneutral evolution from human-chimp-mouse orthologous
 gene trios
 Science 302 (5652), 1960-1963 (2003)
 14671302
 2 (bases 1 to 405)
 Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,
 Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
 Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
 Adams, M.D. and Cargill, M.
 Direct Submission
 Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
 Rockville, MD 20850, USA
 This sequence was made by sequencing genomic exons and ordering
 them based on alignment.
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 Best Local Similarity 79.2%; Fred. No. 9.3e-45;


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Matches 267; Conservative 0; Mismatches 70; Indels 0; Gaps 0;
Qy 9 AGAAATCCCATGAATAGACTGGTGGCAGAGACCTTTGACACTGCTCTCCACTCATCGAAC 68
Db 66 AGAAATCCCATGAATAGACTGGTGGCAGAGACCTTTGACACTGCTCTCCACTCATCGAAC 125
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RESULT 7
CD559608
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ACCESSION CD559608
VERSION CD559608.2 GI:38558942
KEYWORDS EST...
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE 1 (bases 1 to 477)
JOURNAL NIH-MGC http://mgc.nci.nih.gov/.
COMMENT National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
On Jun 10, 2003 this sequence version replaced gi:31585756.
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Narayan Bhat
cDNA Library Preparation: Bhat Laboratory
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: IRBK2 row: g column: 10
High quality sequence start: 107
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/notes="vector: pNR-Dual; Site 1: loxP-Sali; Site 2:
loxP-HindIII; Clones from this library have been
PCR-amplified using gene-specific primers to contain the
complete open reading frame (based on known gene sequences
available from NCBI's RefSeq). Template for PCR is cDNA
```

```
derived from either pooled cytoplasmic polyA RNA from 30
cells lines or pooled total RNA from 10 different tissues
(from BD Biosciences/Clontech and Washington University).
PCR products are directionally cloned into the loxP sites
of the pDNR-Dual vector. Library constructed by Dr.
Narayan Bhat, Earl Bere III and Hongling Liao (Gene
Expression Laboratory, Research Technology Program, SAIC
Frederick, NCI-Frederick, Frederick, MD 21702). For
information on which gene each clone represents, please
visit our anonymous ftp site at
ftp://image.llnl.gov/image/rearrayed_plates/IRBK.presv.dat
a Note: this is a NIH_MGC Library."

ORIGIN
Query Match 64.5%; Score 222.4; DB 14; Length 477;
Best Local Similarity 78.9%; Pred. No. 1.5e-43;
Matches 265; Conservative 0; Mismatches 71; Indels 0; Gaps 0;
Qy 10 GAAATCCCATGAATAGACTGGTGGCAGAGACCTTTGACACTGCTCTCCACTCATCGAAC 69
Db 107 GAATTCCTCCCAAGTGCATTGGTGAAGAGACCTTTGGCAGTCTCTTCTACTCGTCAACT 166
Qy 70 TGGCTGATAGGCGATGGGAACCTGATGATCTCTACTCTCTGAAAATAAAAAATCACCAACTG 129
Db 167 CTGCTGATAGCAATGAGACTCTGAGGATTCCTGTTCTGTATACATAAAAAATCACCAACTG 226
Qy 130 TGCATTAAAGAAAGTTTTCAGGGTATAGACATTTGAAGAACCAAACTGCCACCGGGAG 189
Db 227 TGCATCTGAAGAAATCTTTTCAGGGAAATGACACCTGGAGAGTCAAACTGTGCAAGGGGT 286
Qy 190 GGTGTGGGATAAATCTATTCAAAACCTGTCTTTAAATAAAGAACACATAGAGCGCCAAA 249
Db 287 ACTGTGGAAAGACTATTCAAAAACCTGTCTTTAAATAAAGAAATACATTGACGGGCCAAA 346
Qy 250 AAAAGGTGTCAGGAGAAAGATGGAGAGTGACAAAGTTCTCTAGACTACTCTGCAAGTATT 309
Db 347 AAAAAGCGTGTAGAAAGAAAGACGGAGAGTAAACCAATTCCTTAAACTCTGCAAGAGTT 406
Qy 310 CTTGTGTGTAATAAACACCGAGTGGACACCGGAAAGT 345
Db 407 CTTGTGTGTAATAAACACCGAGTGGATATATATAAGT 442

CD559688 467 bp mRNA linear EST 19-NOV-2003
AGENCOURT 14496964 NIH_MGC 195 Homo sapiens cDNA clone
IMAGE:6971770 5', mRNA sequence.
CD559688
VERSION CD559688.2 GI:38453486
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE 1 (bases 1 to 467)
JOURNAL NIH-MGC http://mgc.nci.nih.gov/.
COMMENT National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
On Jun 10, 2003 this sequence version replaced gi:31585756.
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Narayan Bhat
cDNA Library Preparation: Bhat Laboratory
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: IRBK1 row: g column: 09
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High quality sequence start: 11
High quality sequence stop: 467.
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/clone="IMAGE:6971770"
/tissue_type="mixed"
/lab_host="DH5A (T1 phage-resistant)"
/clone_lib="NIH_MGC_195"
/note="vector: pDNR-Dual; Site 1: loxp-Sall; Site 2: loxp-HindIII; Clones from this library have been PCR-amplified using gene-specific primers to contain the complete open reading frame (based on known gene sequences available from NCBI's RefSeq). Template for PCR is cDNA derived from either pooled cytoplasmic polyA RNA from 30 cells lines or pooled total RNA from 10 different tissues (from BD Biosciences/Clontech and Washington University). PCR products are directionally cloned into the loxp sites of the pDNR-Dual vector. Library constructed by Dr. Narayan Bhat, Earl Bere III and Hongling Liao (Gene Expression Laboratory, Research Technology Program, SAIC Frederick, NCI-Frederick, Frederick, MD 21702). For information on which gene each clone represents, please visit our anonymous ftp site at
ftp://image.llnl.gov/image/rearranged_plates/IRBK.presv.dat
a Note: this is a NIH_MGC Library."

ORIGIN

Query Match 64.1%; Score 221; DB 14; Length 467;
Best Local Similarity 80.4%; Pred. No. 3.3e-43;
Matches 271; Conservative 0; Mismatches 65; Indels 1; Gaps 1;

QY 9 AGAAATCCCATGATGATGTTGGCAGAGACCTTGACACTCTCTCCACTCATCGAAC 68
DB 378 AGAAATCCCATGATGATGTTGGCAGAGACCTTGACACTCTCTCCACTCATCGAAC 319

QY 69 TTGGCTGATAGCGGATGGAACCTGATGATTCCTGTAATTAATAAGAACATCACTCACT 128
DB 318 TCTGCTGATAGCGGATGGAACCTGATGATTCCTGTAATTAATAAGAACATCACTCACT 259

QY 129 GTGCATTAAAGAGAGTTTTCAGGGTATAGACACATTCGAGAACCAACTGCCCGGGA 188
DB 258 GTGCATTAAAGAGAGTTTTCAGGGTATAGACACATTCGAGAACCAACTGCCCGGGA 199

QY 189 GGCTGTGGATAAATACTATTCAAAACCTGCTTTTAATAAAGAACATAGAGCGCCAAA 248
DB 198 TACTGTGGAAGACTATTCAAAACCTGCTTTTAATAAAGAACATAGAGCGCCAAA 139

QY 249 AAAAAGGTGTGCAGGAGAAAGATGGAGAGTGACAAAGTTCCTAGACTACTGCAAGTATT 308
DB 138 AAAA-GTGTGGAGAGAAAGATGGAGAGTGACAAAGTTCCTAGACTACTGCAAGTATT 80

QY 309 TCTTGGTGTAAATAACACCGAGTGGACCCGGAAGT 345
DB 79 TCTTGGTGTAAATAACACCGAGTGGATTAATAGAAAGT 43

RESULT 9
CD559534
LOCUS
DEFINITION
AGENCOURT_14496928 NIH_MGC_195 Homo sapiens cDNA clone
IMAGE:6971770 5', mRNA sequence.
CD559534
CD559534-2 GI:38558949
EST.
KEYWORDS
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 478)
AUTHORS
NTH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
On Jun 10, 2003 this sequence version replaced gi:31585602.
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Narayan Bhat
cDNA Library Preparation: Bhat Laboratory
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: IRBK1 row: g column: 09
High quality sequence start: 3
High quality sequence stop: 478.
Location/Qualifiers
1. 478
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6971770"
/tissue_type="mixed"
/lab_host="DH5A (T1 phage-resistant)"
/clone_lib="NIH_MGC_195"
/note="vector: pDNR-Dual; Site 1: loxp-Sall; Site 2: loxp-HindIII; Clones from this library have been PCR-amplified using gene-specific primers to contain the complete open reading frame (based on known gene sequences available from NCBI's RefSeq). Template for PCR is cDNA derived from either pooled cytoplasmic polyA RNA from 30 cells lines or pooled total RNA from 10 different tissues (from BD Biosciences/Clontech and Washington University). PCR products are directionally cloned into the loxp sites of the pDNR-Dual vector. Library constructed by Dr. Narayan Bhat, Earl Bere III and Hongling Liao (Gene Expression Laboratory, Research Technology Program, SAIC Frederick, NCI-Frederick, Frederick, MD 21702). For information on which gene each clone represents, please visit our anonymous ftp site at
ftp://image.llnl.gov/image/rearranged_plates/IRBK.presv.dat
a Note: this is a NIH_MGC Library."

ORIGIN

Query Match 64.1%; Score 221; DB 14; Length 478;
Best Local Similarity 80.4%; Pred. No. 3.3e-43;
Matches 271; Conservative 0; Mismatches 65; Indels 1; Gaps 1;

QY 9 AGAAATCCCATGATGATGTTGGCAGAGACCTTGACACTCTCTCCACTCATCGAAC 68
DB 110 AGAAATCCCATGATGATGTTGGCAGAGACCTTGACACTCTCTCCACTCATCGAAC 169

QY 69 TTGGCTGATAGCGGATGGAACCTGATGATTCCTGTAATTAATAAGAACATCACTCACT 128
DB 170 TCTGCTGATAGCGGATGGAACCTGATGATTCCTGTAATTAATAAGAACATCACTCACT 229

QY 129 GTGCATTAAAGAGAGTTTTCAGGGTATAGACACATTCGAGAACCAACTGCCCGGGA 188
DB 230 GTGCATTAAAGAGAGTTTTCAGGGTATAGACACATTCGAGAACCAACTGCCCGGGA 289

QY 189 GGCTGTGGATAAATACTATTCAAAACCTGCTTTTAATAAAGAACATAGAGCGCCAAA 248
DB 290 TACTGTGGAAGACTATTCAAAACCTGCTTTTAATAAAGAACATAGAGCGCCAAA 349

QY 249 AAAAAGGTGTGCAGGAGAAAGATGGAGAGTGACAAAGTTCCTAGACTACTGCAAGTATT 308
DB 350 AAAA-GTGTGGAGAGAAAGATGGAGAGTGACAAAGTTCCTAGACTACTGCAAGTATT 408

QY 309 TCTTGGTGTAAATAACACCGAGTGGACCCGGAAGT 345
DB 409 TCTTGGTGTAAATAACACCGAGTGGATTAATAGAAAGT 445

TITLE
JOURNAL
COMMENT

FEATURES
source

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RESULT 10
CD559535
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
On Jun 10, 2003 this sequence version replaced gi:31595603.
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-remail.nih.gov
Tissue Procurement: Narayan Bhat
cDNA Library Preparation: Bhat Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: IRBK1 row: g column: 08
High quality sequence stop: 463.
Location/Qualifiers
1. 463
/organism="Homo sapiens"
/mol_type="mRNA"
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/lab_host="DH5A (T1 phage-resistant)"
/clone_lib="NIH MGC 195"
/notes="Vector: pDNR-Dual; Site 1: loxP-Salt; Site 2:
loxP-HindIII; Clones from this library have been
PCR-amplified using gene-specific primers to contain the
complete open reading frame (based on known gene sequences
available from NCBI's RefSeq). Template for PCR is cDNA
derived from either pooled cytoplasmic polyA RNA from 30
cells lines or pooled total RNA from 10 different tissues
(from BD Biosciences/Clontech and Washington University).
PCR products are directionally cloned into the loxP sites
of the pDNR-Dual vector. Library constructed by Dr.
Narayan Bhat, Earl Bere III and Hongling Liao (Gene
Expression Laboratory, Research Technology Program, SAIC
Frederick, NCI-Frederick, Frederick, MD 21702). For
information on which gene each clone represents, please
visit our anonymous ftp site at
http://image.llnl.gov/image/rearrayed_plates/IRBK.presv.dat
a Note: this is a NIH MGC Library."

ORIGIN
Query Match 63.9%; Score 220.4; DB 14; Length 463;
Best local Similarity 80.2%; Pred No. 4.6e-43;
Matches 271; Conservative 0; Mismatches 66; Indels 1; Gaps 1;

QY 9 AGAAATCCCATGAATAGACGTGGTGGCAGACCTTGACACTGCTTCATCATCGAAC 68
Db 93 AGAAATCCCATGAATAGACGTGGTGGCAGACCTTGACACTGCTTCATCATCGAAC 152
QY 69 TTGGCTGATAGCGGACCTGATGATCTTCTACTCTCTGAATAAATACCAACT 128
Db 153 TCTGCTGATAGCAATGAGACTCTGAGGATTCCTGTTCTGTACATAAATACCAACT 212

RESULT 11
CD559689/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
On Jun 10, 2003 this sequence version replaced gi:31595757.
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-remail.nih.gov
Tissue Procurement: Narayan Bhat
cDNA Library Preparation: Bhat Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: IRBK1 row: g column: 08
High quality sequence stop: 473.
Location/Qualifiers
1. 473
/organism="Homo sapiens"
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/clone="IMAGE:6971769"
/tissue_type="mixed"
/lab_host="DH5A (T1 phage-resistant)"
/clone_lib="NIH MGC 195"
/notes="Vector: pDNR-Dual; Site 1: loxP-Salt; Site 2:
loxP-HindIII; Clones from this library have been
PCR-amplified using gene-specific primers to contain the
complete open reading frame (based on known gene sequences
available from NCBI's RefSeq). Template for PCR is cDNA
derived from either pooled cytoplasmic polyA RNA from 30
cells lines or pooled total RNA from 10 different tissues
(from BD Biosciences/Clontech and Washington University).
PCR products are directionally cloned into the loxP sites
of the pDNR-Dual vector. Library constructed by Dr.
Narayan Bhat, Earl Bere III and Hongling Liao (Gene
Expression Laboratory, Research Technology Program, SAIC
Frederick, NCI-Frederick, Frederick, MD 21702). For
information on which gene each clone represents, please
visit our anonymous ftp site at
http://image.llnl.gov/image/rearrayed_plates/IRBK.presv.dat
a Note: this is a NIH MGC Library."

ORIGIN
Query Match 63.9%; Score 220.4; DB 14; Length 463;
Best local Similarity 80.2%; Pred No. 4.6e-43;
Matches 271; Conservative 0; Mismatches 66; Indels 1; Gaps 1;

QY 9 AGAAATCCCATGAATAGACGTGGTGGCAGACCTTGACACTGCTTCATCATCGAAC 68
Db 93 AGAAATCCCATGAATAGACGTGGTGGCAGACCTTGACACTGCTTCATCATCGAAC 152
QY 69 TTGGCTGATAGCGGACCTGATGATCTTCTACTCTCTGAATAAATACCAACT 128
Db 153 TCTGCTGATAGCAATGAGACTCTGAGGATTCCTGTTCTGTACATAAATACCAACT 212
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ftp://image.llnl.gov/image/rearrayed_plates/IRBK.presv.dat
a Note: this is a NIH_MGC Library."

ORIGIN

Query Match 63.9%; Score 220.4; DB 14; Length 473;
Best Local Similarity 80.2%; Pred. No. 4.5e-43;
Matches 271; Conservative 0; Mismatches 66; Indels 1; Gaps 1;

QY 9 AGAAATCCCATGATGCTGGGAGACCTTGACACTGCTCTCCACTCATCGAAC 68
DB 384 AGAAATCCCATGATGCTGGGAGACCTTGACACTGCTCTCCACTCATCGAAC 325

QY 69 TTGGCTGATAGCGGATGGAACCTTGATGATCTCTCTGAAATATAAATACCAACT 128
DB 324 TCTGCTGATAGCCATGAGACTCTGAGGATCTCTGCTGTACATATAAATACCAACT 265

QY 129 GTGCATTAAGAAGTTTTTCAGGGTATAGACATTAAGAGAACCAACTGCCACGGGA 188
DB 264 GTGCATTAAGAAGTTTTTCAGGGTATAGACATTAAGAGAACCAACTGCCACGGGG 205

QY 189 GGCTGTGATTAACCTATTCCAAACTTGTCTTTAATAAAGACACATAGAGGCC-AAA 247
DB 204 TACTGTGGAAGACTATTCAAAACTTGTCTTTAATAAAGAAATACATTGACGGCCAAA 145

QY 248 AAAAAAGGTGTGAGGAGAAAGATGGAGAGTGACAAAGTTCTCTAGACTTACCTGCAAGTAT 307
DB 144 AAAAAAGGTGTGAGGAGAAAGATGGAGAGTAAACCAATCTCTAGACTTACCTGCAAGT 85

QY 308 TCTCTGGTGTATTAACACCGAGTGGACCGGAAAGT 345
DB 84 TCTCTGGTGTATTAACACCGAGTGGATAATAGAAAGT 47

RESULT 12

CD559536 489 bp mRNA linear EST 26-NOV-2003
LOCUS
DEFINITION AGENCOURT_14496804 NIH MGC 195 Homo sapiens cDNA clone
IMAGE:6971768 5', mRNA sequence.
ACCESSION CD559536
VERSION CD559536.2 GI:38558953
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE NIH-MGC http://mgi.nci.nih.gov/
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999)
On Jun 10, 2003 this sequence version replaced gi:31585604.
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgabs-r@mail.nih.gov
Tissue Procurement: Narayan Bhat
CDNA Library Preparation: Bhat Laboratory
DNA sequencing by: The I.M.A.G.E. Consortium (LLNL)
Clone distribution: Agencourt Bioscience Corporation
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: 138X1 row: 9 column: 07
High quality sequence start: 17
High quality sequence stop: 489.
Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"
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/tissue_type="mixed"
/lab_host="DH5A (T1 phage-resistant)"

FEATURES

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/db_xref="taxon:9606"
/clone="IMAGE:6971768"
/tissue_type="mixed"
/lab_host="DH5A (T1 phage-resistant)"

/clone lib="NIH_MGC 195"
/note="Vector: pDNR-Dual; Site 1: loxP-Sali; Site 2: loxP-HindIII; Clones from this library have been PCR-amplified using gene-specific primers to contain the complete open reading frame (based on known gene sequences available from NCI's RefSeq). Template for PCR is cDNA derived from either pooled cytoplasmic polyA RNA from 30 cells lines or pooled total RNA from 10 different tissues (from BD Biosciences/Clontech and Washington University). PCR products are directionally cloned into the loxP sites of the pDNR-Dual vector. Library constructed by Dr. Narayan Bhat, Earl Bere III and Hongling Liao (Gene Expression Laboratory, Research Technology Program, SAIC Frederick, NCI-Frederick, Frederick, MD 21702). For information on which gene each clone represents, please visit our anonymous ftp site at
ftp://image.llnl.gov/image/rearrayed_plates/IRBK.presv.dat
a Note: this is a NIH_MGC Library."

ORIGIN

Query Match 63.9%; Score 220.4; DB 14; Length 489;
Best Local Similarity 80.2%; Pred. No. 4.5e-43;
Matches 271; Conservative 0; Mismatches 66; Indels 1; Gaps 1;

QY 9 AGAAATCCCATGATGCTGGGAGACCTTGACACTGCTCTCCACTCATCGAAC 68
DB 119 AGAAATCCCATGATGCTGGGAGACCTTGACACTGCTCTCCACTCATCGAAC 178

QY 69 TTGGCTGATAGCGGATGGAACCTTGATGATCTCTCTGAAATATAAATACCAACT 128
DB 179 TCTGCTGATAGCCATGAGACTCTGAGGATCTCTCTGTACATAAATACCAACT 238

QY 129 GTGCATTAAGAAGTTTTTCAGGGTATAGACACATTAAGAGAACCAACTGCCACGGGA 188
DB 239 GTGCATTAAGAAGTTTTTCAGGGTATAGACACATTAAGAGAACCAACTGCCACGGGG 298

QY 189 GGCTGTGATTAACCTATTCCAAACTTGTCTTTAATAAAGAAATACATAGAGGCC-AAA 247
DB 299 TACTGTGGAAGACTATTCAAAACTTGTCTTTAATAAAGAAATACATAGAGGCCAAA 358

QY 248 AAAAAAGGTGTGAGGAGAAAGATGGAGAGTGACAAAGTTCTCTAGACTTACCTGCAAGTAT 307
DB 359 AAAAAAGGTGTGAGGAGAAAGATGGAGAGTAAACCAATCTCTAGACTTACCTGCAAGT 418

QY 308 TCTCTGGTGTATTAACACCGAGTGGACCGGAAAGT 345
DB 419 TCTCTGGTGTATTAACACCGAGTGGATAATAGAAAGT 456

RESULT 13

CD559690 467 bp mRNA linear EST 19-NOV-2003
LOCUS
DEFINITION AGENCOURT_14496838 NIH MGC 195 Homo sapiens cDNA clone
IMAGE:6971768 5', mRNA sequence.
ACCESSION CD559690
VERSION CD559690.2 GI:38453490
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE NIH-MGC http://mgi.nci.nih.gov/
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999)
On Jun 10, 2003 this sequence version replaced gi:31585758.
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgabs-r@mail.nih.gov
Tissue Procurement: Narayan Bhat
CDNA Library Preparation: Bhat Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: IRBKI row: g column: 07
 High quality sequence stop: 467.
 Location/Qualifiers
 1. 467
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:6971768"
 /tissue_type="mixed"
 /lab_host="DH5A (TI phase-resistant)"
 /clone_lib="NIH_MGC_195"
 /notes="vector: pDNR-Dual; Site 1: loxp-Sall; Site 2:
 loxp-RindIII; Clones from this library have been
 PCR-amplified using gene-specific primers to contain the
 complete open reading frame (based on known gene sequences
 available from NCBI's RefSeq). Template for PCR is cDNA
 derived from either pooled cytoplasmic polyA RNA from 30
 cells lines or pooled total RNA from 10 different tissues
 (from BD Biosciences/Clontech and Washington University).
 PCR products are directionally cloned into the loxp sites
 of the pDNR-Dual vector. Library constructed by Dr.
 Narayan Bhat, Earl Bere III and Hongling Liao (Gene
 Expression Laboratory, Research Technology Program, SAIC
 Frederick, NCI-Frederick, Frederick, MD 21702). For
 information on which gene each clone represents, please
 visit our anonymous ftp site at
ftp://image.llnl.gov/image/rearranged_plates/IRBK.presv.dat
 a Note: this is a NIH_MGC Library."

ORIGIN
 Query Match 63.4%; Score 218.8; DB 14; Length 467;
 Best Local Similarity 79.9%; Pred. No. 1.1e-42;
 Matches 270; Conservative 0; Mismatches 67; Indels 1; Gaps 1;
 QY 9 AGAAATCCCATGATGACCTGGGAGAGACCTTGACACTGCTCCACTCATCGAAC 68
 DB 378 AGAAATCCCATGATGACCTGGGAGAGACCTTGACACTGCTCCACTCATCGAAC 319
 QY 69 TTGGCTGATAGCGGATGGAACTGATGATTCCTACTCTCTGAAATATAAATACCAACT 128
 DB 318 TCTGCTGATAGCAATGAGACTTTGAGGATTCCTGCTGTACATATAAATACCAACT 259
 QY 129 GTGCATTAAGAAGTTTTCAGGGTATAGACACTTGAGAACCAAACTGCCCGGGA 188
 DB 258 GTGCATTAAGAAGTTTTCAGGGTATAGACACTTGAGAACCAAACTGCCCGGGA 199
 QY 189 GGCTGTGATTAACCTATTCCTGCTCTTTAATAAAGAACACATAGACGCC-AAA 247
 DB 138 TACTGTGAAGACTATTCAAAACTTGTCTTAAAGAAATACATTGACGCCCAA 139
 QY 248 AAAAAAGGTGTCAGGAGAAAGATGAGAGTGACAAAGTTCTTAGACTACTGCAAGTAT 307
 DB 138 AAAAAAGGTGTCAGGAGAAAGATGAGAGTGACAAAGTTCTTAGACTACTGCAAGT 79
 QY 308 TTCTTGGTGTATTAACACCGAGTGGACACCGGAAAGT 345
 DB 78 TTCTTGGTGTATTAACACCGAGTGGACACCGGAAAGT 41

RESULT 14
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 Mus musculus IL5 gene, VIRTUAL TRANSCRIPT, partial sequence,
 genomic survey sequence.
 ACCESSION
 AY412022
 VERSION
 AY412022.1 GI:39767987
 KEYWORDS
 GSS.
 SOURCE
 Mus musculus (house mouse)

ORGANISM
 Mus musculus
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 1 (bases 1 to 399)
 Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,
 Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
 Ferrera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
 Adams, M.D. and Cargill, M.
 Inferring nonneutral evolution from human-chimp-mouse orthologous
 gene trios
 Science 302 (5652), 1960-1963 (2003)
 14671302
 2 (bases 1 to 399)
 Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,
 Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
 Ferrera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
 Adams, M.D. and Cargill, M.
 Direct Submission
 Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
 Rockville, MD 20850, USA
 This sequence was made by sequencing genomic exons and ordering
 them based on alignment.
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 DB 114 CGGAGCTCTGTTGCAAGCAATGAGNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 173
 QY 123 CCAACTGTGCTAATAAGAGTTTTCAGGGTATAGACACTTGAGAACCAAACTGCCCA 182
 DB 174 CCACTGATGATGGAGAAATCTTTCAGGGGTAGACACTTGAGAAATCAAACTGTCG 233
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 LOCUS
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 genomic survey sequence.
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 CE331159
 VERSION
 CE331159.1 GI:36147469
 KEYWORDS
 GSS.
 SOURCE
 Canis familiaris (dog)
 ORGANISM
 Canis familiaris
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.

REFERENCE 1 (bases 1 to 622)
 AUTHORS Kirkness, E.F., Bafna, V., Halpern, A.L., Levy, S., Remington, K.,
 Rusch, D.B., Delcher, A.L., Pop, M., Wang, W., Fraser, C.M. and
 Venter, J.C.
 TITLE The dog genome: survey sequencing and comparative analysis
 JOURNAL Science 301 (5641), 1998-1903 (2003)
 MEDLINE 22875432
 PUBMED 14512627
 COMMENT Contact: Kirkness EF
 The Institute for Genomic Research
 Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
 Rockville, MD 20850, USA
 Tel: 301-838-0200
 Fax: 301-838-0208
 Email: ekirknes@tigr.org
 Class: shotgun.
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ORIGIN

Query Match 38.2%; Score 131.8; DB 29; Length 622;
 Best Local Similarity 95.1%; Pred. NO. 1.2e-21;
 Matches 136; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
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 95 AACTGCCCCACGGGAGGCTGTGGATAAATATTCCTCAAACTTGTCTTTTAAAGAACCA 154
 QY 234 CATAGAGCGCCAAAAAAGGT 256
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Search completed: August 31, 2004, 13:00:14
 Job time : 1160.04 secs

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Sequence 82, Appl
Sequence 80, Appl
Sequence 82, Appl
Sequence 21, Appl
Sequence 90, Appl
Sequence 8, Appl
Sequence 10, Appl
Sequence 12, Appl
Sequence 14, Appl
Sequence 1236, Ap
Sequence 18, Appl
Sequence 19, Appl
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Sequence 78, Appl
Sequence 2631, Ap
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Sequence 11360, A
Sequence 1018, Ap
Sequence 1030, Ap
Sequence 41750, A
Sequence 136, App
Sequence 27005, A
Sequence 498, App
Sequence 3699, Ap
Sequence 69757, A
Sequence 1168, Ap
Sequence 39049, A
Sequence 60859, A

US-10-218-654-80
US-10-218-654-82
US-10-262-439-80
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US-10-295-074-8
US-10-295-074-10
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US-10-295-074-14
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US-10-424-599-37005
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US-10-437-963-69757
US-10-087-192-1168
US-10-027-632-39049
US-10-027-632-60859

ALIGNMENTS

RESULT 1

US-09-755-633-9
; Sequence 9, Application US/09755633
; Patent No. US20020127200A1
; GENERAL INFORMATION:
; APPLICANT: Yang, Shumin
; APPLICANT: McCall, Catherine A.
; APPLICANT: Weber, Eric R.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF
; FILE REFERENCE: IM-2-C1-C1
; CURRENT APPLICATION NUMBER: US/09/755,633
; PRIOR FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: 09/322,409
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/087,306
; PRIOR FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 9
; LENGTH: 345
; TYPE: DNA
; ORGANISM: Canis familiaris
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(345)
US-09-755-633-9

Query Match 100.0%; Score 345; DB 9; Length 345;
Best Local Similarity 100.0%; Pred. No. 1e-95; 0; Indels 0; Gaps 0;
Matches 345; Conservative 0; Mismatches 0;

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Qy 61 CATCGACTGGCTGATAGCGGATGGAACTGATGCTCTACTCTGAAATAAAAT 120

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

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Run on: August 31, 2004, 01:25:57 ; Search time 204.139 Seconds
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Title: US-10-787-382-9
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Maximum Match 100%

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	345	100.0	345	9	US-09-755-633-11	Sequence 11, Appl
3	345	100.0	345	15	US-10-218-654-85	Sequence 85, Appl
4	345	100.0	345	15	US-10-218-654-87	Sequence 87, Appl
5	345	100.0	345	15	US-10-262-439-85	Sequence 85, Appl
6	345	100.0	345	15	US-10-262-439-87	Sequence 87, Appl
7	345	100.0	402	9	US-09-755-633-7	Sequence 7, Appli
8	345	100.0	402	9	US-09-755-633-8	Sequence 8, Appli
9	345	100.0	402	15	US-10-218-654-83	Sequence 83, Appl
10	345	100.0	402	15	US-10-218-654-84	Sequence 84, Appl
11	345	100.0	402	15	US-10-262-439-83	Sequence 83, Appl
12	345	100.0	402	15	US-10-262-439-84	Sequence 84, Appl
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RESULT 2

US-09-755-633-11/c
; Sequence 11, Application US/09755633
; Patent No. US2002012700A1
; GENERAL INFORMATION:
; APPLICANT: Yang, Shumin
; APPLICANT: McCall, Catherine A.
; APPLICANT: Weber, Eric R.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; FILE REFERENCE: IM-2-C1-C1
; CURRENT APPLICATION NUMBER: US/09/755,633
; PRIOR FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: 09/322,409
; PRIOR FILING DATE: 1999-05-28
; PRIOR FILING DATE: 60/087,306
; PRIOR FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 345
; TYPE: DNA
; ORGANISM: Canis familiaris
US-09-755-633-11

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Best Local Similarity 100.0%; Pred. No. 1e-95;
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 61 CATCGAACTTGGCTGATAGGCGATGGAACTGATGATTCCTCTGAAAAATAAAAAAT 120
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QY 121 CACCAACTGTGCTATTAAGAAAGTTTTCAGGGTATAGACACATTGAAGAACCAAACTGCC 180
225 CACCAACTGTGCTATTAAGAAAGTTTTCAGGGTATAGACACATTGAAGAACCAAACTGCC 166
QY 181 CACGGGGAGGCTGGGATTAACACTATTCAAAACCTTGCTTTAATAAAGAACACATAGAG 240
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RESULT 3

US-10-218-654-85
; Sequence 85, Application US/10218654
; Publication No. US20030099609A1
; GENERAL INFORMATION:
; APPLICANT: Sim, Gek-Kee
; APPLICANT: Yang, Shumin
; APPLICANT: Dreitz, Matthew J.
; APPLICANT: Wonderling, Ramani S.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; FILE REFERENCE: IM-2-C1
; CURRENT APPLICATION NUMBER: US/10/218,654
; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: US/09/322,409
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/087,306
; PRIOR FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 154
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 85
; LENGTH: 345
; TYPE: DNA
; ORGANISM: Canis familiaris
; NAME/KEY: CDS
; LOCATION: (1)..(345)
US-10-218-654-85

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Best Local Similarity 100.0%; Pred. No. 1e-95;
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 241 CGCCAAAAAAAAGGTGTGAGGAGAAAGATGGAGAGTGACAAAAGTTCCCTAGACTACCTG 300
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RESULT 4

US-10-218-654-87/c
; Sequence 87, Application US/10218654
; Publication No. US20030099609A1
; GENERAL INFORMATION:
; APPLICANT: Sim, Gek-Kee
; APPLICANT: Yang, Shumin
; APPLICANT: Dreitz, Matthew J.
; APPLICANT: Wonderling, Ramani S.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; FILE REFERENCE: IM-2-C1
; CURRENT APPLICATION NUMBER: US/10/218,654
; CURRENT FILING DATE: 2002-08-13

Best Local Similarity 100.0%; Pred. No. 1e-95;
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 TTGCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACT 60

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QY 181 CACGGGAGGCTGGGATAAACTATTCAAAACCTGCTCTTAAATAAAGAACACATAGAG 240
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QY 241 CGCCAAAAAAGAGTGTGCGAGGAAAGATGGAGAGTGACAAAAGTTCTTAGACTACCTG 300
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DB 301 CAAGTATTTCTTGGTGTAAATAAACCCGAGTGGACACCGGAAAGT 345

RESULT 5
US-10-262-439-87/c
; Sequence 87, Application US/10262439
; Publication No. US20030143196A1
; GENERAL INFORMATION:
; APPLICANT: Sim, Gek-Kee
; APPLICANT: Yang, Shumin
; APPLICANT: Dreitz, Matthew J.
; APPLICANT: Wonderling, Ramani S.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF
; FILE REFERENCE: IM-2-C2
; CURRENT APPLICATION NUMBER: US/10/262,439
; CURRENT FILING DATE: 2002-09-30
; PRIOR APPLICATION NUMBER: US/09/451,527
; PRIOR FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: 09/322,409
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/087,306
; PRIOR FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 87
; TYPE: DNA
; ORGANISM: Canis familiaris
US-10-262-439-87

Query Match 100.0%; Score 345; DB 15; Length 345;
Best Local Similarity 100.0%; Pred. No. 1e-95;
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 121 CACCAACTGTGCATTAAAGAAAGTTTTCAGGGTATAGACACATTGAAGAACCAAACTGCC 180
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QY 181 CACGGGAGGCTGGGATAAACTATTCAAAACCTGCTCTTAAATAAAGAACACATAGAG 240

PRIOR APPLICATION NUMBER: US/09/322,409
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/087,306
; PRIOR FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 154
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 87
; LENGTH: 345
; TYPE: DNA
; ORGANISM: Canis familiaris
US-10-218-654-87

Query Match 100.0%; Score 345; DB 15; Length 345;
Best Local Similarity 100.0%; Pred. No. 1e-95;
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACT 60
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DB 285 CATCGAACTTGGCTGATAGGCGATGGGAACCTGATGATTCTCTCTGAAAAATAAAAT 226

QY 121 CACCAACTGTGCATTAAAGAAAGTTTTCAGGGTATAGACACATTGAAGAACCAAACTGCC 180
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QY 181 CACGGGAGGCTGGGATAAACTATTCAAAACCTGCTCTTAAATAAAGAACACATAGAG 240
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QY 241 CGCCAAAAAAGAGTGTGCGAGGAAAGATGGAGAGTGACAAAAGTTCTTAGACTACCTG 300
DB 105 CGCCAAAAAAGAGTGTGCGAGGAAAGATGGAGAGTGACAAAAGTTCTTAGACTACCTG 46

QY 301 CAAGTATTTCTTGGTGTAAATAAACCCGAGTGGACACCGGAAAGT 345
DB 45 CAAGTATTTCTTGGTGTAAATAAACCCGAGTGGACACCGGAAAGT 1

RESULT 5
US-10-262-439-85
; Sequence 85, Application US/10262439
; Publication No. US20030143196A1
; GENERAL INFORMATION:
; APPLICANT: Sim, Gek-Kee
; APPLICANT: Yang, Shumin
; APPLICANT: Dreitz, Matthew J.
; APPLICANT: Wonderling, Ramani S.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF
; FILE REFERENCE: IM-2-C2
; CURRENT APPLICATION NUMBER: US/10/262,439
; CURRENT FILING DATE: 2002-09-30
; PRIOR APPLICATION NUMBER: US/09/451,527
; PRIOR FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: 09/322,409
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/087,306
; PRIOR FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 85
; LENGTH: 345
; TYPE: DNA
; ORGANISM: Canis familiaris
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(345)
US-10-262-439-85

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RESULT 7

US-09-755-633-7

; Sequence 7, Application US/09755633

; Patent No. US20020127200A1

; GENERAL INFORMATION:

; APPLICANT: Yang, Shumin

; APPLICANT: McCall, Catherine A.

; APPLICANT: Weber, Eric R.

; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC

; FILE REFERENCE: IM-2-C1-C1

; CURRENT APPLICATION NUMBER: US/09755,633

; PRIOR FILING DATE: 2001-01-05

; PRIOR APPLICATION NUMBER: 09/322,409

; PRIOR FILING DATE: 1999-05-28

; PRIOR APPLICATION NUMBER: 60/087,306

; PRIOR FILING DATE: 1998-05-29

; NUMBER OF SEQ ID NOS: 21

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 7

; LENGTH: 402

; TYPE: DNA

; ORGANISM: Canis familiaris

US-09-755-633-7

Query Match 100.0%; Score 345; DB 9; Length 402;

Best Local Similarity 100.0%; Pred. No. 1.1e-95;

Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTTCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACT 60
Db 58 TTTCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACT 117
Qy 61 CATCGAACTTGGCTGTAGGGATGGGAACCTGATGATTCCTACTCTCTGAAAATAAAAAT 120
Db 118 CATCGAACTTGGCTGTAGGGATGGGAACCTGATGATTCCTACTCTCTGAAAATAAAAAT 177
Qy 121 CACCAACTGTGCATTAAGAAGTTTTTCAGGGTATAGACATTTGAAGAACCAACTGCC 180
Db 178 CACCAACTGTGCATTAAGAAGTTTTTCAGGGTATAGACATTTGAAGAACCAACTGCC 237
Qy 181 CACGGGAGGCTGTGGATAAATATTCCTCAAACTTGTCTTTAATAAAGAACACATAGAG 240
Db 238 CACGGGAGGCTGTGGATAAATATTCCTCAAACTTGTCTTTAATAAAGAACACATAGAG 297
Qy 241 CGCCAAAAAAGTGTGAGGAGAAAGATGGAGAGTGACAAAGTTCCTAGACTACTG 300
Db 298 CGCCAAAAAAGTGTGAGGAGAAAGATGGAGAGTGACAAAGTTCCTAGACTACTG 357
Qy 301 CAAATATTCTTCTGGTGTATTAACACCGAGTGGACACCGGAAAGT 345
Db 358 CAAATATTCTTCTGGTGTATTAACACCGAGTGGACACCGGAAAGT 402

RESULT 8

US-09-755-633-8/c

; Sequence 8, Application US/09755633

; Patent No. US20020127200A1

; GENERAL INFORMATION:

; APPLICANT: Yang, Shumin

; APPLICANT: Weber, Eric R.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; FILE REFERENCE: IM-2-C1-C1
; CURRENT APPLICATION NUMBER: US/09755,633
; CURRENT FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: 09/322,409
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/087,306
; PRIOR FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 402
; TYPE: DNA
; ORGANISM: Canis familiaris
US-09-755-633-8

Query Match 100.0%; Score 345; DB 9; Length 402;

Best Local Similarity 100.0%; Pred. No. 1.1e-95;

Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTTCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACT 60
Db 345 TTTCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACT 286
Qy 61 CATCGAACTTGGCTGTAGGGATGGGAACCTGATGATTCCTACTCTCTGAAAATAAAAAT 120
Db 285 CATCGAACTTGGCTGTAGGGATGGGAACCTGATGATTCCTACTCTCTGAAAATAAAAAT 226
Qy 121 CACCAACTGTGCATTAAGAAGTTTTTCAGGGTATAGACATTTGAAGAACCAACTGCC 180
Db 225 CACCAACTGTGCATTAAGAAGTTTTTCAGGGTATAGACATTTGAAGAACCAACTGCC 166
Qy 181 CACGGGAGGCTGTGGATAAATATTCCTCAAACTTGTCTTTAATAAAGAACACATAGAG 240
Db 165 CACGGGAGGCTGTGGATAAATATTCCTCAAACTTGTCTTTAATAAAGAACACATAGAG 106
Qy 241 CGCCAAAAAAGTGTGAGGAGAAAGATGGAGAGTGACAAAGTTCCTAGACTACTG 300
Db 105 CGCCAAAAAAGTGTGAGGAGAAAGATGGAGAGTGACAAAGTTCCTAGACTACTG 46
Qy 301 CAAATATTCTTCTGGTGTATTAACACCGAGTGGACACCGGAAAGT 345
Db 45 CAAATATTCTTCTGGTGTATTAACACCGAGTGGACACCGGAAAGT 1

RESULT 9

US-10-218-654-83

; Sequence 83, Application US/10218654

; Publication No. US2003009609A1

; GENERAL INFORMATION:

; APPLICANT: Sim, Gek-Ke

; APPLICANT: Yang, Shumin

; APPLICANT: Dreitz, Matthew J.

; APPLICANT: Wonderling, Ramani S.

; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC

; FILE REFERENCE: IM-2-C1

; CURRENT APPLICATION NUMBER: US/10/218,654

; CURRENT FILING DATE: 2002-08-13

; PRIOR APPLICATION NUMBER: US/09/322,409

; PRIOR FILING DATE: 1999-05-28

; PRIOR APPLICATION NUMBER: 60/087,306

; PRIOR FILING DATE: 1998-05-29

; NUMBER OF SEQ ID NOS: 154

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 83

; LENGTH: 402

; TYPE: DNA

; ORGANISM: Canis familiaris

US-10-218-654-83

Query Match 100.0%; Score 345; DB 15; Length 402;
Best Local Similarity 100.0%; Pred. No. 1.1e-95;
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTGCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACT 60
DB 58 TTTGCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACT 117

QY 61 CATCGAACTTGGCTGATAGCGGATGGAACTGATCTCTACTCTCTGAAAATAAAAT 120
DB 118 CATCGAACTTGGCTGATAGCGGATGGAACTGATCTCTACTCTCTGAAAATAAAAT 177

QY 121 CACCAACTGTGCATTAAAGAAAGTTTTTCAGGGTATAGACACATTTGAAGAACCAAACTGCC 180
DB 178 CACCAACTGTGCATTAAAGAAAGTTTTTCAGGGTATAGACACATTTGAAGAACCAAACTGCC 237

QY 181 CACGGGAGGCTGTGATAAAGTATTTCCAAAAGTCTCTTTAATAAAGAACACATAGAG 240
DB 238 CACGGGAGGCTGTGATAAAGTATTTCCAAAAGTCTCTTTAATAAAGAACACATAGAG 297

QY 241 CGCCAAAATAAAAGGTGTGCAGGAGAAAGATGGAGAGTGACAAAAGTTCTTAGACTACCTG 300
DB 298 CGCCAAAATAAAAGGTGTGCAGGAGAAAGATGGAGAGTGACAAAAGTTCTTAGACTACCTG 357

QY 301 CAAGTATTTCTTGGTGTATAAATACACCGAGTGACACCGGAAAGT 345
DB 358 CAAGTATTTCTTGGTGTATAAATACACCGAGTGACACCGGAAAGT 402

RESULT 10
US-10-218-654-84/c
; Sequence 84, Application US/10218654
; Publication No. US20030099609A1
; GENERAL INFORMATION:
; APPLICANT: Sim, Gek-Kee
; APPLICANT: Yang, Shumin
; APPLICANT: Dreitz, Matthew J.
; APPLICANT: Wonderling, Ramani S.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF
; FILE REFERENCE: IM-2-C1
; CURRENT APPLICATION NUMBER: US/10/218,654
; PRIOR FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: US/09/322,409
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/087,306
; PRIOR FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 154
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 84
; LENGTH: 402
; TYPE: DNA
; ORGANISM: Canis familiaris
US-10-218-654-84

Query Match 100.0%; Score 345; DB 15; Length 402;
Best Local Similarity 100.0%; Pred. No. 1.1e-95;
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTGCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACT 60
DB 345 TTTGCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACT 286

QY 61 CATCGAACTTGGCTGATAGCGGATGGAACTGATCTCTACTCTCTGAAAATAAAAT 120
DB 285 CATCGAACTTGGCTGATAGCGGATGGAACTGATCTCTACTCTCTGAAAATAAAAT 226

QY 121 CACCAACTGTGCATTAAAGAAAGTTTTTCAGGGTATAGACACATTTGAAGAACCAAACTGCC 180
DB 225 CACCAACTGTGCATTAAAGAAAGTTTTTCAGGGTATAGACACATTTGAAGAACCAAACTGCC 166

QY 181 CACGGGAGGCTGTGATAAAGTATTTCCAAAAGTCTCTTTAATAAAGAACACATAGAG 240

DB 165 CACGGGAGGCTGTGATAAAGTATTTCCAAAAGTCTCTTTAATAAAGAACACATAGAG 106
QY 241 CGCCAAAATAAAAGGTGTGCAGGAGAAAGATGGAGAGTGACAAAAGTTCTTAGACTACCTG 300
DB 105 CGCCAAAATAAAAGGTGTGCAGGAGAAAGATGGAGAGTGACAAAAGTTCTTAGACTACCTG 46
QY 301 CAAGTATTTCTTGGTGTATAAATACACCGAGTGACACCGGAAAGT 345
DB 45 CAAGTATTTCTTGGTGTATAAATACACCGAGTGACACCGGAAAGT 1

RESULT 11
US-10-262-439-83
; Sequence 83, Application US/10262439
; Publication No. US20030143196A1
; GENERAL INFORMATION:
; APPLICANT: Sim, Gek-Kee
; APPLICANT: Yang, Shumin
; APPLICANT: Dreitz, Matthew J.
; APPLICANT: Wonderling, Ramani S.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF
; FILE REFERENCE: IM-2-C2
; CURRENT APPLICATION NUMBER: US/10/262,439
; CURRENT FILING DATE: 2002-09-30
; PRIOR APPLICATION NUMBER: US/09/451,527
; PRIOR FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: 09/322,409
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/087,306
; PRIOR FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 83
; LENGTH: 402
; TYPE: DNA
; ORGANISM: Canis familiaris
US-10-262-439-83

Query Match 100.0%; Score 345; DB 15; Length 402;
Best Local Similarity 100.0%; Pred. No. 1.1e-95;
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTGCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACT 60
DB 58 TTTGCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACT 117

QY 61 CATCGAACTTGGCTGATAGCGGATGGAACTGATCTCTACTCTCTGAAAATAAAAT 120
DB 118 CATCGAACTTGGCTGATAGCGGATGGAACTGATCTCTACTCTCTGAAAATAAAAT 177

QY 121 CACCAACTGTGCATTAAAGAAAGTTTTTCAGGGTATAGACACATTTGAAGAACCAAACTGCC 180
DB 178 CACCAACTGTGCATTAAAGAAAGTTTTTCAGGGTATAGACACATTTGAAGAACCAAACTGCC 237

QY 181 CACGGGAGGCTGTGATAAAGTATTTCCAAAAGTCTCTTTAATAAAGAACACATAGAG 240
DB 238 CACGGGAGGCTGTGATAAAGTATTTCCAAAAGTCTCTTTAATAAAGAACACATAGAG 297

QY 241 CGCCAAAATAAAAGGTGTGCAGGAGAAAGATGGAGAGTGACAAAAGTTCTTAGACTACCTG 300
DB 298 CGCCAAAATAAAAGGTGTGCAGGAGAAAGATGGAGAGTGACAAAAGTTCTTAGACTACCTG 357

QY 301 CAAGTATTTCTTGGTGTATAAATACACCGAGTGACACCGGAAAGT 345
DB 358 CAAGTATTTCTTGGTGTATAAATACACCGAGTGACACCGGAAAGT 402

RESULT 12
US-10-262-439-84/c
; Sequence 84, Application US/10262439
; Publication No. US20030143196A1
; GENERAL INFORMATION:

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; APPLICANT: Sim, Gek-Kee
; APPLICANT: Yang, Shumin
; APPLICANT: Dreitz, Matthew J.
; APPLICANT: Wonderling, Ramani S.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; FILE REFERENCE: IM-2-C2
; CURRENT APPLICATION NUMBER: US/10/262,439
; CURRENT FILING DATE: 2002-09-30
; PRIOR APPLICATION NUMBER: US/09/451,527
; PRIOR FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: 09/322,409
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/087,306
; PRIOR FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 84
; LENGTH: 402
; TYPE: DNA
; ORGANISM: Canis familiaris
US-10-262-439-84

Query Match      100.0%; Score 345; DB 15; Length 402;
Best Local Similarity 100.0%; Pred. No. 1.1e-95;
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  TTTGCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACT 60
Db      345  TTTGCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACT 286

QY      61  CATCGAACTTGGCTGATAGCGGATGGGAACCTGATGATTCCTACTCTCTGAAAAATAAAAT 120
Db      285  CATCGAACTTGGCTGATAGCGGATGGGAACCTGATGATTCCTACTCTCTGAAAAATAAAAT 226

QY      121  CACCAACTGTGCATTAAGAAGTTTTCAGGGTATAGACATGAGAACCAACTGCC 180
Db      225  CACCAACTGTGCATTAAGAAGTTTTCAGGGTATAGACATGAGAACCAACTGCC 166

QY      181  CACGGGAGGCTGTGGATAAATCTATCCAAACTTGTCTTTAATAAAGAACACATAGAG 240
Db      165  CACGGGAGGCTGTGGATAAATCTATCCAAACTTGTCTTTAATAAAGAACACATAGAG 106

QY      241  CGCCAAAAAAGCTGTGAGAGAAAGATGGAGAGTGACAAAGTTCCTAGACTCCTG 300
Db      105  CGCCAAAAAAGCTGTGAGAGAAAGATGGAGAGTGACAAAGTTCCTAGACTCCTG 46

QY      301  CAAGTATTTCTTGGTGTAAATAAACACCGAGTGGACACCGGAAAGT 345
Db      45  CAAGTATTTCTTGGTGTAAATAAACACCGAGTGGACACCGGAAAGT 1

RESULT 13
US-09-755-633-4
; Sequence 4, Application US/09755633
; Patent No. US20020127200A1
; GENERAL INFORMATION:
; APPLICANT: Yang, Shumin
; APPLICANT: McCall, Catherine A.
; APPLICANT: Weber, Eric R.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; FILE REFERENCE: IM-2-C1-C1
; CURRENT APPLICATION NUMBER: US/09/755,633
; CURRENT FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: 09/322,409
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/087,306
; PRIOR FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 610
; TYPE: DNA
; ORGANISM: Canis familiaris
US-09-755-633-6

Query Match      100.0%; Score 345; DB 9; Length 610;
Best Local Similarity 100.0%; Pred. No. 1.4e-95;
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  TTTGCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACT 60
Db      525  TTTGCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACT 466

QY      61  CATCGAACTTGGCTGATAGCGGATGGGAACCTGATGATTCCTACTCTGAAAAATAAAAT 120
Db      465  CATCGAACTTGGCTGATAGCGGATGGGAACCTGATGATTCCTACTCTGAAAAATAAAAT 406
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; TYPE: DNA
; ORGANISM: Canis familiaris
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (29)..(430)
US-09-755-633-4

Query Match      100.0%; Score 345; DB 9; Length 610;
Best Local Similarity 100.0%; Pred. No. 1.4e-95;
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  TTTGCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACT 60
Db      86  TTTGCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACT 145

QY      61  CATCGAACTTGGCTGATAGCGGATGGGAACCTGATGATTCCTACTCTGAAAAATAAAAT 120
Db      146  CATCGAACTTGGCTGATAGCGGATGGGAACCTGATGATTCCTACTCTCTGAAAAATAAAAT 205

QY      121  CACCAACTGTGCATTAAGAAGTTTTCAGGGTATAGACATGAGAACCAACTGCC 180
Db      206  CACCAACTGTGCATTAAGAAGTTTTCAGGGTATAGACATGAGAACCAACTGCC 265

QY      181  CACGGGAGGCTGTGGATAAATCTATCCAAACTTGTCTTTAATAAAGAACACATAGAG 240
Db      266  CACGGGAGGCTGTGGATAAATCTATCCAAACTTGTCTTTAATAAAGAACACATAGAG 325

QY      241  CGCCAAAAAAGCTGTGAGAGAAAGATGGAGAGTGACAAAGTTCCTAGACTCCTG 300
Db      326  CGCCAAAAAAGCTGTGAGAGAAAGATGGAGAGTGACAAAGTTCCTAGACTCCTG 385

QY      301  CAAGTATTTCTTGGTGTAAATAAACACCGAGTGGACACCGGAAAGT 345
Db      386  CAAGTATTTCTTGGTGTAAATAAACACCGAGTGGACACCGGAAAGT 430

RESULT 14
US-09-755-633-6/c
; Sequence 6, Application US/09755633
; Patent No. US20020127200A1
; GENERAL INFORMATION:
; APPLICANT: Yang, Shumin
; APPLICANT: McCall, Catherine A.
; APPLICANT: Weber, Eric R.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; FILE REFERENCE: IM-2-C1-C1
; CURRENT APPLICATION NUMBER: US/09/755,633
; CURRENT FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: 09/322,409
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/087,306
; PRIOR FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 610
; TYPE: DNA
; ORGANISM: Canis familiaris
US-09-755-633-6

Query Match      100.0%; Score 345; DB 9; Length 610;
Best Local Similarity 100.0%; Pred. No. 1.4e-95;
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  TTTGCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACT 60
Db      525  TTTGCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACT 466

QY      61  CATCGAACTTGGCTGATAGCGGATGGGAACCTGATGATTCCTACTCTGAAAAATAAAAT 120
Db      465  CATCGAACTTGGCTGATAGCGGATGGGAACCTGATGATTCCTACTCTGAAAAATAAAAT 406
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QY 121 CACCAACTGTGCATTAAAGAGTTTTCAGGGTATAGACACATTGAAGAACCAAACTGCC 180
DB 405 CACCAACTGTGCATTAAAGAGTTTTCAGGGTATAGACACATTGAAGAACCAAACTGCC 346
QY 181 CACGGGAGGCTGTGATAAACTATTCCAAAACCTTCTTTTAAATAAAGAACACATAGAG 240
DB 345 CACGGGAGGCTGTGATAAACTATTCCAAAACCTTCTTTTAAATAAAGAACACATAGAG 286
QY 241 CGCCAAAAAAGAGTGTGCAGGAGAAAGATGAGAGTGACAAAAGTTCCTAGACTACCTG 300
DB 285 CGCCAAAAAAGAGTGTGCAGGAGAAAGATGAGAGTGACAAAAGTTCCTAGACTACCTG 226
QY 301 CAAGTATTTCTTGGTGTATATAAACACCGAGTGGACACCGGAAAGT 345
DB 225 CAAGTATTTCTTGGTGTATATAAACACCGAGTGGACACCGGAAAGT 181

RESULT 15

US-10-218-654-80
; Sequence 80, Application US/10218654
; Publication No. US20030099609A1
; GENERAL INFORMATION:
; APPLICANT: Sim, Gek-Kee
; APPLICANT: Yang, Shumin
; APPLICANT: Dreitz, Matthew J.
; APPLICANT: Wonderling, Ramani S.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF
; FILE REFERENCE: IN-2-C1
; CURRENT APPLICATION NUMBER: US/10/218,654
; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: US/09/322,409
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/087,306
; PRIOR FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 154
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 80
; LENGTH: 610
; TYPE: DNA
; ORGANISM: Canis familiaris
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (29)..(430)
US-10-218-654-80

Query Match 100.0%; Score 345; DB 15; Length 610;
Best Local Similarity 100.0%; Pred. No. 1.4e-95;
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTTGCTGTAGAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACT 60
DB 86 TTTGCTGTAGAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACT 145
QY 61 CATCGAACTTGGCTGATAGCGGAACTGTGATTCCTACTCTGAAAATAAAAT 120
DB 146 CATCGAACTTGGCTGATAGCGGAACTGTGATTCCTACTCTGAAAATAAAAT 205
QY 121 CACCAACTGTGCATTAAAGAGTTTTCAGGGTATAGACACATTGAAGAACCAAACTGCC 180
DB 206 CACCAACTGTGCATTAAAGAGTTTTCAGGGTATAGACACATTGAAGAACCAAACTGCC 265
QY 181 CACGGGAGGCTGTGATAAACTATTCCAAAACCTTCTTTTAAATAAAGAACACATAGAG 240
DB 286 CACGGGAGGCTGTGATAAACTATTCCAAAACCTTCTTTTAAATAAAGAACACATAGAG 325
QY 241 CGCCAAAAAAGAGTGTGCAGGAGAAAGATGGAGAGTGACAAAGTTCCTAGACTACCTG 300
DB 326 CGCCAAAAAAGAGTGTGCAGGAGAAAGATGGAGAGTGACAAAGTTCCTAGACTACCTG 385
QY 301 CAAGTATTTCTTGGTGTATATAAACACCGAGTGGACACCGGAAAGT 345
DB 386 CAAGTATTTCTTGGTGTATATAAACACCGAGTGGACACCGGAAAGT 430

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Job time : 205.139 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 30, 2004, 20:51:08 ; Search time 30.7811 Seconds
(without alignments)
6219.989 Million cell updates/sec

Title: US-10-787-382-9
Perfect score: 345
Sequence: 1 ttgtcgtgataatcccat.....ccgagtgacaccggaaagt 345

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	345	100.0	345	4	US-09-322-409-87
3	345	100.0	345	4	US-09-451-527-85
4	345	100.0	345	4	US-09-451-527-87
5	345	100.0	402	4	US-09-322-409-83
6	345	100.0	402	4	US-09-322-409-84
7	345	100.0	402	4	US-09-451-527-83
8	345	100.0	402	4	US-09-451-527-84
9	345	100.0	610	4	US-09-322-409-80
10	345	100.0	610	4	US-09-322-409-82
11	345	100.0	610	4	US-09-451-527-80
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15	229.8	66.6	816	4	US-09-023-655-1236
16	206	59.7	377	4	US-09-180-864-1
17	196.4	56.9	1534	3	US-08-629-643A-4
18	196.4	56.9	1534	3	US-09-155-884-4
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20	90.6	26.3	6727	3	US-09-280-799-1
21	90.6	26.3	6727	3	US-09-155-884-5
22	90.2	26.1	3230	3	US-09-280-799-78
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25	34.4	10.0	4843	3	US-08-986-485-1
26	33.4	9.7	22846	2	US-08-469-461-3
27	33.4	9.7	22846	3	US-07-890-609-3

C 28 32.4 9.4 2797 4 US-09-453-702B-244 Sequence 244, Appl
C 29 31.8 9.2 1902 4 US-09-220-132-74 Sequence 74, Appl
C 30 31.6 9.2 927 4 US-09-134-001C-150 Sequence 150, Appl
C 31 31.6 9.2 1642 4 US-09-737-898B-24 Sequence 24, Appl
C 32 31.6 9.2 1642 4 US-09-737-826A-24 Sequence 24, Appl
C 33 31.6 9.2 9626 4 US-09-150-867-2 Sequence 2, Appl
C 34 31.6 9.2 174493 4 US-09-804-471A-3 Sequence 3, Appl
C 35 31.6 9.2 174493 4 US-10-238-709-3 Sequence 1, Appl
C 36 31.6 9.2 1664976 4 US-08-916-421B-1 Sequence 20, Appl
C 37 31.4 9.1 21338 4 US-09-961-527-20 Sequence 15639, A
C 38 31.2 9.0 505 4 US-09-621-976-15639 Sequence 1, Appl
C 39 31.2 9.0 1664976 4 US-08-916-421B-1 Sequence 1666, Ap
C 40 31 9.0 222 4 US-09-543-681A-1166 Sequence 9, Appl
C 41 31 9.0 3434 4 US-09-388-743-9 Sequence 2806, Ap
C 42 30.8 8.9 1842 4 US-09-328-352-2806 Sequence 2, Appl
C 43 30.8 8.9 9421 2 US-08-370-319C-2 Sequence 2, Appl
C 44 30.8 8.9 9421 3 US-09-224-834-2 Sequence 36, Appl
C 45 30.8 8.9 12124 1 US-08-181-271A-36

ALIGNMENTS

RESULT 1
US-09-322-409-85
; Sequence 85, Application US/09322409
; Patent No. 6471957

GENERAL INFORMATION:

APPLICANT: Sim, Gek-Kee
APPLICANT: Yang, Shumin
APPLICANT: Dreitz, Matthew J.
APPLICANT: Wonderling, Ramani S.
TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF
FILE REFERENCE: IM-2-C1
CURRENT APPLICATION NUMBER: US/09/322,409
CURRENT FILING DATE: 1999-05-28
EARLIER APPLICATION NUMBER: 60/087,306
EARLIER FILING DATE: 1998-05-29
NUMBER OF SEQ ID NOS: 154
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 85
LENGTH: 345
TYPE: DNA
ORGANISM: Canis familiaris
FEATURE:

NAME/KEY: CDS
LOCATION: (1)..(345)

US-09-322-409-85

Query Match 100.0%; Score 345; DB 4; Length 345;
Best Local Similarity 100.0%; Pred. No. 1.4e-100; Indels 0; Gaps 0;
Matches 345; Conservative 0; Mismatches 0;

QY 1 TTTGCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACCTTCACACTGCTCTCCACT 60
DB 1 TTTGCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACCTTCACACTGCTCTCCACT 60
QY 61 CATCGAACTGGCTGATAGCGGACCTGATGATCTCTACTCTGAAATAAATAAT 120
DB 61 CATCGAACTGGCTGATAGCGGACCTGATGATCTCTACTCTGAAATAAATAAT 120
QY 121 CACCACTGTGCATTAAGAAAGTTTTCAGGGTATAGACACATTTGAAGAACCAAACTGCC 180
DB 121 CACCACTGTGCATTAAGAAAGTTTTCAGGGTATAGACACATTTGAAGAACCAAACTGCC 180
QY 181 CACGGGAGGCTGTGGATAAATACTTTCCAAAATCTTGTCTTTTAAATAAAGAACACATAGAG 240
DB 181 CACGGGAGGCTGTGGATAAATACTTTCCAAAATCTTGTCTTTTAAATAAAGAACACATAGAG 240
QY 241 CGCCAAAAAAGAGGTGTCAGAGAGAACATGAGAGTGCACAAAGTTCTTAGACTACCTG 300
DB 241 CGCCAAAAAAGAGGTGTCAGAGAGAACATGAGAGTGCACAAAGTTCTTAGACTACCTG 300

QY 301 CAAGTATTCTTGGTGTAAATACACCGAGTGGACACCGGAAGT 345
 |||||
 Db 301 CAAGTATTCTTGGTGTAAATACACCGAGTGGACACCGGAAGT 345

RESULT 2

US-09-322-409-87/c
 ; Sequence 87, Application US/09322409
 ; Patent No. 6471957
 ; GENERAL INFORMATION:
 ; APPLICANT: Sim, Gek-kee
 ; APPLICANT: Yang, Shumin
 ; APPLICANT: Dreitz, Matthew J.
 ; APPLICANT: Wonderling, Ramani S.
 ; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
 ; TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF
 ; FILE REFERENCE: IM-2-C1
 ; CURRENT APPLICATION NUMBER: US/09/322,409
 ; CURRENT FILING DATE: 1999-05-28
 ; EARLIER APPLICATION NUMBER: 60/087,306
 ; EARLIER FILING DATE: 1998-05-29
 ; NUMBER OF SEQ ID NOS: 154
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 87
 ; LENGTH: 345
 ; TYPE: DNA
 ; ORGANISM: Canis familiaris
 US-09-322-409-87

Query Match 100.0%; Score 345; DB 4; Length 345;
 Best Local Similarity 100.0%; Pred. No. 1.4e-100;
 Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TTTGCTGTAGAAAATCCCATGATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACT 60
 345 TTTGCTGTAGAAAATCCCATGATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACT 286
 Db 345 TTTGCTGTAGAAAATCCCATGATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACT 286
 QY 61 CATCGAACTTGGCTGTAGAGCGATGGGAACCTGATGATTCCTACTCCTGAAAAATAAAAT 120
 Db 285 CATCGAACTTGGCTGTAGAGCGATGGGAACCTGATGATTCCTACTCCTGAAAAATAAAAT 226
 QY 121 CACCAACTGTGCATTAAGAAGTTTTTCAGGGTATAGACATTTGAAGACCAACTGCC 180
 Db 225 CACCAACTGTGCATTAAGAAGTTTTTCAGGGTATAGACATTTGAAGACCAACTGCC 166
 QY 181 CACGGGAGGCTGTGGATAAATCTTCCAAAACCTTGTCTTTAATAAAGAACACATAGAG 240
 Db 165 CACGGGAGGCTGTGGATAAATCTTCCAAAACCTTGTCTTTAATAAAGAACACATAGAG 106
 QY 241 CGCCAAAAAAGAGTGTGAGAGAAAGTGGAGAGTGACAAAGTTCCTAGACTACCTG 300
 Db 105 CGCCAAAAAAGAGTGTGAGAGAAAGTGGAGAGTGACAAAGTTCCTAGACTACCTG 46
 QY 301 CAAGTATTCTTGGTGTAAATACACCGAGTGGACACCGGAAGT 345
 |||||
 Db 45 CAAGTATTCTTGGTGTAAATACACCGAGTGGACACCGGAAGT 1

RESULT 3

US-09-451-527-85
 ; Sequence 85, Application US/09451527
 ; Patent No. 6482403
 ; GENERAL INFORMATION:
 ; APPLICANT: Sim, Gek-kee
 ; APPLICANT: Yang, Shumin
 ; APPLICANT: Dreitz, Matthew J.
 ; APPLICANT: Wonderling, Ramani S.
 ; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
 ; TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF
 ; FILE REFERENCE: IM-2-C2
 ; CURRENT APPLICATION NUMBER: US/09/451,527
 ; CURRENT FILING DATE: 1999-12-01

; EARLIER APPLICATION NUMBER: 09/322,409
 ; EARLIER FILING DATE: 1999-05-28
 ; EARLIER APPLICATION NUMBER: 60/087,306
 ; EARLIER FILING DATE: 1998-05-29
 ; NUMBER OF SEQ ID NOS: 174
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 85
 ; LENGTH: 345
 ; TYPE: DNA
 ; ORGANISM: Canis familiaris
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (1) .. (345)
 US-09-451-527-85

Query Match 100.0%; Score 345; DB 4; Length 345;
 Best Local Similarity 100.0%; Pred. No. 1.4e-100;
 Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TTTGCTGTAGAAAATCCCATGATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACT 60
 Db 1 TTTGCTGTAGAAAATCCCATGATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACT 60
 QY 61 CATCGAACTTGGCTGTAGAGCGATGGGAACCTGATGATTCCTACTCCTGAAAAATAAAAT 120
 Db 61 CATCGAACTTGGCTGTAGAGCGATGGGAACCTGATGATTCCTACTCCTGAAAAATAAAAT 120
 QY 121 CACCAACTGTGCATTAAGAAGTTTTTCAGGGTATAGACATTTGAAGACCAACTGCC 180
 Db 121 CACCAACTGTGCATTAAGAAGTTTTTCAGGGTATAGACATTTGAAGACCAACTGCC 180
 QY 181 CACGGGAGGCTGTGGATAAATCTTCCAAAACCTTGTCTTTAATAAAGAACACATAGAG 240
 Db 181 CACGGGAGGCTGTGGATAAATCTTCCAAAACCTTGTCTTTAATAAAGAACACATAGAG 240
 QY 241 CGCCAAAAAAGAGTGTGAGAGAAAGTGGAGAGTGACAAAGTTCCTAGACTACCTG 300
 Db 241 CGCCAAAAAAGAGTGTGAGAGAAAGTGGAGAGTGACAAAGTTCCTAGACTACCTG 300
 QY 301 CAAGTATTCTTGGTGTAAATACACCGAGTGGACACCGGAAGT 345
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 Db 301 CAAGTATTCTTGGTGTAAATACACCGAGTGGACACCGGAAGT 345

RESULT 4

US-09-451-527-87/c
 ; Sequence 87, Application US/09451527
 ; Patent No. 6482403
 ; GENERAL INFORMATION:
 ; APPLICANT: Sim, Gek-kee
 ; APPLICANT: Yang, Shumin
 ; APPLICANT: Dreitz, Matthew J.
 ; APPLICANT: Wonderling, Ramani S.
 ; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
 ; TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF
 ; FILE REFERENCE: IM-2-C2
 ; CURRENT APPLICATION NUMBER: US/09/451,527
 ; CURRENT FILING DATE: 1999-12-01
 ; EARLIER APPLICATION NUMBER: 09/322,409
 ; EARLIER FILING DATE: 1999-05-28
 ; EARLIER APPLICATION NUMBER: 60/087,306
 ; EARLIER FILING DATE: 1998-05-29
 ; NUMBER OF SEQ ID NOS: 174
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 87
 ; LENGTH: 345
 ; TYPE: DNA
 ; ORGANISM: Canis familiaris
 US-09-451-527-87

Query Match 100.0%; Score 345; DB 4; Length 345;
 Best Local Similarity 100.0%; Pred. No. 1.4e-100;
 Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 5
 US-09-322-409-83.
 ; Sequence 83, Application US/09322409
 ; Patent No. 6471957
 ; GENERAL INFORMATION:
 ; APPLICANT: Sim, Gek-Kee
 ; APPLICANT: Yang, Shumin
 ; APPLICANT: Dreitz, Matthew J.
 ; APPLICANT: Wonderling, Ramani S.
 ; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
 ; TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF
 ; FILE REFERENCE: IM-2-C1
 ; CURRENT APPLICATION NUMBER: US/09/322,409
 ; CURRENT FILING DATE: 1999-05-28
 ; EARLIER APPLICATION NUMBER: 60/087,306
 ; EARLIER FILING DATE: 1998-05-29
 ; NUMBER OF SEQ ID NOS: 154
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 83
 ; LENGTH: 402
 ; TYPE: DNA
 ; ORGANISM: Canis familiaris
 US-09-322-409-83

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301 CAAGTATTCTTCTGGTGAATAAACAACCGAGTGGACCCGGAAAGT 344
358 CAAGTATTCTTGGTGAATAAACAACCGAGTGGACCCGGAAAGT 402

RESULT 6
US-09-322-409-84/c
; Sequence 84, Application US/09322409
; Patent No.: 6471957
; GENERAL INFORMATION:
; APPLICANT: Sim, Gek-Kee
; APPLICANT: Yang, Shumin
; APPLICANT: Dreitz, Matthew J.
; APPLICANT: Wonderling, Ramani S.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEIN
; TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF
; FILE REFERENCE: IM-2-Cl
; CURRENT APPLICATION NUMBER: US/09/322,409
; CURRENT FILING DATE: 1999-05-28
; EARLIER APPLICATION NUMBER: 60/087,306
; EARLIER FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 154
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 84
; LENGTH: 402
; TYPE: DNA
; ORGANISM: Canis familiaris
US-09-322-409-84

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Query Match	100.0%;	Score 345;	DB 4;	Length 402;
Best Local Similarity	100.0%;	Pred. No. 1.5e-100;		
Matches 345;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	TTTCTGTGAGAAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACACTGCTCTCCACT	60	
Db	345	TTTCTGTGAGAAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACT	286	
QY	61	CATCGAACTTGGCTGTAGCGCATGGGAACCTGATGTTCTTACTCTGTGAAATAAAAAAT	120	
Db	285	CATCGAACTTGGCTGTAGCGCATGGGAACCTGATGTTCTTACTCTGTGAAATAAAAAAT	226	
QY	121	CACAACTGTGCATTAAAGAAAGTTTTTCAGGGTATAGACACATTGAAGAACCAACTGCC	180	
Db	225	CACCAACTGTGCATTAAAGAAAGTTTTTCAGGGTATAGACACATTGAAGAACCAACTGCC	166	
QY	181	CACGGGAGGCTGTGGATAAATATTCCAAAACCTGCTCTTTAATAAAGAACACACATAGAG	240	
Db	165	CACGGGAGGCTGTGGATAAATATTCCAAAACCTGCTCTTTAATAAAGAACACACATAGAG	106	
QY	241	CGCCAAAAAAAAGGCTGTGCAGGAGAAAGATGGAGAGTGACAAAGTTCCTAGACTACCTG	300	
Db	105	CGCCAAAAAAAAGGCTGTGCAGGAGAAAGATGGAGAGTGACAAAGTTCCTAGACTACCTG	46	
QY	301	CAAGTATTTCTTGGTGTAAATAACAACCGAGTGGACACCGGAAAGT	345	
Db	45	CAAGTATTTCTTGGTGTAAATAACAACCGAGTGGACACCGGAAAGT	1	

RESULT 7
US-09-451-527-83
; Sequence 83, Application US/09451527
; Patent No. 6482403
; GENERAL INFORMATION:
; APPLICANT: Sim, Gek-Kee
; APPLICANT: Yang, Shumin
; APPLICANT: Dreitz, Matthew J.
; APPLICANT: Wonderling, Ramani S.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF
; FILE REFERENCE: IM-2-C2
; CURRENT APPLICATION NUMBER: US/09/451.527
; CURRENT FILING DATE: 1999-12-01

[illegible]

QY 1 TTTCCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACT 60
Db 525 TTTCCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACT 466
QY 61 CATCGAACTTGGCTGTAGGGGATGGGAACCTGATGATTCCTACTCTCTGAAATATAAAT 120
Db 465 CATCGAACTTGGCTGTAGGGGATGGGAACCTGATGATTCCTACTCTCTGAAATATAAAT 406
QY 121 CACCAACTGTGCATTAAGAAGTTTTCAGGGTATAGACACATGTAAGAACCAACTGCC 180
Db 405 CACCAACTGTGCATTAAGAAGTTTTCAGGGTATAGACACATGTAAGAACCAACTGCC 346
QY 181 CACGGGGAGCTGGGATTAACACTTCCAAAACCTGCTTTTAATAAAGAACACATAGAG 240
Db 345 CACGGGGAGCTGGGATTAACACTTCCAAAACCTGCTTTTAATAAAGAACACATAGAG 286
QY 241 CGCCAAAAAAGAGTGTGAGGAGAAAGATGGAGAGTGACAAAGTTTCCTAGACTACCTG 300
Db 285 CGCCAAAAAAGAGTGTGAGGAGAAAGATGGAGAGTGACAAAGTTTCCTAGACTACCTG 226
QY 301 CAAGTATTTCTGTGTGTAATAAACACCGAGTGGACACCGGAAAGT 345
Db 225 CAAGTATTTCTGTGTGTAATAAACACCGAGTGGACACCGGAAAGT 181

RESULT 13

US-09-371-615A-1

; Sequence 1, Application US/09371615A
; Patent No. 6537781

; GENERAL INFORMATION:

; APPLICANT: IDEXX LABORATORIES

; TITLE OF INVENTION: METHODS AND COMPOSITIONS CONCERNING

; FILE REFERENCE: 03604001700US00

; CURRENT APPLICATION NUMBER: US/09/371,615A

; NUMBER OF SEQ ID NOS: 8

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 1

; LENGTH: 405

; TYPE: DNA

; ORGANISM: Canis familiaris

; US-09-371-615A-1

Query Match 99.1%; Score 341.8; DB 4; Length 405;
Best Local Similarity 99.4%; Pred. No. 1.6e-99;
Matches 343; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TTTCCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACT 60
Db 58 TTTCCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACT 117
QY 61 CATCGAACTTGGCTGTAGGGGATGGGAACCTGATGATTCCTACTCTCTGAAATATAAAT 120
Db 118 CATCGAACTTGGCTGTAGGGGATGGGAACCTGATGATTCCTACTCTCTGAAATATAAAT 177
QY 121 CACCAACTGTGCATTAAGAAGTTTTCAGGGTATAGACACATGTAAGAACCAACTGCC 180
Db 178 CACCAACTGTGCATTAAGAAGTTTTCAGGGTATAGACACATGTAAGAACCAACTGCC 237
QY 181 CACGGGGAGCTGGGATTAACACTTCCAAAACCTGCTTTTAATAAAGAACACATAGAG 240
Db 238 CACGGGGAGCTGGGATTAACACTTCCAAAACCTGCTTTTAATAAAGAACACATAGAG 297
QY 241 CGCCAAAAAAGAGTGTGAGGAGAAAGATGGAGAGTGACAAAGTTTCCTAGACTACCTG 300
Db 298 CGCCAAAAAAGAGTGTGAGGAGAAAGATGGAGAGTGACAAAGTTTCCTAGACTACCTG 357
QY 301 CAAGTATTTCTGTGTGTAATAAACACCGAGTGGACACCGGAAAGT 345
Db 358 CAAGTATTTCTGTGTGTAATAAACACCGAGTGGACACCGGAAAGT 402

RESULT 14
US-09-079-839-2
; Sequence 2, Application US/09079839
; Patent No. 6048726
; GENERAL INFORMATION:
; APPLICANT: Weltman, Joel K.
; APPLICANT: Karim, Aftab S.
; TITLE OF INVENTION: INHIBITION OF EOSINOPHILIC INFLAMMATION
; FILE REFERENCE: 09998/002001
; CURRENT APPLICATION NUMBER: US/09/079,839
; CURRENT FILING DATE: 1998-05-15
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 816
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-079-839-2

Query Match 67.1%; Score 231.4; DB 3; Length 816;
Best Local Similarity 80.4%; Pred. No. 3.6e-64;
Matches 271; Conservative 0; Mismatches 66; Indels 0; Gaps 0;

QY 9 AGAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACTCATCGAAC 68
Db 110 AGAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCTACTCATCGAAC 169
QY 69 TTGGCTGATAGCGGATGGGAACCTTGATGATTCCTACTCTCTGAAATATAAATCACTCAACT 128
Db 170 TCTGCTGATAGCAATGAGACTCTGAGGATTCCTGTTCTGTACATATAAATCACTCAACT 229
QY 129 GTGCATTAAGAAGTTTTCAGGGTATAGACACATGTAAGAACCAACTGCCACGGGGA 188
Db 230 GTGCATTAAGAAGTTTTCAGGGTATAGACACATGTAAGAACCAACTGCCACGGGGA 289
QY 189 GGCTGTGGATAAATCTTCCAAAACCTTGTCTTTTAATAAAGAACACATAGACGGCCAAA 248
Db 290 TACTGTGGAAGACTATTCAAAAACCTTGTCTTTTAATAAAGAACATACATTGACGGCCAAA 349
QY 249 AAAAGGTGTCAGAGAGAGATGGAGAGTGCACAACTTCTAGACTACCTGCAAGTATT 308
Db 350 AAAAGGTGTCAGAGAGAGATGGAGAGTGCACAACTTCTAGACTACCTGCAAGTATT 409
QY 309 TCTTGGTGTATAAACACCGAGTGGACACCGGAAAGT 345
Db 410 TCTTGGTGTATAAACACCGAGTGGACACCGGAAAGT 446

RESULT 15

US-09-023-655-1236

; Sequence 1236, Application US/09023655

; Patent No. 6607879

; GENERAL INFORMATION:

; APPLICANT: Cocks, Benjamin G.

; APPLICANT: Susan G. Stuart

; APPLICANT: Jeffrey J. Sellhamer

; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE

; TITLE OF INVENTION: EXPRESSION

; NUMBER OF SEQUENCES: 1508

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.

; STREET: 3174 PORTER DRIVE

; CITY: PALO ALTO

; STATE: CALIFORNIA

; COUNTRY: USA

; ZIP: 94304

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2

; CURRENT APPLICATION DATA:

Wed Sep 1 08:34:23 2004

APPLICATION NUMBER: US/09/023,655
FILING DATE: HEREMITH
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0001 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1236:
SEQUENCE CHARACTERISTICS:
LENGTH: 816 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GENBANK
CLONE: G288309
US-09-023-655-1236

Query Match 56.6%; Score 229.8; DB 4; Length 816;
Best Local Similarity 80.1%; Pred. No. 1.2e-63;
Matches 270; Conservative 0; Mismatches 67; Indels 0; Gaps 0;

Qy	9	AGAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACACTGCTCTCCACTCATCGAAC	68
Db	110	AGAAATCCCAAGTGCATTTGGTGAAGAGACCTTGGCACTGCTTTCTACTCATCGAAC	169
Qy	69	TTGGCTGATAGGGGATGGGAACCTGATGATTCCTTACTCTCTGAAATAAATAATCACCAACT	128
Db	170	TCCTGCTGATAGCCCAATGAGACTCTGAGGATTCCTGTTCTCTGTACATAAAAAATCACCAACT	229
Qy	129	GTGCATTAAAGAGCTTTTTCAGGGTATAGACACATTGAAGAACCAAACTGCCACGGGGA	188
Db	230	GTGCACCTGAAGAAATCTTTTCAGGGAATAGGCACTCTGGAGTCAAACTGTGAAGGGG	289
Qy	189	GGCTGTGGATAAACTATTCCAAAACTTGTCTTTAATAAAGAAACACATAGAGGCCAAAA	248
Db	290	TACTGTGGAAGACTATTGAAAACTTGTCTTTAATAAAGAAATACATTGACGGCCAAA	349
Qy	249	AAAAAGGTGTCAGAGAGAGATCGAGAGTGACAAAGTTCCTAGACTACCTGCAAGTATT	308
Db	350	AAAAAAGTGTGGAGAGAGACCGGAGAGTAACCAATTCCTAGACTACCTGCAAGAGTT	409
Qy	309	TCITGGTGTATAAACACCGAGTGGACACCGGAAAGT	345
Db	410	TCITGGTGTATGAACACCGAGTGGATAATAGAAAGT	446

Search completed: August 31, 2004, 06:34:47
Job time : 31.7811 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 30, 2004, 15:56:41 ; Search time 164.547 Seconds
(without alignments)
8907.036 Million cell updates/sec

Title: US-10-787-382-9

Perfect score: 345

Sequence: 1 ttgtgctgtagaaatcccat.....ccgagtgacacggaaagt 345

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124098041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_29Jan04:*
1: Geneseq1980s:*
2: Geneseq1990s:*
3: Geneseq2000s:*
4: Geneseq2001as:*
5: Geneseq2001bs:*
6: Geneseq2002s:*
7: Geneseq2003as:*
8: Geneseq2003bs:*
9: Geneseq2003cs:*
10: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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C 2	345	100.0	345	3 AAZ5551	Canine ma
3	345	100.0	402	3 AAZ5548	Canine in
C 4	345	100.0	402	3 AAZ5549	Canine in
5	345	100.0	610	3 AAZ5546	Canine in
C 6	345	100.0	610	3 AAZ5547	Canine in
7	341.8	99.1	405	4 AAF74300	Canine in
8	289.6	83.9	838	3 AAZ44265	Porcine I
9	287.4	83.3	393	4 AAF74306	Canine in
10	274.8	79.7	399	2 AAT50756	Ovine IL-
11	274.8	79.7	520	2 AAT50755	Ovine IL-
12	231.4	67.1	816	3 AAA34857	Human ade
13	231.4	67.1	816	3 AAA13338	Human int
14	231.4	67.1	816	3 AAF20979	Human low
15	231.4	67.1	816	7 ABZ96673	Human nuc
16	231.4	67.1	816	7 ACF63368	Human int
17	231.4	67.1	858	8 AAL61293	h115-P2-P
18	231.4	67.1	858	8 AAL61294	h115-P30-
19	231.4	67.1	864	8 AAL61296	h115.37 v
20	231.4	67.1	864	8 AAL61295	h115.36 v
21	231.4	67.1	4057	3 AAZ34858	Human ade
22	231.4	67.1	4057	3 AAF20980	Human low
23	231.4	67.1	4057	7 ABZ96674	Human nuc

24	229.8	66.6	402	1 AAN81380	Aan81380 A human B
25	224.6	65.1	370	1 AAN91647	Aan91647 Synthetic
26	206	59.7	377	1 Aav01595	Aav01595 Human int
27	196.4	56.9	348	2 AAT14922	Aat14922 T cell re
28	196.4	56.9	399	2 AAV64061	Aav64061 T cell re
29	196.4	56.9	402	2 AAT14921	Aat14921 T cell re
30	196.4	56.9	1533	1 AAN82431	Aan82431 B cell di
31	196.4	56.9	1534	2 AAT88013	Aat88013 Murine in
32	196.4	56.9	1623	2 AAT14925	Aat14925 T cell re
33	196.4	56.9	1623	2 AAV64062	Aav64062 Plasmid p
34	195	55.5	252	4 AAF74305	Aaf74305 Canine in
35	194.6	56.4	342	2 AAT14923	Aat14923 T cell re
36	194.2	56.3	339	2 AAT14924	Aat14924 T cell re
37	190.6	55.2	1945	9 ADB53890	ADB53890 Primary r
38	190	55.1	481	1 AAN80461	Aan80461 Clone 115
39	183.6	53.2	385	3 AAA43842	Aaa43842 Human sec
40	178.4	51.7	375	3 AAC68870	Aac68870 Modified
41	175.6	50.9	357	3 AAC68871	Aac68871 Modified
42	169.2	49.0	381	3 AAC68867	Aac68867 Modified
43	166.4	48.2	399	3 AAC68873	Aac68873 Modified
44	166	48.1	444	3 AAC68875	Aac68875 Modified
45	165.6	48.0	375	3 AAC68872	Aac68872 Modified

ALIGNMENTS

RESULT 1
AAZ55550
ID AAZ55550 standard; cDNA; 345 BP.

XX AC AAZ55550;

XX DT 14-MAR-2000 (first entry)

XX DE Canine mature interleukin-5 (IL-5) cDNA.

XX KW Interleukin-5; IL-5; antibody; canine; inhibitor; immune response;
immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.

XX OS Canis familiaris.

XX PN WO9961618-A2.

XX PD 02-DEC-1999.

XX PF 28-MAY-1999; 99WO-US011942.

XX PR 29-MAY-1998; 98US-0087306P.

XX (HESK-) HESKA CORP.

XX PI Sim G, Yang S, Dreitz MJ, Wonderling RS;

XX DR WPI; 2000-072623/06.

XX P-P8DB; AAY58220.

XX PT Nucleic acids encoding immunoregulatory proteins from cats or dogs,
useful for treating or preventing e.g. tumors or autoimmune disease.

XX PS Claim 1h; Page 226-227; 264pp; English.

XX CC Sequences AAZ55546-255551 represent cDNA sequences encoding canine
interleukin-5 (IL-5). The invention relates to canine IL-4, canine or
feline Flt-3 ligand, canine or feline CD40, canine or feline (IFN-alpha)
ligand, canine IL-5, canine IL-13, feline interferon-alpha (IFN-alpha)
and feline granulocyte macrophage colony-stimulating factor (GM-CSF), and
nucleotides which encode these immunoregulatory proteins. The proteins,
their associated nucleic acids, specific antibodies and inhibitors may be
used as vaccines for therapeutic or prophylactic regulation of an immune
response in animals (particularly cats, dogs, horses and humans). They
may be used to treat autoimmune or infectious diseases including
allergies, tumours, inflammation and graft rejection, and to increase the

CC response from a co-administered antigen. The nucleotide sequences can
 CC also be used for the recombinant production of a protein, while
 CC nucleotide fragments are useful as probes, as amplification primers and
 CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).
 CC The proteins may be used to raise antibodies and to screen for modulators
 CC of activity, while the antibodies may be used in detection, and in drug
 CC targeting

XX Sequence 345 BP; 120 A; 68 C; 78 G; 79 T; 0 U; 0 Other;

Query Match 100.0%; Score 345; DB 3; Length 345;

Best Local Similarity 100.0%; Pred. No. 4e-93;

Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTCGCTAGAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACT 60

DB 1 TTTCGCTAGAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACT 60

QY 61 CATCGAACTTGGCTGATAGCGCATGGGAACCTGATGATTCCTACTCTCTGAAAAATAAAAT 120

DB 61 CATCGAACTTGGCTGATAGCGCATGGGAACCTGATGATTCCTACTCTCTGAAAAATAAAAT 120

QY 121 CACCAACTGTGCATTAAGAAGTTTTCAGGGTATAGACATGTAAGAACCAAACTGCC 180

DB 121 CACCAACTGTGCATTAAGAAGTTTTCAGGGTATAGACATGTAAGAACCAAACTGCC 180

QY 181 CACGGGAGGCTGGGATAAATCTTCCAAAACCTGTCTTTTAAATAAAGAACACATAGAG 240

DB 181 CACGGGAGGCTGGGATAAATCTTCCAAAACCTGTCTTTTAAATAAAGAACACATAGAG 240

QY 241 CGCCAAAAAAGGCTGTGAGGAGAAAGATGGAGAGTGACAAAGTTCTTAGACTACCTG 300

DB 241 CGCCAAAAAAGGCTGTGAGGAGAAAGATGGAGAGTGACAAAGTTCTTAGACTACCTG 300

QY 301 CAAGTATTTCTTGGTGTAAATAAACACCGAGTGGACACCGGAAAGT 345

DB 301 CAAGTATTTCTTGGTGTAAATAAACACCGAGTGGACACCGGAAAGT 345

RESULT 2

AAZ5551/G

ID AAZ5551 standard; cDNA; 345 BP.

XX AAZ5551;

AC AAZ5551;

XX AAZ5551;

DT 14-MAR-2000 (first entry)

XX Canine mature interleukin-5 (IL-5) cDNA complement.

DE Canine mature interleukin-5 (IL-5) cDNA complement.

XX Interleukin-5; IL-5; antibody; canine; inhibitor; immune response;

KW immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.

XX Canis familiaris.

XX Canis familiaris.

XX WO9961618-A2.

XX 02-DEC-1999.

XX 28-MAY-1999; 99WO-US011942.

XX 29-MAY-1998; 98US-0087306P.

XX (HESK-) HESKA CORP.

XX Sim G, Yang S, Dreitz MJ, Wonderling RS;

XX WPI; 2000-072623/06.

XX P-PSDB; AAY58220.

XX Nucleic acids encoding immunoregulatory proteins from cats or dogs,

XX useful for treating or preventing e.g. tumours or autoimmune disease.

XX Claim 1h; Page 228; 264pp; English.

XX PS

XX Sequences AAZ55546-255551 represent cDNA sequences encoding canine
 CC interleukin-5 (IL-5). The invention relates to canine IL-4, canine or
 CC feline Flt-3 ligand, canine or feline CD40, canine or feline CD154 (CD40
 CC ligand), canine IL-5, canine IL-13, feline interferon-alpha (IFN-alpha)
 CC and feline granulocyte macrophage colony-stimulating factor (GM-CSF), and
 CC nucleotides which encode these immunoregulatory proteins. The proteins,
 CC their associated nucleic acids, specific antibodies and inhibitors may be
 CC used as vaccines for therapeutic or prophylactic regulation of an immune
 CC response in animals (particularly cats, dogs, horses and humans). They
 CC may be used to treat autoimmune or infectious diseases, including
 CC allergies, tumours, inflammation and graft rejection, and to increase the
 CC response from a co-administered antigen. The nucleotide sequences can
 CC also be used for the recombinant production of a protein, while
 CC nucleotide fragments are useful as probes, as amplification primers and
 CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).
 CC The proteins may be used to raise antibodies and to screen for modulators
 CC of activity, while the antibodies may be used in detection, and in drug
 CC targeting

XX Sequence 345 BP; 79 A; 78 C; 68 G; 120 T; 0 U; 0 Other;

Query Match 100.0%; Score 345; DB 3; Length 345;

Best Local Similarity 100.0%; Pred. No. 4e-93;

Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTCGCTAGAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACT 60

DB 345 TTTCGCTAGAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACT 285

QY 61 CATCGAACTTGGCTGATAGCGCATGGGAACCTGATGATTCCTACTCTGAAAAATAAAAT 120

DB 285 CATCGAACTTGGCTGATAGCGCATGGGAACCTGATGATTCCTACTCTGAAAAATAAAAT 225

QY 121 CACCAACTGTGCATTAAGAAGTTTTCAGGGTATAGACATGTAAGAACCAAACTGCC 180

DB 225 CACCAACTGTGCATTAAGAAGTTTTCAGGGTATAGACATGTAAGAACCAAACTGCC 166

QY 181 CACGGGAGGCTGGGATAAATCTTCCAAAACCTGTCTTTTAAATAAAGAACACATAGAG 240

DB 165 CACGGGAGGCTGGGATAAATCTTCCAAAACCTGTCTTTTAAATAAAGAACACATAGAG 106

QY 241 CGCCAAAAAAGGCTGTGAGGAGAAAGATGGAGAGTGACAAAGTTCTTAGACTACCTG 300

DB 105 CGCCAAAAAAGGCTGTGAGGAGAAAGATGGAGAGTGACAAAGTTCTTAGACTACCTG 46

QY 301 CAAGTATTTCTTGGTGTAAATAAACACCGAGTGGACACCGGAAAGT 345

DB 45 CAAGTATTTCTTGGTGTAAATAAACACCGAGTGGACACCGGAAAGT 1

RESULT 3

AAZ55548

ID AAZ55548 standard; cDNA; 402 BP.

XX AAZ55548;

AC AAZ55548;

XX AAZ55548;

DT 14-MAR-2000 (first entry)

XX Canine interleukin-5 (IL-5) cDNA coding region.

DE Canine interleukin-5 (IL-5) cDNA coding region.

XX Interleukin-5; IL-5; antibody; canine; inhibitor; immune response;

KW immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.

XX Canis familiaris.

XX Canis familiaris.

XX WO9961618-A2.

XX 02-DEC-1999.

XX 28-MAY-1999; 99WO-US011942.

XX 29-MAY-1998; 98US-0087306P.

XX PS


```
XX (HESK-) HESKA CORP.
PA
XX Sim G, Yang S, Dreitz MJ, Wonderling RS;
XX
XX WPI; 2000-072623/06.
XX P-PSDB; AAY58219.
XX
XX Nucleic acids encoding immunoregulatory proteins from cats or dogs,
XX useful for treating or preventing e.g. tumors or autoimmune disease.
XX
XX Claim 1h; Page 225; 264pp; English.
XX
XX Sequences AAZ55546-Z55551 represent cDNA sequences encoding canine
XX interleukin-5 (IL-5). The invention relates to canine IL-4, canine or
XX feline Flt-3 ligand, canine or feline CD40, canine or feline CD154 (CD40
XX ligand), canine IL-5, canine IL-13, feline interferon-alpha (IFN-alpha)
XX and feline granulocyte macrophage colony-stimulating factor (GM-CSF), and
XX nucleotides which encode these immunoregulatory proteins. The proteins,
XX their associated nucleic acids, specific antibodies and inhibitors may be
XX used as vaccines for therapeutic or prophylactic regulation of an immune
XX response in animals (particularly cats, dogs, horses and humans). They
XX may be used to treat autoimmune or infectious diseases including
XX allergies, tumours, inflammation and graft rejection, and to increase the
XX response from a co-administered antigen. The nucleotide sequences can
XX also be used for the recombinant production of a protein, while
XX nucleotide fragments are useful as probes, as amplification primers and
XX as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).
XX The proteins may be used to raise antibodies and to screen for modulators
XX of activity, while the antibodies may be used in detection, and in drug
XX targeting.
XX
XX Sequence 402 BP; 129 A; 79 C; 93 G; 101 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 345; DB 3; Length 402;
XX Best Local Similarity 100.0%; Pred. No. 4.2e-93;
XX Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 TTGCTGTAGAAATCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACT 60
DB 58 TTGCTGTAGAAATCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACT 117
QY 61 CATCGAACTTGGCTGTAGCGGATGGGAACCTGATGATTCCTACTCTGAAAATAAAAT 120
DB 118 CATCGAACTTGGCTGTAGCGGATGGGAACCTGATGATTCCTACTCTGAAAATAAAAT 177
QY 121 CACCACTGTGCATTAAAGAGTTTTCAGGGTATAGACACATTTGAGACCAACTGCC 180
DB 178 CACCACTGTGCATTAAAGAGTTTTCAGGGTATAGACACATTTGAGACCAACTGCC 237
QY 181 CACGGGAGGCTGTGGATAAACTATTCCAAAACCTTGTCTTTAATAAAGAACACATAGAG 240
DB 238 CACGGGAGGCTGTGGATAAACTATTCCAAAACCTTGTCTTTAATAAAGAACACATAGAG 297
QY 241 CGCCAAAAAAGGTGTGAGGAAAGATGGAGTGCACAAAGTTCCTAGACTACCTG 300
DB 298 CGCCAAAAAAGGTGTGAGGAAAGATGGAGTGCACAAAGTTCCTAGACTACCTG 357
QY 301 CAAGTATTTCTTGGTGTAAATAAACACCGAGTGGACACCGGAAAGT 345
DB 358 CAAGTATTTCTTGGTGTAAATAAACACCGAGTGGACACCGGAAAGT 402
XX
RESULT 4
AAZ55549/c
ID AAZ55549 standard; cDNA; 402 BP.
XX
XX AAZ55549;
AC AAZ55549;
XX
XX 14-MAR-2000 (first entry)
DT
XX Canine interleukin-5 (IL-5) cDNA coding region complement.
DE
XX
```

```
XX Interleukin-5; IL-5; antibody; canine; inhibitor; immune response;
XX immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.
XX
XX Canis familiaris.
XX
XX WO9561618-A2.
XX
XX 02-DEC-1999.
XX
XX 28-MAY-1999; 99WO-US011942.
XX
XX 29-MAY-1998; 98US-0087306P.
XX
XX (HESK-) HESKA CORP.
XX
XX Sim G, Yang S, Dreitz MJ, Wonderling RS;
XX
XX WPI; 2000-072623/06.
XX P-PSDB; AAY58219.
XX
XX Nucleic acids encoding immunoregulatory proteins from cats or dogs,
XX useful for treating or preventing e.g. tumors or autoimmune disease.
XX
XX Claim 1h; Page 226; 264pp; English.
XX
XX Sequences AAZ55546-Z55551 represent cDNA sequences encoding canine
XX interleukin-5 (IL-5). The invention relates to canine IL-4, canine or
XX feline Flt-3 ligand, canine or feline CD40, canine or feline CD154 (CD40
XX ligand), canine IL-5, canine IL-13, feline interferon-alpha (IFN-alpha)
XX and feline granulocyte macrophage colony-stimulating factor (GM-CSF), and
XX nucleotides which encode these immunoregulatory proteins. The proteins,
XX their associated nucleic acids, specific antibodies and inhibitors may be
XX used as vaccines for therapeutic or prophylactic regulation of an immune
XX response in animals (particularly cats, dogs, horses and humans). They
XX may be used to treat autoimmune or infectious diseases including
XX allergies, tumours, inflammation and graft rejection, and to increase the
XX response from a co-administered antigen. The nucleotide sequences can
XX also be used for the recombinant production of a protein, while
XX nucleotide fragments are useful as probes, as amplification primers and
XX as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).
XX The proteins may be used to raise antibodies and to screen for modulators
XX of activity, while the antibodies may be used in detection, and in drug
XX targeting.
XX
XX Sequence 402 BP; 101 A; 93 C; 79 G; 129 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 345; DB 3; Length 402;
XX Best Local Similarity 100.0%; Pred. No. 4.2e-93;
XX Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 TTGCTGTAGAAATCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACT 60
DB 345 TTGCTGTAGAAATCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACT 286
QY 61 CATCGAACTTGGCTGTAGCGGATGGGAACCTGATGATTCCTCTGAAAATAAAAT 120
DB 285 CATCGAACTTGGCTGTAGCGGATGGGAACCTGATGATTCCTCTCTGAAAATAAAAT 226
QY 121 CACCAACTGTGCATTAAAGAGTTTTCAGGGTATAGACACATTTGAGACCAACTGCC 180
DB 225 CACCAACTGTGCATTAAAGAGTTTTCAGGGTATAGACACATTTGAGACCAACTGCC 166
QY 181 CACGGGAGGCTGTGGATAAACTATTCCAAAACCTTGTCTTTAATAAAGAACACATAGAG 240
DB 165 CACGGGAGGCTGTGGATAAACTATTCCAAAACCTTGTCTTTAATAAAGAACACATAGAG 106
QY 241 CGCCAAAAAAGGTGTGAGGAAAGATGGAGTGCACAAAGTTCCTAGACTACCTG 300
DB 105 CGCCAAAAAAGGTGTGAGGAAAGATGGAGTGCACAAAGTTCCTAGACTACCTG 46
QY 301 CAAGTATTTCTTGGTGTAAATAAACACCGAGTGGACACCGGAAAGT 345
DB 45 CAAGTATTTCTTGGTGTAAATAAACACCGAGTGGACACCGGAAAGT 1
```

Dd		146	CATCGAACTTGGCTGATAGCCGATGGGAACCTGTACTTCCTTTCAATAAATAAAAAAT	207
Qy		121	CACCAACTGTGCATTAAAGAAGTTTTTTCAGGGTATAGACACATTTGAAGAACCAAACCTGCC	180
Dd		206	CACCAACTGTGCATTAAAGAAGTTTTTTCAGGGTATAGACACATTTGAAGAACCAAACCTGCC	265
Qy		181	CACGGGAGCCTGTGGATAAACTATTCCAAAACCTTGCTTTTAATAAAGAACACATAGAG	240
Dd		266	CACGGGAGCCTGTGGATAAACTATTTCAAAACCTTGCTTTTAATAAAGAACACATAGAG	325
Qy		241	CGCAAAAAAAAAAGGTGTCAGAGAGAAAGATCGAGAGTGACAAGTTCCTAGACTACCCTG	300
Dd		326	CGCAAAAAAAAAAGGTGTCAGAGAGAAAGATCGAGAGTGACAAGTTCCTAGACTACCCTG	385
Qy		301	CAAGTATTTCTTGGTGTAAATAAACACCGAGTGGACACCGGAAAGT	345
Dd		386	CAAGTATTTCTTGGTGTAAATAAACACCGAGTGGACACCGGAAAGT	430
 RESULT 6 AAZ55547/c ID AAZ55547 standard; cDNA; 610 BP.				
XX	Key	AAC	AAZ55547;	
XX	CDS	AAZ55547;		
DT	Location/Qualifiers	(first entry)		
DE	Canine interleukin-5 (IL-5) cDNA complement.			
XX	Interleukin-5; IL-5; antibody; canine; inhibitor; immune response;			
KW	immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.			
OS	Canis familiaris.			
FX	Key	Location/Qualifiers		
FT	CDS	/tag= a		
FT	Product= "Canine IL-5"			
PN	WO9961618-A2.			
XX	02-DEC-1999.			
PF	28-MAY-1999;	99WO-USO11942.		
PR	29-MAY-1998;	98US-0087306P.		
PA	(HESK-) HESKA CORP.			
PI	Sim G, Yang S, Dreitz MJ, Wonderling RS;			
DR	WPI; 2000-072623/06.			
DR	P-PSDB; AA558219.			
XX	Nucleic acids encoding immunoregulatory proteins from cats or dogs,			
PT	useful for treating or preventing e.g. tumors or autoimmune disease.			
XX	Claim 1h; Page 223-224; 264pp; English.			
CC	Sequences AAZ55546-255551 represent cDNA sequences encoding canine			
CC	interleukin-5 (IL-5). The invention relates to canine IL-4, canine or			
CC	feline Flt-3 ligand, canine or feline CD40, canine or feline CD154 (CD40			
CC	ligand), canine IL-5, canine IL-13, feline interferon-alpha (IFN-alpha)			
CC	and feline granulocyte macrophage colony-stimulating factor (GM-CSF), and			
CC	nucleotides which encode these immunoregulatory proteins. The proteins,			
CC	their associated nucleic acids, specific antibodies and inhibitors may be			
CC	used as vaccines for therapeutic or prophylactic regulation of an immune			
CC	response in animals (particularly cats, dogs, horses and humans). They			
CC	may be used to treat autoimmune or infectious diseases including			
CC	allergies, tumours, inflammation and graft rejection, and to increase the			
CC	response from a co-administered antigen. The nucleotide sequences can			
CC	also be used for the recombinant production of a protein, while			
CC	nucleotide fragments are useful as probes, as amplification primers and			
CC	as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).			
CC	The proteins may be used to raise antibodies and to screen for modulators			
CC	of activity, while the antibodies may be used in detection, and in drug			
CC	targeting			
XX	Sequence 610 BP; 202 A; 114 C; 139 G; 155 T; 0 U; 0 Other;			
SQ	Query Match 100.0%; Score 345; DB 3; Length 610;			
	Best Local Similarity 100.0%; Pred. No. 4.9e-93;			
	Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
QY	1 TTTCGTGTAGAAATCCCAGATAGCTGGTGAGAGACCTTGACACTGCTCCACT	60		
Dd	86 TTTCGTGTAGAAATCCCAGATAGCTGGTGAGAGACCTTGACACTGCTCCACT	145		
QY	61 CATCGAACTTGGCTGATAGCCGATGGGAACCTGTACTTCCTTTCAATAAATAAAAAAT	120		

CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).
 CC The proteins may be used to raise antibodies and to screen for modulators
 CC of activity, while the antibodies may be used in detection, and in drug
 CC targeting

SQ Sequence 610 BP; 155 A; 139 C; 114 G; 202 T; 0 U; 0 Other;
 Query Match 100.0%; Score 345; DB 3; Length 610;
 Best Local Similarity 100.0%; Pred. No. 4.9e-93;
 Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTGCTGTAGAAATCCCATGATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACT 60
 DB 525 TTTGCTGTAGAAATCCCATGATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACT 466
 QY 61 CATCGAATCTGGCTGATAGCGGATGGAACTGATCTCTACTCTCTGAAATATAAAAT 120
 DB 465 CATCGAATCTGGCTGATAGCGGATGGAACTGATCTCTACTCTCTGAAATATAAAAT 406
 QY 121 CACCACTGTCATTAAGAGCTTTTCAGGGTATAGACACATTTGAAGAACCAACTGCC 180
 DB 405 CACCACTGTCATTAAGAGCTTTTCAGGGTATAGACACATTTGAAGAACCAACTGCC 346
 QY 181 CACGGGAGGCTGTGGATAAACTATTCCAAAACCTTCTTTTATAAAGAACACATAGAG 240
 DB 345 CACGGGAGGCTGTGGATAAACTATTCCAAAACCTTCTTTTATAAAGAACACATAGAG 286
 QY 241 CGCCAAAAAAGGCTGCAGAGAAAGATGGAGAGTGACAAAGTTCCTAGACTACCTG 300
 DB 285 CGCCAAAAAAGGCTGCAGAGAAAGATGGAGAGTGACAAAGTTCCTAGACTACCTG 226
 QY 301 CAAGTATTTCTTGGTGTAAATAAACACCGAGTGCACACCGGAAAGT 345
 DB 225 CAAGTATTTCTTGGTGTAAATAAACACCGAGTGCACACCGGAAAGT 181

RESULT 7
 AAF74300
 ID AAF74300 standard; DNA; 405 BP.
 AC AAF74300;
 XX
 DT 04-MAY-2001 (first entry)
 DE Canine interleukin-5 coding sequence #1.
 DE Dog; interleukin-5; IL-5; allergy; cancer; gene therapy;
 KW inflammatory reaction; ds.
 KW
 OS Canis sp.
 OS
 PN WO200111049-A2.
 PN
 PD 15-FEB-2001.
 PD
 XX 09-AUG-2000; 2000WO-US021651.
 XX
 PF 10-AUG-1999; 99US-00371615.
 XX
 PR (IDEX-) IDEX LAB INC.
 XX
 PA Guo H, Lawton R, Mermer B, Aiyappa AP;
 PI WPI; 2001-191542/19.
 XX
 DR P-PSDB; AAB72615.
 DR
 XX Novel canine interleukin 5 polynucleotide and polypeptides are used for
 PT generating antibodies which are useful in treating allergies in dogs.
 XX
 PS Claim 31; Page 46; 48pp; English.
 PS
 CC The present invention provides the protein and coding sequences of the
 CC canine interleukin-5 (IL-5) protein. This can be used to treat allergies.

CC cancer and inflammatory reactions in dogs. The present sequence is one
 CC version of the IL-5 coding sequence shown in the specification
 XX
 SQ Sequence 405 BP; 131 A; 77 C; 94 G; 103 T; 0 U; 0 Other;

Query Match 99.1%; Score 341.8; DB 4; Length 405;
 Best Local Similarity 99.4%; Pred. No. 3.8e-92;
 Matches 343; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TTTGCTGTAGAAATCCCATGATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACT 60
 DB 58 TTTGCTGTAGAAATCCCATGATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACT 117
 QY 61 CATCGAATCTGGCTGATAGCGGATGGAACTGATCTCTACTCTGAAATATAAAAT 120
 DB 118 CATCGAATCTGGCTGATAGCGGATGGAACTGATCTCTACTCTGAAATATAAAAT 177
 QY 121 CACCACTGTGCATTAAGAGCTTTTCAGGGTATAGACACATTTGAAGAACCAACTGCC 180
 DB 178 CACCACTGTGCATTAAGAGCTTTTCAGGGTATAGACACATTTGAAGAACCAACTGCC 237
 QY 181 CACGGGAGGCTGTGGATAAACTATTCCAAAACCTTCTTTTATAAAGAACACATAGAG 240
 DB 238 CACGGGAGGCTGTGGATAAACTATTCCAAAACCTTCTTTTATAAAGAACACATAGAG 297
 QY 241 CGCCAAAAAAGGCTGCAGAGAAAGATGGAGAGTGACAAAGTTCCTAGACTACCTG 300
 DB 298 CGCCAAAAAAGGCTGCAGAGAAAGATGGAGAGTGACAAAGTTCCTAGACTACCTG 357
 QY 301 CAAGTATTTCTTGGTGTAAATAAACACCGAGTGCACACCGGAAAGT 345
 DB 358 CAAGTATTTCTTGGTGTAAATAAACACCGAGTGCACACCGGAAAGT 402

RESULT 8
 AAZ44265
 ID AAZ44265 standard; DNA; 838 BP.
 AC AAZ44265;
 XX
 DT 31-MAR-2000 (first entry)
 DT
 XX Porcine IL-5 DNA.
 DE
 XX Pig; vaccine; cysticercosis; protective antigen; cCl; cC3; cC4; ss.
 KW tenial cysticercus; gamma interferon; IFN-gamma; interleukin 5; IL-5;
 XX
 OS Sus scrofa.
 OS
 XX CN1231339-A.
 XX
 PD 13-OCT-1999.
 XX
 PF 29-JAN-1999; 99CN-00113447.
 XX
 PR 29-JAN-1999; 99CN-00113447.
 XX
 PA (UYTW-) UNIV NO 2 MILITARY MEDICAL PLA.
 XX
 PI Sun S, Dai J;
 XX
 DR WPI; 2000-087904/08.
 XX
 PT Nucleic acid vaccine for cysticercosis co-contracted by human and pig.
 XX
 PS Claim 3; Page 9; 21pp; Chinese.

CC This invention describes a novel nucleic acid vaccine for preventing and
 CC curing human and porcine cysticercosis. The invention involves the formation
 CC of a eukaryotic expression plasmid from fusion transcript expression unit
 CC consisting of three protective antigen genes (cCl, cC3 and cC4) of pig
 CC tenial cysticercus and coexpression unit of related cell factor gamma
 CC interferon (IFN-gamma) and pork interleukin 5 (IL-5)] genes. The

CC Ovine IL-5 or IL-12 are used to treat and/or prevent infections in
CC livestock (esp. cows and sheep), particularly where the animals are
CC stressed, e.g. during transport. IL-5 and IL-12 can also be used as
CC adjuvants in vaccines for veterinary use (partic. weakly immunogenic
CC subunit or synthetic peptide vaccines). They may also be used to treat
CC cancer, immunosuppression and allergy. They may also be used to treat
CC reproductive system and to promote growth or early maturity. Optionally
CC interleukin can be delivered from constructs or delivery cells and
CC antibodies are useful in enzyme immunoassays for rapid diagnosis of
CC infection. The interleukins are immunopotentiators, especially IL-5
CC promotes growth of early haematopoietic progenitor cells and generation
CC of cytotoxic cells from thymocytes, also it stimulates production and
CC secretion of IgM and IgA (in synergism with bacterial endotoxin). IL-12
CC induces production of gamma-interferon by, and proliferation of, T and NK
CC cells and increases the (non-)specific cytolytic lymphocyte response. The
CC genetic constructs can also be used for in vitro production of IL-5 or -
CC 12. (Updated on 17-OCT-2003 to standardise OS field)

XX Sequence 399 BP; 130 A; 77 C; 93 G; 99 T; 0 U; 0 Other;

Query Match 79.7%; Score 274.8; DB 2; Length 399;

Best Local Similarity 87.7%; Pred. No. 4.3e-72;
Matches 300; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

QY 3 TGCTGTAGAAAAATCCCATGATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACTCA 62

Db 54 TGCTGTAGAAAGTACCATGATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACGCA 113

QY 63 TCGAACTTGCTGATAGCGGATGGGAACCTGATGATTCCTACTCCTGAAATTAATAATCA 122

Db 114 TCAAACTCTGCTGATAGGTGGAACCTTGATGATTCCTACTCCTGACATACAAATCA 173

QY 123 CCAACTCTGATTAAGAAAGTTTTCAGGGTATAGACACATTTGAAGAACCAACTGCCCA 182

Db 174 CCAACTATGATTAAGAAAGTTTTCAGGGATAGACACATTTGAAGAACTCAACTGCACA 233

QY 183 CGGGAGGCTGTGATGATTAATTCCTAAACTTGTCTTTAATAAAGAACACATAGAGCG 242

Db 234 AGGGATGCTGTGAAAAAATATTCGAAACTTGTCTTTAATAAAGAACATACATAGACCT 293

QY 243 CCAAAAAAAGGTGTCAGGAGAAATGAGAGTGGAGTGCACAAAGTCTCTAGACTACCTGCA 302

Db 294 CCAAAAAAAGAAAGTGTGGAGAGAAATGAGAGTGGAGTGCACAAATTCCTGACTACTGCA 353

QY 303 AGTATTTCCTGGTGTAAATCAACCGAGTGGACACCGGAAAG 344

Db 354 AGTATTCCTGGTGTGATAAACACAGAGTGGACGATGGAAG 395

RESULT 11

AAT50755

XX AAT50755 standard; DNA; 520 BP.

XX AAT50755;

XX 17-OCT-2003 (revised)

DT 24-SEP-1997 (first entry)

XX Ovine IL-5 gene.

XX Cytokine; ovine; sheep; interleukin-5; interleukin-12; IL-5; IL-12;

KW livestock; cow; stress; transport; vaccine adjuvant; veterinary; cancer;

KW immunosuppression; allergy; reproductive system; growth; early maturity;

KW antibody; diagnosis; immunopotentiator;

KW early haematopoietic progenitor cell; cytotoxic cell; thymocyte;

KW secretion; IgM; IgA; bacterial endotoxin; gamma-interferon; ss.

XX Ovis aries.

OS Location/Qualifiers

XX Key 46..444

FT CDS /tag= a

FT /product= "Ovine_IL-5"

FT

FT exon 46..183
FT /tag= b
FT /number= 1
FT exon 184..216
FT /tag= c
FT /number= 2
FT exon 217..345
FT /tag= d
FT /number= 3
FT exon 346..480
FT /tag= e
FT /number= 4

PN WO9700321-A1.

XX 03-JAN-1997.

XX 14-JUN-1996; 96WO-AU0000360.

XX 14-JUN-1995; 95AU-00003502.

PR 27-OCT-1995; 95AU-00006244.

XX (CSR) COMMONWEALTH SCI & IND RES ORG.

XX Seow H, Wood P;

XX WPI: 1997-077528/07.

DR P-PSDB; AAW08479.

XX Nucleic acid encoding ovine interleukin-5 or -12 - used as vaccine

PT adjuvants and to treat or prevent microbial infections in livestock.

PT Claim 6; Page 39-40; 78pp; English.

XX The sequences given in AAT50755-56 encode ovine interleukin-5 (IL-5).

XX Ovine IL-5 or IL-12 are used to treat and/or prevent infections in

CC livestock (esp. cows and sheep), particularly where the animals are

CC stressed, e.g. during transport. IL-5 and IL-12 can also be used as

CC adjuvants in vaccines for veterinary use (partic. weakly immunogenic

CC subunit or synthetic peptide vaccines). They may also be used to treat

CC cancer, immunosuppression and allergy. They may also be used to treat

CC reproductive system and to promote growth or early maturity. Optionally

CC interleukin can be delivered from constructs or delivery cells and

CC antibodies are useful in enzyme immunoassays for rapid diagnosis of

CC infection. The interleukins are immunopotentiators, especially IL-5

CC promotes growth of early haematopoietic progenitor cells and generation

CC of cytotoxic cells from thymocytes, also it stimulates production and

CC secretion of IgM and IgA (in synergism with bacterial endotoxin). IL-12

CC induces production of gamma-interferon by, and proliferation of, T and NK

CC cells and increases the (non-)specific cytolytic lymphocyte response. The

CC genetic constructs can also be used for in vitro production of IL-5 or -

CC 12. (Updated on 17-OCT-2003 to standardise OS field)

XX Sequence 520 BP; 166 A; 99 C; 124 G; 131 T; 0 U; 0 Other;

SQ Query Match 79.7%; Score 274.8; DB 2; Length 520;

Best Local Similarity 87.7%; Pred. No. 4.7e-72;

Matches 300; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

QY 3 TGCTGTAGAAAAATCCCATGATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACTCA 62

Db 99 TGCTGTAGAAAGTACCATGATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACGCA 158

QY 63 TCGAACTTGCTGATAGCGGATGGGAACCTGATGATTCCTACTCCTGAAATTAATAATCA 122

Db 159 TCAAACTCTGCTGATAGGTGGAACCTTGATGATTCCTACTCCTGACATACAAATCA 218

QY 123 CCAACTGTGCATTAAAGAAAGTTTTCAGGGTATAGACACATTTGAAGAACCAAACTGCCCA 182

Db 219 CCAACTATGATTAAGAAAGTTTTCAGGGATAGACACATTTGAAGAACTCAACTGCACA 278

QY 183 CGGGAGGCTGTGGATAAACTATTCCAAACTTGTCTTTAATAAAGAACACATAGAGCG 242

Db 279 AGGGATCTGTGAAAAAATATTCGGAACCTTCTCTTTAATAAAGATACATAGACCT 338
 Qy 243 CCAAAAAAAGGTGTGAGGAGAAAGATGAGAGTGCACAAAGTTCCTAGACTACCTGCA 302
 Db 339 CCAAAAAAGAGTGTGAGGAGAAAGATGAGAGTGCACAAATTCCTGACTACTGCA 398
 Qy 303 AGTATTTCTTGTGTAATAACACCGAGTGCACACCGGAAAG 344
 Db 399 AGTTTCTTCTGTGATAAACACAGAGTGCACGATGGAAG 440

RESULT 12

ID AAA34857 standard; DNA; 816 BP.
 AC AAA34857;

28-JUL-2000 (first entry)

Human adenosine receptor related polynucleotide SEQ ID NO:2546..

Human; adenosine receptor; low adenosine antisense oligonucleotide;
 phosphorothioate; impaired respiration; inflammation; allergy;
 allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
 antiasthmatic; cytoskeletal; cytoskeletal; analgesic; impaired airway;
 lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
 respiratory distress syndrome; pain; cystic fibrosis; emphysema;
 pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
 cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.

Homo sapiens.

WO200009525-A2.

24-FEB-2000.

03-AUG-1999; 99WO-US017712.

03-AUG-1998; 98US-0095212P.

(UYEC-) UNIV EAST CAROLINA.

Nyce JW;

WPI; 2000-205971/18.

New antisense oligonucleotides useful for treating e.g. pulmonary
 vasoconstriction, inflammation, allergies, asthma, hypertension,
 bronchitis, emphysema, respiratory distress syndrome, ischemia or
 cancers.

Disclosure; Page 716; 1343pp; English.

The present invention describes a new composition comprising an antisense
 oligonucleotide (ON) with low adenosine (up to 15%), which targets
 nucleic acids involved in bronchoconstriction, allergies, and/or
 inflammation. The ON can have antiinflammatory, antiasthmatic,
 antiasthmatic, cytoskeletal and analgesic activities. The compositions are
 useful for the treatment of diseases associated with inflammation,
 impaired airways, including lung disease and diseases whose secondary
 effects afflict the lungs of a subject. They can be used for treating
 e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma,
 fibrosis, pulmonary hypertension, emphysema, chronic obstructive
 pulmonary disease (COPD), and cancers such as leukaemias, lymphomas,
 carcinomas, and cancers which may metastasize to the lungs, including
 breast and prostate cancer. The reduction of the adenosine content of the
 ONs reduces side effects. The A-containing ONs break down with the
 release of deoxyadenosine which activates adenosine receptors causing
 bronchoconstriction and inflammation. AAA32313 to AAA35312 represent the
 nucleotide sequences given in the sequence listing from the present
 invention, which correspond to SEQ ID NO:1 to 2815, and then the last 185
 sequences are also called SEQ ID NO:1 to 185, but the sequences differ

CC from the previously named sequences. SEQ ID NO:11 to 1680 (AAA32323 to
 CC AAA33992) are specifically claimed ONs from the present invention. N.B.
 CC Sequences given in the disclosure of the present invention do not match
 CC up with their corresponding SEQ ID NO: sequences given in the sequence
 CC listing

XX
 SQ Sequence 816 BP; 277 A; 137 C; 164 G; 238 T; 0 U; 0 Other;

Query Match 67.1%; Score 231.4; DB 3; Length 816;

Best Local Similarity 80.4%; Pred. No. 5.4e-59; Indels 0; Gaps 0;

Matches 271; Conservative 0; Mismatches 66; Indels 0; Gaps 0;

Qy 9 AGAAAAATCCCATGATAGACTGGTGGCAGAGACCTTGACACTGTCTCTCATCGAAC 68

Db 110 AGAAATTCACCAAGTGCATTGGTGAAGAGACCTTGGCACTGCTTCTACTCATCGAAC 169

Qy 69 TTGGCTGATAGCGGATGGAACTGATGATTCCTACTCTCTGAAAATAAATACCAACT 128

Db 170 TCTGTGATAGCAATGAGACTCTGAGGATTCCTGTTCTGTACATAAATACCAACT 229

Qy 129 GTGCATTAAGAAGTTTTTTCAGGGTATAGACACATTCAGAAACCAACTGCCACGGGA 188

Db 230 GTGCATGAGAAATCTTTCAGGGAATAGGCACACTGGAGAGTCAACTGTGCAAGGGG 289

Qy 189 GGCTGTGATTAACATATTCCTCAAACTTGTCTTTTAAATAAGAACACATAGAGCGCCAAA 248

Db 250 TACTGTGGAAGACTTATTCAAAAAATTTGCTCTTAATAAGAAATACATTGACGGCCAAA 349

Qy 249 AAAAAGGTGTCCAGGAGAAAGTGCAGAGTGCACAAAGTTCCTAGACTACCTGCAAGTATT 308

Db 350 AAAAAGTGTGGAGAGAAAGACCGAGAGTAACCAATTCCTAGACTACCTGCAAGATT 409

Qy 309 TCTTGGTGTATAAACACCGAGTGCACACCGGAAAGT 345

Db 410 TCTTGGTGTATAAACACCGAGTGCATAATAGAAAGT 446

RESULT 13

ID AAA13338 standard; cDNA; 816 BP.

XX
 AC AAA13338;

25-JUL-2000 (first entry)

Human interleukin-5 (IL-5) nucleotide sequence.

Human; interleukin-5; IL-5; inflammatory disease; asthma; eczema;
 antisense oligonucleotide; allergic rhinitis; inflammatory skin disease;
 allergic conjunctivitis; inhibitor; ss.

Homo sapiens.

US6048726-A.

11-APR-2000.

15-MAY-1998; 98US-00079839.

15-MAY-1998; 98US-00079839.

(WELT/) WELTMAN J K.

(KARI/) KARIM A S.

Weltman JK, Karim AS;

WPI; 2000-302784/26.

Oligonucleotide comprising non-natural internucleoside linkage, useful
 for inhibiting interleukin-5 expression and treating inflammatory
 diseases, asthma, allergic rhinitis, allergic conjunctivitis.
 Disclosure; Col 3-4; 11pp; English.

	XX	This sequence represents the human interleukin-5 (IL-5) encoding nucleotide sequence. Interleukin-5 is involved in eosinophilic inflammation and inflammatory disorders. The present invention relates to an IL-5 antisense oligonucleotide (see AAL1337) which inhibits the expression of IL-5. The antisense oligonucleotide has at least one non-natural internucleoside linkage. The oligonucleotide is able to inhibit IL-5 secretion in a dose dependent manner, and is useful for inhibiting IL-5 expression and therefore treating inflammatory diseases, asthma, allergic rhinitis, allergic conjunctivitis and inflammatory skin diseases such as eczema
	XX	
	SQ	Sequence 816 BP; 277 A; 137 C; 164 G; 238 T; 0 U; 0 Other;
		Query Match 67.1%; Score 231.4; DB 3; Length 816;
		Best Local Similarity 80.4%; Pred. No. 5.4e-59;
		Matches 271; Conservative 0; Mismatches 66; Indels 0; Gaps 0;
QY	9	AGNAAATCCCATGAATAGACTGCTGGCAGAGACCTTGACACTGTCTTCCACTCATCGAAC 68
DB	110	AGNAAATTCCTCCCAAGTGCATTGGTGAAGAAGACCTTGGCACCTGCTTTTCTACTCATCGAAC 169
QY	69	T*GGCTGATAGGCGATGGGAACCTCATGATTCCTACTCTTGAAAATAAAAAATACCACAAC 128
DB	170	TCTGCTGATAGCCANTGACACTTCAGAGATTCCTGCTGTACATAAANTCACCACCT 229
QY	129	GTGCATTAAGAAGATTTTTTCAGGTPATAGACACATTTGAAGAACAAACCTGCCACGGGGA 188
DB	230	GTGCAC TGAAGAAATCTTTTCAGGGAATAGGCACACTTGGAGAGTCACAACTGTGCAAGGGG 289
QY	189	GGCTGTGGATAACTATTCCAAAACCTTGCTCTTTAATAAAGAACACATAGGGCCCAA 248
DB	290	TACTGTGGAAAGACTATTCAA AAAACCTTGCTCTTAATAAAGAAATACATTGACGCCCAA 349
QY	249	AAAAAGCTGTGAGGAGAAAGATGAGAGTGTGACAAAGTTCCCTAGACTACCTGCAAGTATT 308
DB	350	AAAAAGTGTGAGAGAGAAAGACGAGAGTAAACCAATTCCTAGACTACCTGCAAGAGTT 409
QY	309	TCTTGTGTAATAAACACCCGAGTGGACACCGGAAAGT 345
DB	410	TCTTGTGTAAATGAACACCGAGTGGATTAATAGAAAGT 446

RESULT 14

REF ID: AAF20979

ID AAF20979















































Best Local Similarity 80.4%; Pred. No. 5.4e-59;
Matches 271; Conservative 0; Mismatches 66; Indels 0; Gaps 0;

9 AGAATAATCCCATGAATAGACTGTGGCAGAGACCTTGACATGCTCTCCATCATCGAAC 68

XX
Human Law order

DE Human low adenoc

Low average m.w. \overline{M}_w \overline{M}_n \overline{M}_z

human: airway disorder: bronch

KW surfactant depletion: respira

X
A (IIVFC-) INTV EAST CAROLINA

A (NYCE-) UNIV EAST
A (NYCE/) NYCE J W.

[illegible]

Nyce JW:

WPI; 2000-679539/66.

Disclosure; Page 788; 1592pp; English.

The present invention describes low adenosine (A) content antisense oligonucleotides and compositions (I) comprising them. In the antisense oligonucleotides the A is replaced by a 'Universal' or alternative base. (I) can have respiratory, bronchodilator, antiinflammatory, analgesic, immunosuppressive, antiasthmatic, hypertensive and cytostatic activities. The antisense oligonucleotides and (I) can be used to down-regulate the expression and/or activity of target polypeptides associated with lung/respiratory disorders and malignancies, such as stimulating and activating peptide factors and transmitters, transcription factors, immunoglobulins and antibodies, antibody receptors, cytokines and chemokines, endogenously produced specific and non-specific enzymes, binding proteins, adhesion molecules and their receptors, cytokine and chemokine receptors, adenosine receptors, bradykinin receptors, central nervous system (CNS) and peripheral nervous and non-nervous system receptors, CNS and peripheral nervous and non-nervous system peptide transmitters, defensins, growth factors, vasoactive peptides and receptors, binding proteins and malignancy associated proteins. The antisense oligonucleotides may be used in this way to treat disorders including respiratory obstruction (especially pulmonary obstruction and/or bronchoconstriction) and/or lung inflammation, allergies (I) and/or surfactant hypoproduction which are associated with a disease or condition selected from pulmonary vasoconstriction, inflammation, allergies, asthma impeded respiration, respiratory distress syndrome (ARDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary hypertension, emphysema, chronic obstructive pulmonary disease (COPD), pulmonary transplantation rejection, pulmonary infections, bronchitis, and/or cancer. AAF18434 to AAF21543 represent human polynucleotide fragments and antisense oligonucleotides used in the exemplification of the present invention.

Sequence 816 BP: 277 A; 137 C; 164 G; 238 T; 0 U; 0 Other;

100

Query Match 67.1%; Score 231.4; DB 3; Length 816;

Best Local Similarity	80.4%	Pred. No. 5,4e-59;	
Matches 271;	Conservative	0;	Mismatches 66;
			Indels 0;
			Gaps 0

9 AGAATATCCCATGATATGACTGGTGGCAGAGACCTTGACACTGCTCTCCACTCATCGAAC 68

3 AGAATATCCACAAAGTGCATTTGGTGAAGAGACCTTGGCACTGCTTTCTACTCATCGAAC 169

110 AGAATATCCACAAAGTGCATTTGGTGAAGAGACCTTGGCACTGCTTTCTACTCATCGAAC 169

69 TTGGCTGATAGGCGATGGGAACCTGATGATTCTCTGAAATAATAAATCACCACCT 128

170 TCCTGTATAGCCAATGAGACTCTGAGATTCTGTTCTGTACATAAAATCACCACT 229

129 GTGCATTAAAGAAGTTTTTTCAGGGTATAGACACATTGAAGAACCAAACTGCCACGGGA 189

230 GTGCACTGAAGAAATCTTTCAGGGAAATAGGCACACTGGAGAGTCAAACTGTGCAAGGGG 289b

189 GGCTGTGGATAAACATATTCCTCCAAAACTTGTCTTTTATAAAGAACACATAGAGCGGCCAAAA 248

290 TACTGTGGAAGACTATTCAAAAATTGTCCTTAATAAAGAAATACATTGACGGCCAAA 349b

249 AAAAGGTGTCAGGAGAAAGATGGAGAGTGACAAAGTCTCTAGACTACCTGCAAGTATT 308

350 AAAAAAGTGTGGAGAGAAAGACGGAGAGTAACCAATTCCTAGACTACCTGCAAGAGTT 409db

309 TCTTGGTGTAATAAACACCGAGTGGACACCGGAAGT 345

A

RESULT 15

ABZ96673
ID ABZ96673 standard; DNA; 816 BP.

XX AC ABZ96673;

XX DT 17-OCT-2003 (first entry)

XX DE Human nucleic acid sequence.

XX KW Human; antisense; lung dysfunction; nasal airway dysfunction;
antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
XX KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
antisense gene therapy; respiratory; lung; adenosine sensitivity;
XX KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
lung inflammation; respiratory disease; ds.

XX OS Homo sapiens.

XX PN WO200285308-A2.

XX PD 31-OCT-2002.

XX PF 23-APR-2002; 2002WO-US013135.

XX PR 24-APR-2001; 2001US-0286137P.

XX PX (EPIC-) EPIGENESIS PHARM INC.

XX PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;

XX DR WPI; 2003-229219/22.

XX PT Pharmaceutical composition for treating ailments associated with impaired
respiration, has oligo(s) antisense to specific gene(s) or its
corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
ubiquinone.

XX PS Disclosure; SEQ ID NO 11915; 872pp; English.

XX CC The invention relates to a novel pharmaceutical composition, which has a
first active agent comprising an oligonucleotide antisense to the
initiation codon, coding region, 5' or 3' end genomic flanking regions,
5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
junctions of genes encoding a polypeptide associated with lung and/or
nasal airway dysfunction and a second active agent comprising an
antiinflammatory steroid and ubiquinone. A composition of the invention
has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
immunosuppressive, and cytostatic activity. The composition may have a
use in antisense gene therapy. The composition is useful for treating or
preventing a respiratory, lung or malignant disease or condition, also
for enhancing the prophylactic or therapeutic respiratory effect of an
antiinflammatory steroid in a subject, for reducing or depleting levels
of, or reducing sensitivity to adenosine, reducing levels of adenosine
receptor, producing bronchodilation, increasing levels of ubiquinone or
lung surfactant in a subject's tissue, or treating bronchoconstriction,
lung inflammation, lung allergies, or a respiratory disease or condition.
XX CC Note: The sequence data for this patent is not represented in the printed
specification, but was obtained in electronic format directly from WIPO
at ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 816 BP; 277 A; 137 C; 164 G; 238 T; 0 U; 0 Other;

Query Match 67.1%; Score 231.4; DB 7; Length 816;

Best Local Similarity 80.4%; Pred. No. 5.4e-59;

Matches 271; Conservative 0; Mismatches 66; Indels 0; Gaps 0;

QY 9 AGAAATCCCATGAATAGACTGTGGCAGAGACCTTGACACTGCTCCACTCATCGAAC 69

Db 110 AGAAATCCCATGAATAGACTGTGGCAGAGACCTTGACACTGCTCCACTCATCGAAC 169

QY	69	TTGGCTGATAGCGGATGGGAACCTGATGATTCTTACTCTCTGAAATAAAAAATCACTCAACT	128
Db	170	TCTGCTGATAGCCAAATGAGACTCTGAGGATTCTTCTGTATATAAAATCACCACACT	229
QY	129	GTGCATTAAAGAGTCTTTTTCAGGGTATAGACACATTTGAGAACCAAACTGCCACGGGA	188
Db	230	GTGCACCTGAAGAAATCTTTTCAGGGATAGGCACACTGGAGAGTCAAACTGTGCAAGGGG	289
QY	189	GGCTGTGGATAAACTATTTCAAAACCTTCTTTTAAATAAAGAACACATAGAGCGCCAAA	248
Db	290	TACTGTGGAAGACTATTTCAAAACCTTCTTTTAAATAAAGAAATACATTGACGGCCAAA	349
QY	249	AAAAAGGTGTGAGGAGAAAGATGGAGAGTGCACAAAGTTCTTAGACTACCTGCAAGTATT	308
Db	350	AAAAAAGTGTGAGAGAAAGACCGGAGAGTAAACCAATTCTTAGACTACCTGCAAGATT	409
QY	309	TCTTGTGTAAATAACACCGGAGTGGACACCGGAAAGT	345
Db	410	TCTTGTGTAAATGACACCGGAGTGGATAATAGAAAGT	446

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OM nucleic - nucleic search, using sw model

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Listing first 45 summaries

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- 39: em_htgo_hum:**
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- 41: em_htgo_other:**

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
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2	345	100.0	345	6	AR241541	AR241541 Sequence
3	345	100.0	345	6	AR254496	AR254496 Sequence
4	345	100.0	345	6	AR254497	AR254497 Sequence
5	345	100.0	345	6	BD211562	BD211562 Canine an
6	345	100.0	345	6	BD211563	BD211563 Canine an
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8	345	100.0	402	6	AR241539	AR241539 Sequence
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12	345	100.0	402	6	BD211561	BD211561 Canine an
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14	345	100.0	610	6	AR241536	AR241536 Sequence
15	345	100.0	610	6	AR241537	AR241537 Sequence
16	345	100.0	610	6	AR254492	AR254492 Sequence
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18	345	100.0	610	6	BD211558	BD211558 Canine an
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24	289.6	83.9	838	4	AF025436	AF025436 Felis cat
25	285.4	82.7	405	4	AF068770	AF068770 Felis cat
26	283.8	82.3	405	4	BTINTLEUS	Z67872 B.taurus mR
27	280	81.2	529	4	SSC133452	AJ133452 Sus scrof
28	278.4	80.7	405	4	SSC010088	U35038 Ovis aries
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32	234.6	68.0	405	9	AF294756	AF294756 Salmir s
33	231.4	67.1	405	9	CEYIN5A	L26033 Cercocebus
34	231.4	67.1	816	6	E01639	E01639 cDNA encodi
35	231.4	67.1	816	6	E13591	E13591 cDNA encodi
36	231.4	67.1	816	9	HSIL5R	X04688 Human mRNA
37	231.4	67.1	858	6	AX766521	AX766521 Sequence
38	231.4	67.1	858	6	AX766523	AX766523 Sequence
39	231.4	67.1	864	6	AX766525	AX766525 Sequence
40	231.4	67.1	864	6	AX766527	AX766527 Sequence
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ALIGNMENTS

RESULT 1
AR241540

LOCUS AR241540
DEFINITION Sequence 85 from patent US 6471957.
ACCESSION AR241540
VERSION AR241540.1 GI:27287249
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.

REFERENCE 1 (bases 1 to 345)

AUTHORS Sim.G.-K., Yang,S., Dreitz,M.J. and Wonderling,R.S.

TITLE Canine IL-4 immunoregulatory proteins and uses thereof

JOURNAL Patent: US 6471957-A 85 29-OCT-2002;

FEATURES Location/Qualifiers

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linear FAT 20-DEC-2002

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/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Query Match 100.0%; Score 345; DB 6; Length 345;
Best Local Similarity 100.0%; Pred. No. 3.3e-83;
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTGCTGTAGAAAATCCCATGATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACT 60
DB 1 TTTGCTGTAGAAAATCCCATGATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACT 60

QY 61 CATCGAACTTGGCTGATAGGCGATGGCACTGATGATTCCTACTCTCTGAAATATAAAT 120
DB 61 CATCGAACTTGGCTGATAGGCGATGGCACTGATGATTCCTACTCTCTGAAATATAAAT 120

QY 121 CACCAACTGTGCATTAAGAAGTTTTTTCAGGGTATAGACACATTGAAGAACCAACTGCC 180
DB 121 CACCAACTGTGCATTAAGAAGTTTTTTCAGGGTATAGACACATTGAAGAACCAACTGCC 180

QY 181 CACGGGAGGCTGGGATTAACCTATTCCTGCTCTTATTAAGAAGACACATAGAG 240
DB 181 CACGGGAGGCTGGGATTAACCTATTCCTGCTCTTATTAAGAAGACACATAGAG 240

QY 241 CGCCAAAAAAGAGTGTGAGGAGAAAGATGGAGAGTGACAAAGTTCTTAGACTACCTG 300
DB 241 CGCCAAAAAAGAGTGTGAGGAGAAAGATGGAGAGTGACAAAGTTCTTAGACTACCTG 300

QY 301 CAAGTATTTCTTGGTGTAAATAACACCGAGTGGACCCGGAAGT 345
DB 301 CAAGTATTTCTTGGTGTAAATAACACCGAGTGGACCCGGAAGT 345

RESULT 2
RE241541/c
LOCUS AR241541 345 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 87 from patent US 6471957.
ACCESSION AR241541
VERSION AR241541.1 GI:27287250
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 345)
AUTHORS Sim, G.-K., Yang, S., Dreitz, M.J. and Wonderling, R.S.
TITLE Canine IL-4 immunoregulatory proteins and uses thereof
JOURNAL Patent: US 6471957-A 87 29-Oct-2002;
FEATURES
source 1. .345
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Query Match 100.0%; Score 345; DB 6; Length 345;
Best Local Similarity 100.0%; Pred. No. 3.3e-83;
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTGCTGTAGAAAATCCCATGATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACT 60
DB 345 TTTGCTGTAGAAAATCCCATGATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACT 286

QY 61 CATCGAACTTGGCTGATAGGCGATGGCACTGATGATTCCTACTCTCTGAAATATAAAT 120
DB 285 CATCGAACTTGGCTGATAGGCGATGGCACTGATGATTCCTACTCTCTGAAATATAAAT 226

QY 121 CACCAACTGTGCATTAAGAAGTTTTTTCAGGGTATAGACACATTGAAGAACCAACTGCC 180
DB 225 CACCAACTGTGCATTAAGAAGTTTTTTCAGGGTATAGACACATTGAAGAACCAACTGCC 166

QY 181 CACGGGAGGCTGGGATTAACCTATTCCTGCTCTTATTAAGAAGACACATAGAG 240
DB 165 CACGGGAGGCTGGGATTAACCTATTCCTGCTCTTATTAAGAAGACACATAGAG 106

QY 241 CGCCAAAAAAGAGTGTGAGGAGAAAGATGGAGAGTGACAAAGTTCTTAGACTACCTG 300
DB 105 CGCCAAAAAAGAGTGTGAGGAGAAAGATGGAGAGTGACAAAGTTCTTAGACTACCTG 46

QY 301 CAAGTATTTCTTGGTGTAAATAACACCGAGTGGACCCGGAAGT 345
DB 45 CAAGTATTTCTTGGTGTAAATAACACCGAGTGGACCCGGAAGT 1

RESULT 3
AR254496 345 bp DNA linear PAT 20-DEC-2002
LOCUS AR254496
DEFINITION Sequence 85 from patent US 6482403.
ACCESSION AR254496
VERSION AR254496.1 GI:27303384
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 345)
AUTHORS Sim, G.-K., Yang, S., Dreitz, M.J. and Wonderling, R.S.
TITLE Canine IL-13 immunoregulatory proteins and uses thereof
JOURNAL Patent: US 6482403-A 85 19-NOV-2002;
FEATURES
source 1. .345
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Query Match 100.0%; Score 345; DB 6; Length 345;
Best Local Similarity 100.0%; Pred. No. 3.3e-83;
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTGCTGTAGAAAATCCCATGATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACT 60
DB 1 TTTGCTGTAGAAAATCCCATGATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACT 60

QY 61 CATCGAACTTGGCTGATAGGCGATGGCACTGATGATTCCTACTCTCTGAAATATAAAT 120
DB 61 CATCGAACTTGGCTGATAGGCGATGGCACTGATGATTCCTACTCTCTGAAATATAAAT 120

QY 121 CACCAACTGTGCATTAAGAAGTTTTTTCAGGGTATAGACACATTGAAGAACCAACTGCC 180
DB 121 CACCAACTGTGCATTAAGAAGTTTTTTCAGGGTATAGACACATTGAAGAACCAACTGCC 180

QY 181 CACGGGAGGCTGGGATTAACCTATTCCTGCTCTTATTAAGAAGACACATAGAG 240
DB 181 CACGGGAGGCTGGGATTAACCTATTCCTGCTCTTATTAAGAAGACACATAGAG 240

QY 241 CGCCAAAAAAGAGTGTGAGGAGAAAGATGGAGAGTGACAAAGTTCTTAGACTACCTG 300
DB 241 CGCCAAAAAAGAGTGTGAGGAGAAAGATGGAGAGTGACAAAGTTCTTAGACTACCTG 300

QY 301 CAAGTATTTCTTGGTGTAAATAACACCGAGTGGACCCGGAAGT 345
DB 301 CAAGTATTTCTTGGTGTAAATAACACCGAGTGGACCCGGAAGT 345

RESULT 4
AR254497/c
LOCUS AR254497 345 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 87 from patent US 6482403.
ACCESSION AR254497
VERSION AR254497.1 GI:27303385
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 345)
AUTHORS Sim, G.-K., Yang, S., Dreitz, M.J. and Wonderling, R.S.
TITLE Canine IL-13 immunoregulatory proteins and uses thereof
JOURNAL Patent: US 6482403-A 87 19-NOV-2002;

FEATURES		Location/Qualifiers	
source		1. .345	
		/organism="unknown"	
		/mol_type="genomic DNA"	
ORIGIN			
Query Match 100.0%; Score 345; DB 6; Length 345;			
Best Local Similarity 100.0%; Pred. No. 3.3e-83;			
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
QY	1	TTTGTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACT	60
DB	345	TTTGTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACT	286
QY	61	CATCGAACTTGGCTGATAGCGATGGCAACCTGATGATTCCTACTCCTGAAAAATAAAAT	120
DB	285	CATCGAACTTGGCTGATAGCGATGGCAACCTGATGATTCCTACTCCTGAAAAATAAAAT	226
QY	121	CACCAACTGTGCATTAAGAAGTTTTTCAGGGTATAGACACATTTGAAGAACCAACTGCC	180
DB	225	CACCAACTGTGCATTAAGAAGTTTTTCAGGGTATAGACACATTTGAAGAACCAACTGCC	166
QY	181	CACGGGAGGCTGTGGATAAATCTTCCAAAACCTTGCTTTAATAAAGAACACATAGAG	240
DB	165	CACGGGAGGCTGTGGATAAATCTTCCAAAACCTTGCTTTAATAAAGAACACATAGAG	106
QY	241	CGCCAAAAAAGGCTGCAGGAGAAAGATGGAGAGTGACAAAGTTCTCTAGACTACCTG	300
DB	105	CGCCAAAAAAGGCTGCAGGAGAAAGATGGAGAGTGACAAAGTTCTCTAGACTACCTG	46
QY	301	CAAGTATTTCTTGGTGTATTAACACCGAGTGGACACCGGAAAGT	345
DB	45	CAAGTATTTCTTGGTGTATTAACACCGAGTGGACACCGGAAAGT	1
RESULT 5			
BD211562			
LOCUS			
DEFINITION			
Canine and feline immunoregulatory proteins, nucleic acid molecules			
and method of using the same.			
ACCESSION			
BD211562			
VERSION			
BD211562.1 GI:33021332			
KEYWORDS			
JP 2002516104-A/68.			
SOURCE			
Canis familiaris (dog)			
ORGANISM			
Canis familiaris			
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.			
REFERENCE			
1 (bases 1 to 345)			
Sim,G., Yang,S., Dreitz,M.J. and Wonderling,R.S.			
Canine and feline immunoregulatory proteins, nucleic acid molecules			
and method of using the same			
Patent: JP 2002516104-A 68 04-JUN-2002;			
JOURNAL			
HESKA CORP			
COMMENT			
OS Canis familiaris (dog)			
PN JP 2002516104-A/68			
PD 04-JUN-2002			
PF 28-MAY-1999 JP 2000551002			
PR 29-MAY-1998 US 60/087306			
PI GEKKEE SIM,SHUMIN YANG,MATTHEW J DREITZ,RAMANI S WONDERLING PC			
C12N15/09,A61K31/7088,A61K38/00,A61K39/00,A61K39/395,			
PC A61K39/395,			
PC A61K45/00,A61K48/00,A61P37/02,A61P37/04,C07K14/475,C07K14/535,			
PC C07K14/54,			
PC C07K14/56,C07K16/24,C07K16/28,C12N1/21,C12N5/10, PC			
G01N33/15,			
PC G01N33/50,C12N15/00,A61K37/02,A61K37/66,C12N5/00 CC Canine			
and feline immunoregulatory proteins, nucleic acid			
molecules and			
CC method of using the same			
FH Key Location/Qualifiers			
(1)..(345).			
FT CDS Location/Qualifiers			
1. .345			
FEATURES			
source			

FEATURES		Location/Qualifiers	
source		1. .345	
		/organism="Canis familiaris"	
		/mol_type="genomic DNA"	
		/db_xref="taxon:9615"	
ORIGIN			
Query Match 100.0%; Score 345; DB 6; Length 345;			
Best Local Similarity 100.0%; Pred. No. 3.3e-83;			
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
QY	1	TTTGTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACT	60
DB	1	TTTGTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACT	60
QY	61	CATCGAACTTGGCTGATAGCGATGGGAACTGATGATTCCTACTCCTGAAAAATAAAAT	120
DB	61	CATCGAACTTGGCTGATAGCGATGGGAACTGATGATTCCTACTCCTGAAAAATAAAAT	120
QY	121	CACCAACTGTGCATTAAGAAGTTTTTCAGGGTATAGACACATTTGAAGAACCAACTGCC	180
DB	121	CACCAACTGTGCATTAAGAAGTTTTTCAGGGTATAGACACATTTGAAGAACCAACTGCC	180
QY	181	CACGGGGAGGCTGTGGATAAATCTTCCAAAACCTTGCTTTAATAAAGAACACATAGAG	240
DB	181	CACGGGGAGGCTGTGGATAAATCTTCCAAAACCTTGCTTTAATAAAGAACACATAGAG	240
QY	241	CGCCAAAAAAGGCTGCAGGAGAAAGATGGAGAGTGACAAAGTTCTCTAGACTACCTG	300
DB	241	CGCCAAAAAAGGCTGCAGGAGAAAGATGGAGAGTGACAAAGTTCTCTAGACTACCTG	300
QY	301	CAAGTATTTCTTGGTGTATTAACACCGAGTGGACACCGGAAAGT	345
DB	301	CAAGTATTTCTTGGTGTATTAACACCGAGTGGACACCGGAAAGT	345
RESULT 6			
BD211563/c			
LOCUS			
DEFINITION			
Canine and feline immunoregulatory proteins, nucleic acid molecules			
and method of using the same.			
ACCESSION			
BD211563			
VERSION			
BD211563.1 GI:33021333			
KEYWORDS			
JP 2002516104-A/69.			
SOURCE			
Canis familiaris (dog)			
ORGANISM			
Canis familiaris			
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.			
REFERENCE			
1 (bases 1 to 345)			
Sim,G., Yang,S., Dreitz,M.J. and Wonderling,R.S.			
Canine and feline immunoregulatory proteins, nucleic acid molecules			
and method of using the same			
Patent: JP 2002516104-A 69 04-JUN-2002;			
JOURNAL			
HESKA CORP			
COMMENT			
OS Canis familiaris (dog)			
PN JP 2002516104-A/69			
PD 04-JUN-2002			
PF 28-MAY-1999 JP 2000551002			
PR 29-MAY-1998 US 60/087306			
PI GEKKEE SIM,SHUMIN YANG,MATTHEW J DREITZ,RAMANI S WONDERLING PC			
C12N15/09,A61K31/7088,A61K38/00,A61K39/00,A61K39/395,			
PC A61K39/395,			
PC A61K45/00,A61K48/00,A61P37/02,A61P37/04,C07K14/475,C07K14/535,			
PC C07K14/54,			
PC C07K14/56,C07K16/24,C07K16/28,C12N1/21,C12N5/10, PC			
G01N33/15,			
PC G01N33/50,C12N15/00,A61K37/02,A61K37/66,C12N5/00 CC Canine			
and feline immunoregulatory proteins, nucleic acid			
molecules and			
CC method of using the same			
FH Key Location/Qualifiers			
1. .345			
FT source			
/organism='Canis familiaris (dog)'			
Location/Qualifiers			
1. .345			

ORIGIN
 /organism="Canis familiaris"
 /mol_type="genomic DNA"
 /db_xref="taxon:9615"

Query Match 100.0%; Score 345; DB 6; Length 345;
 Best Local Similarity 100.0%; Pred. No. 3.2e-83;
 Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTGCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACT 60
 DB 345 TTTGCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACT 286

QY 61 CATCGAACTTGGCTGTAGAGCGATGGGAACCTGATGATTTCTTCTTCTGAAATATAAAT 120
 DB 285 CATCGAACTTGGCTGTAGAGCGATGGGAACCTGATGATTTCTTCTTCTGAAATATAAAT 226

QY 121 CACCAACTGTGCATTAAAGAGTTTTCAGGGTATAGACACATTGAAGAACCAACTGCC 180
 DB 225 CACCAACTGTGCATTAAAGAGTTTTCAGGGTATAGACACATTGAAGAACCAACTGCC 166

QY 181 CACGGGAGGCTGGGATAAATCTTCCAAAACCTGTCTTTTAATAAAGAACACATAGAG 240
 DB 165 CACGGGAGGCTGGGATAAATCTTCCAAAACCTGTCTTTTAATAAAGAACACATAGAG 106

QY 241 CGCCAAAAAAGGCTGTGAGGAGAAAGATGAGAGTGGACAAAGTTCTAGACTACCTG 300
 DB 105 CGCCAAAAAAGGCTGTGAGGAGAAAGATGAGAGTGGACAAAGTTCTAGACTACCTG 46

QY 301 CAAGTATTTCTTGGTGTAAATAAACACCGAGTGGACCGGAAAGT 345
 DB 45 CAAGTATTTCTTGGTGTAAATAAACACCGAGTGGACCGGAAAGT 1

RESULT 7
 AR241538
 LOCUS AR241538 402 bp DNA linear PAT 20-DEC-2002
 DEFINITION Sequence 83 from patent US 6471957.
 ACCESSION AR241538
 VERSION AR241538.1 GI:27287247
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 UNCLASSIFIED.
 REFERENCE 1 (bases 1 to 402)
 AUTHORS Sim,G.-K., Yang,S., Dreitz,M.J. and Wonderling,R.S.
 TITLE Canine IL-4 immunoregulatory proteins and uses thereof
 JOURNAL Patent: US 6471957-A 83 29-OCT-2002;
 FEATURES Location/Qualifiers
 source 1..402
 /organism="unknown"
 /mol_type="genomic DNA"

Query Match 100.0%; Score 345; DB 6; Length 402;
 Best Local Similarity 100.0%; Pred. No. 3.2e-83;
 Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTGCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACT 60
 DB 58 TTTGCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACT 117

QY 61 CATCGAACTTGGCTGTAGAGCGATGGGAACCTGATGATTTCTTCTTCTGAAATATAAAT 120
 DB 118 CATCGAACTTGGCTGTAGAGCGATGGGAACCTGATGATTTCTTCTTCTGAAATATAAAT 177

QY 121 CACCAACTGTGCATTAAAGAGTTTTCAGGGTATAGACACATTGAAGAACCAACTGCC 180
 DB 178 CACCAACTGTGCATTAAAGAGTTTTCAGGGTATAGACACATTGAAGAACCAACTGCC 237

QY 181 CACGGGAGGCTGGGATAAATCTTCCAAAACCTGTCTTTTAATAAAGAACACATAGAG 240
 DB 238 CACGGGAGGCTGGGATAAATCTTCCAAAACCTGTCTTTTAATAAAGAACACATAGAG 297

QY 241 CGCCAAAAAAGGCTGTGAGGAGAAAGATGAGAGTGGACAAAGTTCTTAGACTACCTG 300
 DB 298 CGCCAAAAAAGGCTGTGAGGAGAAAGATGAGAGTGGACAAAGTTCTTAGACTACCTG 357

QY 301 CAAGTATTTCTTGGTGTAAATAAACACCGAGTGGACCGGAAAGT 345
 DB 358 CAAGTATTTCTTGGTGTAAATAAACACCGAGTGGACCGGAAAGT 402

RESULT 8
 AR241539/c
 LOCUS AR241539 402 bp DNA linear PAT 20-DEC-2002
 DEFINITION Sequence 84 from patent US 6471957.
 ACCESSION AR241539
 VERSION AR241539.1 GI:27287248
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 UNCLASSIFIED.
 REFERENCE 1 (bases 1 to 402)
 AUTHORS Sim,G.-K., Yang,S., Dreitz,M.J. and Wonderling,R.S.
 TITLE Canine IL-4 immunoregulatory proteins and uses thereof
 JOURNAL Patent: US 6471957-A 84 29-OCT-2002;
 FEATURES Location/Qualifiers
 source 1..402
 /organism="unknown"
 /mol_type="genomic DNA"

Query Match 100.0%; Score 345; DB 6; Length 402;
 Best Local Similarity 100.0%; Pred. No. 3.2e-83;
 Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTGCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACT 60
 DB 345 TTTGCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACT 286

QY 61 CATCGAACTTGGCTGTAGAGCGATGGGAACCTGATGATTTCTTCTTCTGAAATATAAAT 120
 DB 285 CATCGAACTTGGCTGTAGAGCGATGGGAACCTGATGATTTCTTCTTCTGAAATATAAAT 226

QY 121 CACCAACTGTGCATTAAAGAGTTTTCAGGGTATAGACACATTGAAGAACCAACTGCC 180
 DB 225 CACCAACTGTGCATTAAAGAGTTTTCAGGGTATAGACACATTGAAGAACCAACTGCC 166

QY 181 CACGGGAGGCTGGGATAAATCTTCCAAAACCTGTCTTTTAATAAAGAACACATAGAG 240
 DB 165 CACGGGAGGCTGGGATAAATCTTCCAAAACCTGTCTTTTAATAAAGAACACATAGAG 106

QY 241 CGCCAAAAAAGGCTGTGAGGAGAAAGATGAGAGTGGACAAAGTTCTTAGACTACCTG 300
 DB 105 CGCCAAAAAAGGCTGTGAGGAGAAAGATGAGAGTGGACAAAGTTCTTAGACTACCTG 46

QY 301 CAAGTATTTCTTGGTGTAAATAAACACCGAGTGGACCGGAAAGT 345
 DB 45 CAAGTATTTCTTGGTGTAAATAAACACCGAGTGGACCGGAAAGT 1

RESULT 9
 AR254494
 LOCUS AR254494 402 bp DNA linear PAT 20-DEC-2002
 DEFINITION Sequence 83 from patent US 6482403.
 ACCESSION AR254494
 VERSION AR254494.1 GI:27303382
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 UNCLASSIFIED.
 REFERENCE 1 (bases 1 to 402)
 AUTHORS Sim,G.-K., Yang,S., Dreitz,M.J. and Wonderling,R.S.
 TITLE Canine IL-13 immunoregulatory proteins and uses thereof
 JOURNAL Patent: US 6482403-A 83 19-NOV-2002;

FEATURES Location/Qualifiers
source 1..402
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match 100.0%; Score 345; DB 6; Length 402;
Best Local Similarity 100.0%; Pred. No. 3.2e-83;
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTCGTGTAGAAATCCCATGAATAGACTGGTGGCGAGACCTTGACACTGCTCTCCACT 60
DB 58 TTTCGTGTAGAAATCCCATGAATAGACTGGTGGCGAGACCTTGACACTGCTCTCCACT 117
QY 61 CATCGAACTTGGCTGTAGAGCGATGGGAACCTCATGATTCCTACTCTGAAATAAAAT 120
DB 118 CATCGAACTTGGCTGTAGAGCGATGGGAACCTCATGATTCCTACTCTGAAATAAAAT 177
QY 121 CACCAACTGTGCATTAAAGAAGTTTTTCAGGGTATAGACACATTGAAGAACCAAACTGCC 180
DB 178 CACCAACTGTGCATTAAAGAAGTTTTTCAGGGTATAGACACATTGAAGAACCAAACTGCC 237
QY 181 CACGGGAGGCTGTGGATAAACAATTCCTCAAACTTGCTTTTAATAAAGAACACATAGAG 240
DB 238 CACGGGAGGCTGTGGATAAACAATTCCTCAAACTTGCTTTTAATAAAGAACACATAGAG 297
QY 241 CGCCAAAAAAGGTGTGCAGGAGAAAGATGAGAGTGAACAAAGTTCCCTAGACTACCTG 300
DB 298 CGCCAAAAAAGGTGTGCAGGAGAAAGATGAGAGTGAACAAAGTTCCCTAGACTACCTG 357
QY 301 CAAGTATTTCTTGTTGTAATAAACAACCGAGTGGACACCGGAAAGT 345
DB 358 CAAGTATTTCTTGTTGTAATAAACAACCGAGTGGACACCGGAAAGT 402

RESULT 10
AR254495/c
LOCUS AR254495 402 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 84 from patent US 6482403.
ACCESSION AR254495
VERSION AR254495.1 GI:27303383
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 402)
AUTHORS Sim,G.-K., Yang,S., Dreitz,M.J. and Wonderling,R.S.
TITLE Caniney IL-13 immunoregulatory proteins and uses thereof
JOURNAL Patent: US 6482403-A 84 19-NOV-2002;
FEATURES Location/Qualifiers
source 1..402
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match 100.0%; Score 345; DB 6; Length 402;
Best Local Similarity 100.0%; Pred. No. 3.2e-83;
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTCGTGTAGAAATCCCATGAATAGACTGGTGGCGAGACCTTGACACTGCTCTCCACT 60
DB 345 TTTCGTGTAGAAATCCCATGAATAGACTGGTGGCGAGACCTTGACACTGCTCTCCACT 286
QY 61 CATCGAACTTGGCTGTAGAGCGATGGGAACCTCATGATTCCTACTCTGAAATAAAAT 120
DB 285 CATCGAACTTGGCTGTAGAGCGATGGGAACCTCATGATTCCTACTCTGAAATAAAAT 226
QY 121 CACCAACTGTGCATTAAAGAAGTTTTTCAGGGTATAGACACATTGAAGAACCAAACTGCC 180
DB 225 CACCAACTGTGCATTAAAGAAGTTTTTCAGGGTATAGACACATTGAAGAACCAAACTGCC 166
QY 181 CACGGGAGGCTGTGGATAAACAATTCCTCAAACTTGCTTTTAATAAAGAACACATAGAG 240

DB 165 CACGGGAGGCTGTGGATAAACAATTCCTCAAACTTGCTTTTAATAAAGAACACATAGAG 106
QY 241 CGCCAAAAAAGGTGTGCAGGAGAAAGATGAGAGTGAACAAAGTTCCCTAGACTACCTG 300
DB 105 CGCCAAAAAAGGTGTGCAGGAGAAAGATGAGAGTGAACAAAGTTCCCTAGACTACCTG 46
QY 301 CAAGTATTTCTTGTTGTAATAAACAACCGAGTGGACACCGGAAAGT 345
DB 45 CAAGTATTTCTTGTTGTAATAAACAACCGAGTGGACACCGGAAAGT 1

RESULT 11
BD211560 402 bp DNA linear PAT 17-JUL-2003
LOCUS BD211560
DEFINITION Canine and feline immunoregulatory proteins, nucleic acid molecules and method of using the same.
ACCESSION BD211560
VERSION BD211560.1 GI:33021330
KEYWORDS JP 2002516104-A/66.
SOURCE Canis familiaris (dog)
ORGANISM Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE 1 (bases 1 to 402)
AUTHORS Sim,G., Yang,S., Dreitz,M.J. and Wonderling,R.S.
TITLE Canine and feline immunoregulatory proteins, nucleic acid molecules and method of using the same
JOURNAL Patent: JP 2002516104-A 66 04-JUN-2002;
COMMENT HESKA CORP
OS Canis familiaris (dog)
PN JP 2002516104-A/66
PD 04-JUN-2002
PF 28-MAY-1999 JP 2000551002
PR 29-MAY-1998 US 60/087306
PI GEKKEE SIM,SHUMIN YANG,MATTHEW J DREITZ,RAMANI S WONDERLING PC C12N15/09,A61K31/7088,A61K38/00,A61K38/21,A61K39/00,A61K39/395,A61K39/395.
PC A61K35/00,A61K48/00,A61P37/02,A61P37/04,C07K14/475,C07K14/535,C07K14/54,C07K14/56,C07K14/705,C07K16/24,C07K16/28,C12N1/21,C12N5/10,PC G01N33/50,C12N15/00,A61K37/02,A61K37/66,C12N5/00 CC Canine and feline immunoregulatory proteins, nucleic acid CC molecules and method of using the same
FH Key Location/Qualifiers
FT source 1..402
FT /organism="Canis familiaris (dog)".
FEATURES Location/Qualifiers
source 1..402
/organism="Canis familiaris"
/mol_type="genomic DNA"
/db_xref="taxon:9615"

ORIGIN
Query Match 100.0%; Score 345; DB 6; Length 402;
Best Local Similarity 100.0%; Pred. No. 3.2e-83;
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTCGTGTAGAAATCCCATGAATAGACTGGTGGCGAGACCTTGACACTGCTCTCCACT 60
DB 58 TTTCGTGTAGAAATCCCATGAATAGACTGGTGGCGAGACCTTGACACTGCTCTCCACT 117
QY 61 CATCGAACTTGGCTGTAGAGCGATGGGAACCTCATGATTCCTACTCTGAAATAAAAT 120
DB 118 CATCGAACTTGGCTGTAGAGCGATGGGAACCTCATGATTCCTACTCTGAAATAAAAT 177
QY 121 CACCAACTGTGCATTAAAGAAGTTTTTCAGGGTATAGACACATTGAAGAACCAAACTGCC 180
DB 178 CACCAACTGTGCATTAAAGAAGTTTTTCAGGGTATAGACACATTGAAGAACCAAACTGCC 237
QY 181 CACGGGAGGCTGTGGATAAACAATTCCTCAAACTTGCTTTTAATAAAGAACACATAGAG 240

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Db      238  CACGGGAGGCTGTGGATAAATATTCCAAAACCTTGTCTTTAATAAAGAACACATAGAG 297
Qy      241  CGCCAAAAAAGAGTGTGAGGAGAAAGATGGAGAGTGACAAAGTTCTTAGACTACCTG 300
Db      298  CGCCAAAAAAGAGTGTGAGGAGAAAGATGGAGAGTGACAAAGTTCTTAGACTACCTG 357
Qy      301  CAAGTATTCTTGGTGTAAATAACACCGAGTGGACACCGGAAAGT 345
Db      358  CAAGTATTCTTGGTGTAAATAACACCGAGTGGACACCGGAAAGT 402

RESULT 12
BD211561/c
LOCUS      402 bp DNA linear PAT 17-JUL-2003
DEFINITION Canine and feline immunoregulatory proteins, nucleic acid molecules
and method of using the same.
ACCESSION BD211561
VERSION    BD211561.1 GI:33021331
KEYWORDS   JP 2002516104-A/67.
SOURCE     Canis familiaris (dog)
ORGANISM   Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE 1 (bases 1 to 402)
AUTHORS   S.M.G., Yang,S., Dreitz,M.J. and Wonderling,R.S.
TITLE      Canine and feline immunoregulatory proteins, nucleic acid molecules
and method of using the same
JOURNAL    Patent: JP 2002516104-A 67 04-JUN-2002;
HESKA CORP
COMMENT    OS Canis familiaris (dog)
PN JP 2002516104-A/67
PD 04-JUN-2002
PF 28-MAY-1999 JP 2000551002
PI 29-MAY-1998 US 60/087306
PR GEKKEE SIM, SHUMIN YANG, MATTHEW J DREITZ, RAWANI S WONDERLING PC
C12N15/09, A61K31/7088, A61K38/00, A61K38/21, A61K39/00, A61K39/395,
PC A61K39/395,
PC A61K45/00, A61K48/00, A61P37/02, A61P37/04, C07K14/475, C07K14/535,
PC C07K14/54,
PC C07K14/56, C07K14/705, C07K16/24, C07K16/28, C12N1/21, C12N5/10, PC
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PC G01N33/50, C12N15/00, A61K37/02, A61K37/66, C12N5/00 CC Canine
and feline immunoregulatory proteins, nucleic acid CC
molecules and method of using the same
CC method of using the same
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Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DEFINITION Canis familiaris interleukin-5 mRNA, complete cds.
ACCESSION AF331919
VERSION    AF331919.1 GI:15919180
KEYWORDS
SOURCE     Canis familiaris (dog)
ORGANISM   Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE 1 (bases 1 to 610)
AUTHORS   Yang,S., Sellins,K.S., Weber,E. and McCall,C.
TITLE      Canine interleukin-5: molecular characterization of the gene and
expression of biologically active recombinant protein
JOURNAL    J. Interferon Cytokine Res. 21 (6), 361-367 (2001)
MEDLINE    21334408
PUBMED     11440633
REFERENCE 2 (bases 1 to 610)
AUTHORS   Yang,S.
TITLE      Direct Submission
JOURNAL    Submitted (22-DEC-2000) Immunology, Heska Corporation, 1613
Prospect Parkway, Ft Collins, CO 80525, USA
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DEFINITION Sequence 80 from patent US 6471957.
ACCESSION AR241536
VERSION AR241536.1 GI:27287245
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 610)
AUTHORS Sim,G.-K., Yang,S., Dretz,M.J. and Wonderling,R.S.
TITLE Canine IL-4 immunoregulatory proteins and uses thereof
JOURNAL Patent: US 6471957-A 80 29-OCT-2002;
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DEFINITION Sequence 82 from patent US 6471957.
ACCESSION AR241537
VERSION AR241537.1 GI:27287246
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 610)
AUTHORS Sim,G.-K., Yang,S., Dretz,M.J. and Wonderling,R.S.
TITLE Canine IL-4 immunoregulatory proteins and uses thereof
JOURNAL Patent: US 6471957-A 82 29-OCT-2002;
FEATURES Location/Qualifiers
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Best Local Similarity 100.0%; Pred. NO. 3.1e-83;
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Db 345 CACGGGAGCTGTGGTAACTATTCCAAACTTGTCTTTAATAAAGAACACATAGAG 286
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

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Minimum DB seq length: 0

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SUMMARIES

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4	600.6	36.2	3230	17	US-10-679-532-78
5	406	24.5	671	9	US-09-755-633-21
6	171.8	10.4	610	9	US-09-755-633-4
7	171.8	10.4	610	9	US-09-755-633-6
8	171.8	10.4	610	15	US-10-218-654-80
9	171.8	10.4	610	15	US-10-218-654-82
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32 89 5.4 864 15 US-10-295-074-12 Sequence 12, Appl
33 89 5.4 864 15 US-10-295-074-14 Sequence 14, Appl
34 61.8 3.7 7348 13 US-10-221-714A-57 Sequence 57, Appl
35 61.2 3.7 4661 17 US-10-433-793-52 Sequence 52, Appl
36 61.2 3.7 3673778 15 US-10-312-841-1 Sequence 1, Appl
37 60.8 3.7 6876 15 US-10-311-455-954 Sequence 954, Appl
38 60.6 3.7 6280 17 US-10-240-589C-74 Sequence 74, Appl
39 60 3.6 10328 15 US-10-311-455-1517 Sequence 1517, Appl
40 58.4 3.5 6365 15 US-10-311-455-98 Sequence 98, Appl
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ALIGNMENTS

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US-09-755-633-18
; Sequence 18, Application US/09755633
; Patent No. US20020127200A1
; GENERAL INFORMATION:
; APPLICANT: Yang, Shumin
; APPLICANT: McCall, Catherine A.
; APPLICANT: Weber, Eric R.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; FILE REFERENCE: IM-2-C1-C1
; CURRENT APPLICATION NUMBER: US/09755,633
; CURRENT FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: 09/322,409
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/087,306
; PRIOR FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
; LENGTH: 1658
; TYPE: DNA
; ORGANISM: Canis familiaris
; FEATURE:
; NAME/KEY: Intron
; LOCATION: (171)..(373)
; NAME/KEY: Intron
; LOCATION: (407)..(1275)
; NAME/KEY: Intron
; LOCATION: (1405)..(1522)
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RESULT 2

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; Patent No. US20020127200A1
; GENERAL INFORMATION:
; APPLICANT: Yang, Shumin
; APPLICANT: McCall, Catherine A.
; APPLICANT: Weber, Eric R.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; FILE OF INVENTION: ACID MOLECULES, AND USES THEREOF
; FILE REFERENCE: IM-2-C1-C1
; CURRENT APPLICATION NUMBER: US/09/755,633
; PRIOR FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: 09/322,409
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/087,306
; PRIOR FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.1
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; LENGTH: 1658
; TYPE: DNA
; ORGANISM: Canis familiaris
US-09-755-633-19

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Best Local Similarity 99.8%; Pred. No. 0;
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Db 707 TTAATGATCTCAGTCTCTGTAAGTGCATAGGTAATCATTTGGTGGTCTTTACTAT 766
Qy 235 -TTTAAAGATCCATTAATGAATGAATGAGTGTAAATAATAATAATAATGGTAAAC 293
Db 767 ATATAGAGATCTGTTATATAATAATAAGATCTGAG-CACATTAGTACATGGGTGATACT 825
Qy 294 ATGTTACTCAGAGAAATTAATAAGATGATGAACCTTACATATCAATTAATAAGTAA 353
Db 826 ACATCAACAGCAACATTTCTTAAAGATGATGAATGCTGGTGTCTGTAAATAAGTATG 885
Qy 354 TTGCTTCTCTTCTTTCAGAACCTGATGATTCCTACTCTGAAATAATAATAATAATGTA 413
Db 886 -TATTTCTCTCTCTCCAGACTCTGAGGATTCCTGTTCTGTACATAATAATGTAAGTT 944
Qy 414 AAATATGATTTGATTAATGATTAATGAATCAG-----TTTCATATTTTAAAGCTATAA 469
Db 945 AAATATGATTTGATTAATGATGATGATGAATGAATGAATTTCTCTTTTAAAGCTATAA 1004
Qy 470 GTATCAGTTAAATTTGGGATGATTAATTTTATCTATTTTGTGTTTATGTTGGGATG 529
Db 1005 TCATTAGTTATCAATGGAATTAATTTTATTTTCTATTTTGTGTTTCTATGTTGGTCT 1064
Qy 530 AAAT-TATGCTGTTTGAATTAATGGAATGCTGTAGGAATGCTCTACAAATTAATGA 588
Db 1065 GAATGCTGTACTTATAAATATGAGGAATGACATTT-----TTATCAAGTA 1109
Qy 589 GAATCCATTAAGCAAGTGGATCAGGCTTTTGTGTTGATGTTGCTCAGTCTCCATCTCAA 648
Db 1110 GAATCTCTTAAACAGTGGATAGGCTTTTGTGATGTTTGTGATGTTGCTTCCCAAG 1169
Qy 649 AGCTCTGTCAGGCTCTTTTCCAAAGAAATCCATATTTGGTGCAGATATCTTCTAG 708
Db 1170 AGCATCTGTGAGG-ATTTCTTCCAGAGGATTTCCACACTGAGTGGTGGTGGCTAG 1228
Qy 709 GCTCCATTCCTCTGCTGGTGGCTTTCTCTCACTCACTGCTTTTCTGAAAGTACTAGCA 768
Db 1229 TCTCCGTGCTAGTTCTGAC-----TCTTTCTCACTCTAACTGTTTCTGAAAGTATTAGCA 1283
Qy 769 ACTTGGGTTATATTTTGAATTTATGCTAGTACATGAAATATACAGTGAAGTCT 828
Db 1284 ACTCAGAAATTAATTTTGAACCATGATCAGTAGACATTAATAATATATAACAAATGCC- 1342
Qy 829 ATATTAATAGTCACTCCACATATTTAAATGAATTTTAACTCTAATGGAATCATATACAT 888
Db 1343 --CTATATTAATTTCTGCATCTTAAATAATATGACTATATGATGTTGGTGTGTATGAT 1400
Qy 889 CTGAGTATGTCATGCTATTAATAATGTTAAATGTTGATATCATATGCTAAATAGA 948
Db 1401 TGAATATG---CCTGGTCAATTAATAATGTAATAATATATAGTTT-ATTAGTCTAAATAGA 1456
Qy 949 ATAAATACCAGCTAGAACATATACAGGAAATTTCTGAGGTGAGGTAAATCAGTAGGCA 1008
Db 1457 ATAAACTACCAGCTAGAACATGTAAGACAT--TGATATGAGTTTAAATGATATAATGC- 1513
Qy 1009 GTTGTATTAATACCTGTAAGCAATTTATTTTCAATATCATCTTCAATTTATCATTTGTA 1068
Db 1514 -----ATTACATCTCCAAACATTTTTCAGTTACATAATTAAGTTATATCTTTATA 1568
Qy 1069 ACATCTCTCAGTAATTAATAAATCATCTTTAC--TTATGGTAATTAAGTTAGTATAAG 1127

Db 1569 AAATCTCTCAGTAATCATATAAGCTTCACTACTCTTTTGAATAATTTATCTTAATATGTG 1628
Qy 1128 GTGCTTTCCACCTGGGAAAGACACAAGTAAACCTCTTTGGGAGAAAGGAACCTTGCTA 1187
Db 1629 GTGCTTTGTTGCTCTAGAAA-----ACAAACAAATAACTCTTTGGGAAAGGAACCTCATGTA 1684
Qy 1188 AACCCCAAAACAAAGTCTAACTTTT----- 1214
Db 1685 AATACCAAAACAAAGCTTAACTTTTGGGACCAAAATTTGTTTAAATAATTTTAA 1744
Qy 1215 ----- 1214
Db 1745 TTGATGAATTAATAAGTATATATTTATTGTGTACAAATATGATGTTTGAAGTATGTAT 1804
Qy 1215 -----TGGACCAAAATTTTATGCTCTTTTGTGTAATTAATTTT 1256
Db 1805 ACATGAGAAATGACAAATTTTATACCTTTGCTTGTATTTTGA-TTTT 1863
Qy 1257 TAAATCTTCTCTATTTAGCACCAACTGTGCAATTAAGAAGTTTTTCAAGGTATAGACAC 1316
Db 1864 AATAATTTCTCTATTTAGCACCAACTGTGCACTGAAGAAATCTTTCAGGGAATAGGCAC 1923
Qy 1317 ATTGAAGAACCAACTGCGGAGGCTGTGTAATAACTATTTCCAAACCTTGTCTTT 1376
Db 1924 ACTGAGAGTCAAACTGTGCAAGGGGTACTGTGGAAGACTATTCAAAACCTTGTCTT 1983
Qy 1377 AATAAAGAACACATAGAGCGCCAAAGTAAAGTAAAGACATTTGSCAAACCTTAAGT 1436
Db 1984 AATAAAGAAATACATTTGACGCGCAAAAGTAAAGTTACACATTTCAATGGAAGCTATAT 2043
Qy 1437 ATATTGCTGACTCTGCTCTTTT-----TGCCTATTCTATGGAATTTGACAGTTTCTGT 2085
Db 1497 CAATATCT-----CCTCTGTTCTTTAAACAGAAAGGTGTGAGGAGAAAGATGGAGAG 1550
Qy 2086 TAATACCTTATTGCTATTTTCTTTTTCACAGAAAGTGTGGAAGAAAGACGAGAG 2145
Db 1551 TGACAAAGTCTCTAGACTACCTGCAAGTATTTCTTGTGTATTAACACCGAGTGGACAC 1610
Qy 2146 TAAACCAATCTCTAGACTACCTGCAAGTATTTCTTGTGTATTAACACCGAGTGGATA 2205
Db 1611 CGGAAAGTGTAGAACAAACCGCTTATTGTAGTGGAGATTTTGGAG 1657
Qy 2206 TAGAAAGTGTAGACTAAACTGTTTGTGAGCCAAAGATTTTGGAG 2252

RESULT 5

US-09-755-633-21
; Sequence 21, Application US/09755633
; Patent No. US20020127200A1
; GENERAL INFORMATION:
; APPLICANT: Yang, Shumin
; APPLICANT: McCall, Catherine A.
; APPLICANT: Weber, Eric R.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; FILE REFERENCE: IM-2-Cl-Cl
; CURRENT APPLICATION NUMBER: US/09/755,633
; PRIOR FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: 09/322,409
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/087,306
; PRIOR FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 671
; TYPE: DNA
; ORGANISM: Canis familiaris
US-09-755-633-21

Query Match 24.5%; Score 406; DB 9; Length 671;

Best Local Similarity 100.0%; Pred. No. 9e-76;
Matches 406; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGGCAAACTGAACATTTTCAGAGCTATGAGATGCTTCTGAAATTTGAGTTTCTAGCTC 60
DB 1 AGGCAAACTGAACATTTTCAGAGCTATGAGATGCTTCTGAAATTTGAGTTTCTAGCTC 60

QY 61 TTGGGGCTGCTATGTTTCTGCTTCTCTAGAAAATCCCATGAATAGACTGGTGGCAG 120
DB 61 TTGGGGCTGCTATGTTTCTGCTTCTCTAGAAAATCCCATGAATAGACTGGTGGCAG 120

QY 121 AGACCTTGACACTGCTCCACATCATGCACTGGCTGATAGCGGATGGGTAATTTCT 180
DB 121 AGACCTTGACACTGCTCCACATCATGCACTGGCTGATAGCGGATGGGTAATTTCT 180

QY 181 TTTTGATTCCTACAGTCTTTAAATGCAATGCTGTAATTTGGTGGTGGCTAGTTTAA 240
DB 181 TTTTGATTCCTACAGTCTTTAAATGCAATGCTGTAATTTGGTGGTGGCTAGTTTAA 240

QY 241 GATCCATATCAATGAAGTAATGAGTGTAAATATATATATATATATATATATATATAT 300
DB 241 GATCCATATCAATGAAGTAATGAGTGTAAATATATATATATATATATATATATATAT 300

QY 301 TCAGAAGAT 360
DB 301 TCAGAAGAT 360

QY 361 CTTTCTTTTCAGAACCTGATGATCTCTACTCTGAAATATAAAAT 406
DB 361 CTTTCTTTTCAGAACCTGATGATCTCTACTCTGAAATATAAAAT 406

RESULT 6
US-09-755-633-4
; Sequence 4, Application US/09755633
; Patent No. US20020127200A1
; GENERAL INFORMATION:
; APPLICANT: Yang, Shumin
; APPLICANT: McCall, Catherine A.
; APPLICANT: Weber, Eric R.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; FILE REFERENCE: IM-2-CI-C1
; CURRENT APPLICATION NUMBER: US/09/755,633
; PRIOR FILING DATE: 2001-01-05
; PRIOR FILING DATE: 1999-05-28
; PRIOR FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 4
; LENGTH: 610
; TYPE: DNA
; ORGANISM: Canis familiaris
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (29)..(430)
US-09-755-633-4

Query Match
Best Local Similarity 100.0%; Score 171.8; DB 9; Length 610;
Matches 179; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 1 AGGCAAACTGAACATTTTCAGAGCTATGAGATGCTTCTGAAATTTGAGTTTCTAGCTC 60
DB 3 AGGCAAACTGAACATTTTCAGAGCTATGAGATGCTTCTGAAATTTGAGTTTCTAGCTC 62

QY 61 TTGGGGCTGCTATGTTTCTGCTTCTCTAGAAAATCCCATGAATAGACTGGTGGCAG 120
DB 63 TTGGGGCTGCTATGTTTCTGCTTCTCTAGAAAATCCCATGAATAGACTGGTGGCAG 122

QY 121 AGACCTTGACACTGCTCTCCACATCATGCACTGGCTGATAGCGGATGGGTAATTTCT 180

DB 123 AGACCTTGACACTGCTCTCCACATCATGCACTTGCTGATAGCGGATGGGTAATTTCT 182
QY 181 TTTTGATTCCT 191
DB 183 TTCCTACTCT 193

RESULT 7
US-09-755-633-6/c
; Sequence 6, Application US/09755633
; Patent No. US20020127200A1
; GENERAL INFORMATION:
; APPLICANT: Yang, Shumin
; APPLICANT: McCall, Catherine A.
; APPLICANT: Weber, Eric R.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; FILE REFERENCE: IM-2-CI-C1
; CURRENT APPLICATION NUMBER: US/09/755,633
; PRIOR FILING DATE: 2001-01-05
; PRIOR FILING DATE: 1999-05-28
; PRIOR FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: Patent In Ver. 2.1
; LENGTH: 610
; TYPE: DNA
; ORGANISM: Canis familiaris
US-09-755-633-6

Query Match
Best Local Similarity 10.4%; Score 171.8; DB 9; Length 610;
Matches 179; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 1 AGGCAAACTGAACATTTTCAGAGCTATGAGATGCTTCTGAAATTTGAGTTTCTAGCTC 60
DB 608 AGGCAAACTGAACATTTTCAGAGCTATGAGATGCTTCTGAAATTTGAGTTTCTAGCTC 549

QY 61 TTGGGGCTGCTATGTTTCTGCTTCTCTAGAAAATCCCATGAATAGACTGGTGGCAG 120
DB 548 TTGGGGCTGCTATGTTTCTGCTTCTCTAGAAAATCCCATGAATAGACTGGTGGCAG 489

QY 121 AGACCTTGACACTGCTCTCCACATCATGCACTGGCTGATAGCGGATGGGTAATTTCT 180
DB 488 AGACCTTGACACTGCTCTCCACATCATGCACTGGCTGATAGCGGATGGGTAATTTCT 429

QY 181 TTTTGATTCCT 191
DB 428 TTCCTACTCT 418

RESULT 8
US-10-218-654-80
; Sequence 80, Application US/10218654
; Publication No. US20030099609A1
; GENERAL INFORMATION:
; APPLICANT: Sim, Gek-Kee
; APPLICANT: Yang, Shumin
; APPLICANT: Dreitz, Matthew J.
; APPLICANT: Wonderling, Ramani S.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; FILE REFERENCE: IM-2-C1
; CURRENT APPLICATION NUMBER: US/10/218,654
; CURRENT FILING DATE: 2002-08-13
; PRIOR FILING DATE: US/09/322,409
; PRIOR FILING DATE: 1999-05-28
; PRIOR FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 154

SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 80
LENGTH: 610
TYPE: DNA
ORGANISM: Canis familiaris
FEATURE:
NAME/KEY: CDS
LOCATION: (29)..(430)
US-10-218-654-80

Query Match 10.4%; Score 171.8; DB 15; Length 610;
Best Local Similarity 93.7%; Pred. No. 3e-26;
Matches 179; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 181 TTTTGATTCCT 191
Db 428 TTCTACTCCT 418

RESULT 10
US-10-262-439-80
Sequence 80, Application US/10262439
Publication No. US20030143196A1
GENERAL INFORMATION:
APPLICANT: Sim, Gek-Kee
APPLICANT: Yang, Shumin
APPLICANT: Dreitz, Matthew J.
APPLICANT: Wonderling, Ramani S.
TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
FILE OF INVENTION: ACID MOLECULES, AND USES THEREOF
FILE REFERENCE: IM-2-C2
CURRENT APPLICATION NUMBER: US/10/262,439
CURRENT FILING DATE: 2002-09-30
PRIOR APPLICATION NUMBER: US/09/451,527
PRIOR FILING DATE: 1999-12-01
PRIOR APPLICATION NUMBER: 09/322,409
PRIOR FILING DATE: 1999-05-28
PRIOR APPLICATION NUMBER: 60/087,306
PRIOR FILING DATE: 1998-05-29
NUMBER OF SEQ ID NOS: 174
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 80
LENGTH: 610
TYPE: DNA
ORGANISM: Canis familiaris
NAME/KEY: CDS
LOCATION: (29)..(430)
US-10-262-439-80

Query Match 10.4%; Score 171.8; DB 15; Length 610;
Best Local Similarity 93.7%; Pred. No. 3e-26;
Matches 179; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 1 AGGCAAACTGAACTTTCAGAGCTATGAGAAATGCTTCTGAAATTCGATTGCTAGCTC 60
Db 3 AGGCAAACTGAACTTTCAGAGCTATGAGAAATGCTTCTGAAATTCGATTGCTAGCTC 62

QY 61 TTGGGGCTGCTATGTTTCTGCTGTAGAAATCCCATGAAATCCCATGAAATAGACTGGTGGCAG 120
Db 63 TTGGGGCTGCTATGTTTCTGCTGTAGAAATCCCATGAAATCCCATGAAATAGACTGGTGGCAG 122

QY 121 AGACCTTGACACTGCTCTCCACTCATCGAACTTGGCTGATAGGCGATGGGTAATTTTCT 180
Db 123 AGACCTTGACACTGCTCTCCACTCATCGAACTTGGCTGATAGGCGATGGGTAATTTTCT 182

QY 181 TTTTGATTCCT 191
Db 193 TTCTACTCCT 193

RESULT 11
US-10-262-439-82/c
Sequence 82, Application US/10262439
Publication No. US20030143196A1
GENERAL INFORMATION:
APPLICANT: Sim, Gek-Kee
APPLICANT: Yang, Shumin
APPLICANT: Dreitz, Matthew J.
APPLICANT: Wonderling, Ramani S.
TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
FILE OF INVENTION: ACID MOLECULES, AND USES THEREOF
FILE REFERENCE: IM-2-C2
CURRENT APPLICATION NUMBER: US/10/262,439
CURRENT FILING DATE: 2002-09-30
PRIOR APPLICATION NUMBER: US/09/451,527
PRIOR FILING DATE: 1999-12-01

SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 80
LENGTH: 610
TYPE: DNA
ORGANISM: Canis familiaris
FEATURE:
NAME/KEY: CDS
LOCATION: (29)..(430)
US-10-218-654-80

Query Match 10.4%; Score 171.8; DB 15; Length 610;
Best Local Similarity 93.7%; Pred. No. 3e-26;
Matches 179; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 1 AGGCAAACTGAACTTTCAGAGCTATGAGAAATGCTTCTGAAATTCGATTGCTAGCTC 60
Db 3 AGGCAAACTGAACTTTCAGAGCTATGAGAAATGCTTCTGAAATTCGATTGCTAGCTC 62

QY 61 TTGGGGCTGCTATGTTTCTGCTGTAGAAATCCCATGAAATCCCATGAAATAGACTGGTGGCAG 120
Db 63 TTGGGGCTGCTATGTTTCTGCTGTAGAAATCCCATGAAATCCCATGAAATAGACTGGTGGCAG 122

QY 121 AGACCTTGACACTGCTCTCCACTCATCGAACTTGGCTGATAGGCGATGGGTAATTTTCT 180
Db 123 AGACCTTGACACTGCTCTCCACTCATCGAACTTGGCTGATAGGCGATGGGTAATTTTCT 182

QY 181 TTTTGATTCCT 191
Db 183 TTCTACTCCT 193

RESULT 9
US-10-218-654-82/c
Sequence 82, Application US/10218654
Publication No. US20030099609A1
GENERAL INFORMATION:
APPLICANT: Sim, Gek-Kee
APPLICANT: Yang, Shumin
APPLICANT: Dreitz, Matthew J.
APPLICANT: Wonderling, Ramani S.
TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
FILE OF INVENTION: ACID MOLECULES, AND USES THEREOF
FILE REFERENCE: IM-2-C1
CURRENT APPLICATION NUMBER: US/10/218,654
CURRENT FILING DATE: 2002-08-13
PRIOR APPLICATION NUMBER: US/09/322,409
PRIOR FILING DATE: 1999-05-28
PRIOR APPLICATION NUMBER: 60/087,306
PRIOR FILING DATE: 1998-05-29
NUMBER OF SEQ ID NOS: 154
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 82
LENGTH: 610
TYPE: DNA
ORGANISM: Canis familiaris
US-10-218-654-82

Query Match 10.4%; Score 171.8; DB 15; Length 610;
Best Local Similarity 93.7%; Pred. No. 3e-26;
Matches 179; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 1 AGGCAAACTGAACTTTCAGAGCTATGAGAAATGCTTCTGAAATTCGATTGCTAGCTC 60
Db 608 AGGCAAACTGAACTTTCAGAGCTATGAGAAATGCTTCTGAAATTCGATTGCTAGCTC 549

QY 61 TTGGGGCTGCTATGTTTCTGCTGTAGAAATCCCATGAAATCCCATGAAATAGACTGGTGGCAG 120
Db 548 TTGGGGCTGCTATGTTTCTGCTGTAGAAATCCCATGAAATCCCATGAAATAGACTGGTGGCAG 489

QY 121 AGACCTTGACACTGCTCTCCACTCATCGAACTTGGCTGATAGGCGATGGGTAATTTTCT 180
Db 488 AGACCTTGACACTGCTCTCCACTCATCGAACTTGGCTGATAGGCGATGGGTAATTTTCT 429


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; PRIOR APPLICATION NUMBER: 09/322,409
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/087,306
; PRIOR FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 82
; LENGTH: 610
; TYPE: DNA
; ORGANISM: Canis familiaris
US-10-262-439-82

Query Match
Best Local Similarity 10.4%; Score 171.8; DB 15; Length 610;
Matches 179; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 1 AGCAAAACACTGAACATTTTCAGAGCTATGAAATGCTTCTGAATTTGAGTTTGTAGCTC 60
DB 608 AGCAAAACACTGAACATTTTCAGAGCTATGAAATGCTTCTGAATTTGAGTTTGTAGCTC 549

QY 61 TTGGGGCTGCTATGTTTCTGCTTTCCTCTAGAAAATCCCATGAATAGCTGGTGGCAG 120
DB 548 TTGGGGCTGCTATGTTTCTGCTTTCCTCTAGAAAATCCCATGAATAGCTGGTGGCAG 489

QY 121 AGACCTTGACACTGCTCTCCACTCATGCACTTGGCTGTAGCGATGGGTAATTTTCT 180
DB 488 AGACCTTGACACTGCTCTCCACTCATGCACTTGGCTGTAGCGATGGGTAATTTTCT 429

QY 181 TTTGATTTCT 191
DB 428 TTTGATTTCT 418

RESULT 12
US-10-311-455-1017
; Sequence 1017, Application US/10311455
; Publication No. US20030143606A1
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIEPENBROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Determining Cytosine Methylation
; FILE OF INVENTION: cytosine methylation
; FILE REFERENCE: 5013.1014
; CURRENT FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: US/10/311,455
; PRIOR FILING DATE: 2001-07-02
; PRIOR APPLICATION NUMBER: DE 10032529.7
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 2424
; SEQ ID NO 1017
; LENGTH: 5397
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-311-455-1017

Query Match
Best Local Similarity 9.1%; Score 150.6; DB 15; Length 5397;
Matches 250; Conservative 0; Mismatches 119; Indels 8; Gaps 2;

QY 1 AGCAAAACACTGAACATTTTCAGAGCTATGAAATGCTTCTGAATTTGAGTTTGTAGCTC 60
DB 5019 AGGTAAACGTAGACGCTTTTAGAGTTATGAGATGTTTGTATTTGAGTTTGTAGTT 5078

QY 61 TTGGGGCTGCTATGTTTCTGCTTTCCTCTAGAAAATCCCATGAATAGCTGGTGGCAG 120
DB 5079 TTGGAGTTTGTACGTGTATGTTTATTTTATAGAAAATTTTATAGAAATTTTATAGTGTATTTGGTGAAG 5138

; PRIOR APPLICATION NUMBER: 09/322,409
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/087,306
; PRIOR FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 82
; LENGTH: 610
; TYPE: DNA
; ORGANISM: Canis familiaris
US-10-262-439-82

Query Match
Best Local Similarity 93.7%; Score 171.8; DB 15; Length 610;
Matches 179; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 1 AGCAAAACACTGAACATTTTCAGAGCTATGAAATGCTTCTGAATTTGAGTTTGTAGCTC 60
DB 608 AGCAAAACACTGAACATTTTCAGAGCTATGAAATGCTTCTGAATTTGAGTTTGTAGCTC 549

QY 61 TTGGGGCTGCTATGTTTCTGCTTTCCTCTAGAAAATCCCATGAATAGCTGGTGGCAG 120
DB 548 TTGGGGCTGCTATGTTTCTGCTTTCCTCTAGAAAATCCCATGAATAGCTGGTGGCAG 489

QY 121 AGACCTTGACACTGCTCTCCACTCATGCACTTGGCTGTAGCGATGGGTAATTTTCT 180
DB 488 AGACCTTGACACTGCTCTCCACTCATGCACTTGGCTGTAGCGATGGGTAATTTTCT 429

QY 181 TTTGATTTCT 191
DB 428 TTTGATTTCT 418

RESULT 13
US-09-755-633-7
; Sequence 7, Application US/09755633
; Patent No. US20020127200A1
; GENERAL INFORMATION:
; APPLICANT: Yang, Shumin
; APPLICANT: McCall, Catherine A.
; APPLICANT: Weber, Eric R.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC ACID MOLECULES, AND USES THEREOF
; FILE REFERENCE: IM-2-Cl-C1
; CURRENT APPLICATION NUMBER: US/09/755,633
; CURRENT FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: 09/322,409
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/087,306
; PRIOR FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 402
; TYPE: DNA
; ORGANISM: Canis familiaris
US-09-755-633-7

Query Match
Best Local Similarity 8.8%; Score 145.8; DB 9; Length 402;
Matches 153; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 27 ATGAGATGCTTCTGAATTTGAGTTTGTAGCTTCTGGGGCTCCCTATGTTCTGCTTT 86
DB 1 ATGAGATGCTTCTGAATTTGAGTTTGTAGCTTCTGGGGCTCCCTATGTTCTGCTTT 60

QY 87 GCTGTAGAAAATCCCATGAATAGACTGGTGGCAGACCTTGACACTGCTTCCACTCAT 146
DB 61 GCTGTAGAAAATCCCATGAATAGACTGGTGGCAGACCTTGACACTGCTTCCACTCAT 120

QY 147 CGAAGTTGGCTGATAGCGATGGGTAATTTCTTTTGTATTCCT 191
DB 121 CGAAGTTGGCTGATAGCGATGGGTAATTTCTTTTGTATTCCT 165

RESULT 14
US-09-755-633-8/c
; Sequence 8, Application US/09755633
; Patent No. US20020127200A1
; GENERAL INFORMATION:
; APPLICANT: Yang, Shumin
; APPLICANT: McCall, Catherine A.
; APPLICANT: Weber, Eric R.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC ACID MOLECULES, AND USES THEREOF

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Search completed: August 31, 2004, 14:03:44
Job time : 985.052 secs

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FILE REFERENCE: IM-2-C1-C1
CURRENT APPLICATION NUMBER: US/09/755,633
CURRENT FILING DATE: 2001-01-05
PRIOR APPLICATION NUMBER: 09/322,409
PRIOR FILING DATE: 1999-05-28
PRIOR APPLICATION NUMBER: 60/087,306
PRIOR FILING DATE: 1998-05-29
NUMBER OF SEQ ID NOS: 21
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 8
LENGTH: 402
TYPE: DNA
ORGANISM: Canis familiaris
US-09-755-633-8

Query Match      8.8%; Score 145.8; DB 9; Length 402;
Best Local Similarity 92.7%; Pred. No. 7.5e-21;
Matches 153; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 27 ATGAGAATCCTTCTGAAATTTGAGTTTGCTAGCTCTTGGGGCTGCCTATGTTTCTGCCTTT 86
Db 402 ATGAGAATCCTTCTGAAATTTGAGTTTGCTAGCTCTTGGGGCTGCCTATGTTTCTGCCTTT 343

QY 87 GCTGTAGAAAATCCCATGATAGACTGTGGGAGAGACCTTGACACTGCTCTCCACTCAT 146
Db 342 GCTGTAGAAAATCCCATGATAGACTGTGGGAGAGACCTTGACACTGCTCTCCACTCAT 283

QY 147 CGAACTTGGCTGATAGCGGATGGGTAATTTCTTTTTCATTCT 191
Db 282 CGAACTTGGCTGATAGCGGATGGGTAATTTCTTTTTCATTCT 238

RESULT 15
US-10-218-654-83
Sequence 83, Application US/10218654
Publication No. US20030099609A1
GENERAL INFORMATION:
APPLICANT: Sim, Gek-kee
APPLICANT: Yang, Shumin
APPLICANT: Dreitz, Matthew J.
APPLICANT: Wonderling, Ramani S.
TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF
FILE REFERENCE: IM-2-C1
CURRENT APPLICATION NUMBER: US/10/218,654
CURRENT FILING DATE: 2002-08-13
PRIOR APPLICATION NUMBER: US/09/322,409
PRIOR FILING DATE: 1999-05-28
PRIOR APPLICATION NUMBER: 60/087,306
PRIOR FILING DATE: 1998-05-29
NUMBER OF SEQ ID NOS: 154
SOFTWARE: PatentIn ver. 2.0
SEQ ID NO 83
LENGTH: 402
TYPE: DNA
ORGANISM: Canis familiaris
US-10-218-654-83

Query Match      8.8%; Score 145.8; DB 15; Length 402;
Best Local Similarity 92.7%; Pred. No. 7.5e-21;
Matches 153; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 27 ATGAGAATCCTTCTGAAATTTGAGTTTGCTAGCTCTTGGGGCTGCCTATGTTTCTGCCTTT 86
Db 1 ATGAGAATCCTTCTGAAATTTGAGTTTGCTAGCTCTTGGGGCTGCCTATGTTTCTGCCTTT 60

QY 87 GCTGTAGAAAATCCCATGATAGACTGTGGGAGAGACCTTGACACTGCTCTCCACTCAT 146
Db 61 GCTGTAGAAAATCCCATGATAGACTGTGGGAGAGACCTTGACACTGCTCTCCACTCAT 120

QY 147 CGAACTTGGCTGATAGCGGATGGGTAATTTCTTTTTCATTCT 191
Db 121 CGAACTTGGCTGATAGCGGATGGGTAATTTCTTTTTCATTCT 165
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Blank Sheet

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 30, 2004, 21:24:28 ; Search time 5570.11 Seconds
(without alignments)
8889.782 Million cell updates/sec

Title: US-10-787-382-18

Perfect score: 1658

Sequence: 1 aggaacaactgaacatttc.....gtagtgaagatttggaga 1658

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estnu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_est1:*
10: gb_est2:*
11: gb_hic:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_man:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_phg:*
27: em_gss_vrl:*
28: gb_gss1:*
29: gb_gss2:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	398	24.0	622	29	CE331159 tigr-gss-
2	114.8	6.9	463	14	CD559535 AGENCOURT
C 3	114.4	6.9	467	14	CD559688 AGENCOURT
C 4	114.4	6.9	467	14	CD559690 AGENCOURT

RESULT 1
CE331159
LOCUS
DEFINITION
tigr-gss-dog-1700033986568 DOG Library Canis familiaris genomic,
genomic survey sequence.
ACCESSION
CE331159
VERSION
CE331159.1 GI:36147469
KEYWORDS
GSS:
SOURCE
Canis familiaris (dog)
ORGANISM
Canis familiaris
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE
1 (bases 1 to 622)
AUTHORS
Kirkness E.F., Bafna V., Halpern A.L., Levy S., Remington K.,
Rusch D.B., Delcher A.L., Pop M., Wang W., Fraser C.M. and
Venter J.C.
TITLE
The dog genome: survey sequencing and comparative analysis
JOURNAL
Science 301 (5641), 1898-1903 (2003)
MEDLINE
22875432
PUBMED
14512627
COMMENT
Contact: Kirkness EF
The Institute for Genomic Research
Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
Rockville, MD 20850, USA
Tel: 301-838-0200
Fax: 301-838-0208
Email: ekirkness@tigr.org

ALIGNMENTS

CE331159 622 bp DNA linear GSS 26-SEP-2003
tigr-gss-dog-1700033986568 DOG Library Canis familiaris genomic,
genomic survey sequence.
CE331159 GI:36147469
GSS:
Canis familiaris (dog)
Canis familiaris
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
Kirkness E.F., Bafna V., Halpern A.L., Levy S., Remington K.,
Rusch D.B., Delcher A.L., Pop M., Wang W., Fraser C.M. and
Venter J.C.
The dog genome: survey sequencing and comparative analysis
Science 301 (5641), 1898-1903 (2003)
MEDLINE
22875432
PUBMED
14512627
COMMENT
Contact: Kirkness EF
The Institute for Genomic Research
Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
Rockville, MD 20850, USA
Tel: 301-838-0200
Fax: 301-838-0208
Email: ekirkness@tigr.org

C 5	114.4	6.9	470	14	CD559687
C 6	114.4	6.9	473	14	CD559689
C 7	114.4	6.9	478	14	CD559534
8	114.4	6.9	492	14	CD559533
9	113.2	6.8	489	14	CD559536
C 10	111.2	6.7	456	14	CD559686
C 11	110.8	6.7	456	14	CD559532
12	97.8	5.9	405	29	AY412020
13	96.2	5.8	405	29	AY412021
14	95.8	5.8	407	14	CD559608
C 15	95.2	5.7	503	13	BQ598873
C 16	85.8	5.2	399	29	AY412022
C 17	83	5.0	1101	29	CNS0039G
18	78.4	4.7	1200	13	EX437758
19	72.8	4.4	987	29	CNS014PQ
20	71.2	4.3	1200	13	EX437739
21	70	4.2	854	9	AL522840
C 22	69.8	4.2	1200	13	EX437758
C 23	69.2	4.2	1200	13	EX415878
C 24	69	4.2	994	13	EX414650
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26	68	4.1	1101	29	CNS0039G
C 27	68	4.1	1190	29	CNS020N7
C 28	67.6	4.1	1201	13	EX443774
C 29	67.4	4.1	1201	13	EX355654
30	67	4.0	1201	9	AL532464
C 31	66.6	4.0	1101	29	CNS017L2
C 32	66.4	4.0	1201	13	EX439779
C 33	66.2	4.0	1165	13	EX338369
C 34	65.8	4.0	1101	29	CNS00EVL
35	65.6	4.0	1124	13	EX436282
36	65.2	3.9	928	29	CNS00DKY
37	65	3.9	1101	29	CNS00EVL
38	64.6	3.9	508	28	AQ248202
39	64.6	3.9	1146	13	EX462546
C 40	64.2	3.9	1056	13	EX415058
41	64.2	3.9	1200	13	EX415878
42	64	3.9	999	13	EX380865
C 43	64	3.9	1101	29	CNS004ZW
C 44	63.4	3.8	1190	29	CNS020N7
C 45	63	3.8	1201	13	EX442997

Class: shotgun.
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 /mol_type="genomic DNA"
 /strain="Standard Poodle"
 /db_xref="taxon:9615"
 /clone_lib="Dog Library"
 /note="Site 1: BatXI; Libraries were prepared from peripheral blood"

FEATURES
 source

ORIGIN

Query Match 24.0%; Score 398; DB 29; Length 622;
 Best Local Similarity 96.4%; Pred. No. 4.2e-09;
 Matches 407; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 1237 TTTTGTGATGAATATATATTTTAAATCTTCTCATTTAGCACCAACTGTGCAATTAAGAA 1296
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 Db 3 TTGTTTGTGATGAATATATTTTAAATCTTCTCATTTAGCACCAACTGTGCAATTAAGAA 62

QY 1297 GTTTTTCAGGTATAGACACATTAAGAACCAAACTGCCACGGGAGGCTGTGGATAA 1356
 |||||
 Db 63 GTTTTTCAGGTATAGACACATTAAGAACCAAACTGCCACGGGAGGCTGTGGATAA 122

QY 1357 CTATTTCCAAAACCTGTCTTTAAATAAAGAACACATAGAGCGCCAAAAGTAAGTTAAAGA 1416
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 Db 123 CTATTTCCAAAACCTGTCTTTAAATAAAGAACACATAGAGCGCCAAAAGTAAGTTAAAGA 182

QY 1417 CATTTGCAAAAACCTTAAGATATATTTGCTGACTCTGCTGTTTTTTTTTTTTTTT 1476
 |||||
 Db 183 CATTTGCAAAAACCTTAAGATATATTTGCTGACTCTGCTGTTTTTTTTTTTTTTT 242

QY 1477 CAAAGATTGACAGTTTCTTCAATATCTCTCTGTTCTTTTAAACAAAGGTCGACG 1536
 |||||
 Db 243 CAAAGATTGACAGTTTCTTCAATATCTCTCTGTTCTTTTAAACAAAGGTCGACG 302

QY 1537 AGAAAGTGGAGAGTGACAAAGTTCTTAGACTACCTGCAAGTATTTCTTGGTGATAA 1596
 |||||
 Db 303 AGAAAGTGGAGAGTGACAAAGTTCTTAGACTACCTGCAAGTATTTCTTGGTGATAA 362

QY 1597 CACCGATGGACACCGCAAGTTGAGAACAAACCGGCTATTCTAGTGGAGATTTTGA 1656
 |||||
 Db 363 CACCGATGGACACCGCAAGTTGAGAACAAACCGGCTATTCTAGTGGAGATTTTGA 422

QY 1657 GA 1658
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 Db 423 GA 424

RESULT 2
 LOCUS CD559535
 DEFINITION AGENCOURT 14496865 NIH MGC 195 Homo sapiens cDNA clone
 IMAGE:6971769 5', mRNA sequence.
 ACCESSION CD559535
 VERSION CD559535.2 GI:38558950
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 463)
 NIH-MGC <http://mgi.nci.nih.gov/>.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 On Jun 10, 2003 this sequence version replaced gi:31585603.
 Contact: Daniela S. Gerhard, Ph.D.
 Office of Cancer Genetics / NIH
 National Cancer Institute / NIH
 Bldg. 31 Rm10A07 Bethesda, MD 20892
 Email: cgaps-remail.nih.gov
 Tissue Procurement: Narayan Bhat
 cDNA Library Preparation: Bhat Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone Distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: IRBKI row: g column: 08
 High quality sequence stop: 463.
 Location/Qualifiers
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 /mol_type="mRNA"
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 /clone="IMAGE:6971769"
 /tissue_type="mixed"
 /lab_host="DH5A (TI phage-resistant)"
 /clone_lib="NIH MGC 195"
 /note="Vector: pDNR-Dual; Site 1: loxP-Sali; Site 2:
 loxP-HindIII; Clones from this library have been
 PCR-amplified using gene-specific primers to contain the
 complete open reading frame (based on known gene sequences
 available from NCBI's RefSeq). Template for PCR is cDNA
 derived from either pooled cytoplasmic polyA RNA from 30
 cells lines or pooled total RNA from 10 different tissues
 (from BD Biosciences/Clontech and Washington University).
 PCR products are directionally cloned into the loxP sites
 of the pDNR-Dual vector. Library constructed by Dr.
 Narayan Bhat, Earl Bere III and Hongling Liao (Gene
 Expression Laboratory, Research Technology Program, SAIC
 Frederick, NCI-Frederick, Frederick, MD 21702). For
 information on which gene each clone represents, please
 visit our anonymous ftp site at
ftp://image.llnl.gov/image/rearrayed_plates/IRBK.presv.dat
 A Note: this is a NIH_MGC Library."

ORIGIN

Query Match 6.9%; Score 114.8; DB 14; Length 463;
 Best Local Similarity 75.3%; Pred. No. 1.2e-09;
 Matches 143; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

QY 2 GCGAAACACATGACATTCAGAGCTATGAGATGCTTCTGAATTTGAGTTTGTAGCTCT 61
 |||||
 Db 3 GACAAACGACAGATTCAGAGCTATGAGATGCTTCTGAATTTGAGTTTGTAGCTCT 62

QY 62 TGGGGCTGCTTATCTTCTGCTTTGCTGTAGAAAATCCCATGAATAGACTGTGGCAGA 121
 |||||
 Db 63 TGGAGCTGCTTATCTTCTGCTGTATGCCATCCCAAGAAATCCCAAGTGCATTTGGTGAAGA 122

QY 122 GACCTTGACACTGCTTCTCCACTCATCGAATCTGGCTATAGGCGATGGGTAAATTTCTT 181
 |||||
 Db 123 GACCTTGACACTGCTTCTTCTACTCATCGAATCTGCTGATAGCAATGAGACTCTGAGGAT 182

QY 182 TTTGATTTCTT 191
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 Db 183 TCCTGTTCTT 192

RESULT 3
 LOCUS CD559688/c
 DEFINITION AGENCOURT 14496964 NIH MGC 195 Homo sapiens cDNA clone
 IMAGE:6971770 5', mRNA sequence.
 ACCESSION CD559688
 VERSION CD559688.2 GI:38453486
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 467)
 NIH-MGC <http://mgi.nci.nih.gov/>.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 On Jun 10, 2003 this sequence version replaced gi:31585756.

Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Narayan Bhat
cDNA Library Preparation: Bhat Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov

Plate: IRBK1 row: g column: 09
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High quality sequence stop: 467.
Location/Qualifiers

FEATURES

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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6971770"
/tissue_type="mixed"
/lab_host="DH5A (T1 phage-resistant)"
/clone_lib="NIH_MGC 195"
/notes="Vector: pDNR-Dual; Site 1: loxp-SalI; Site 2:
loxP-HindIII; Clones from this library have been
PCR-amplified using gene-specific primers to contain the
complete open reading frame (based on known gene sequences
available from NCBI's RefSeq). Template for PCR is cDNA
derived from either pooled cytoplasmic polyA RNA from 30
cells lines or pooled total RNA from 10 different tissues
(from BD Biosciences/Clontech and Washington University).
PCR products are directionally cloned into the loxp sites
of the pDNR-Dual vector. Library constructed by Dr.
Narayan Bhat, Earl Bere III and Hongling Liao (Gene
Expression Laboratory, Research Technology Program, SAIC
Frederick, NCI-Frederick, Frederick, MD 21702). For
information on which gene each clone represents, please
visit our anonymous ftp site at
ftp://image.llnl.gov/image/rearrayed_plates/IRBK.presv.dat
a Note: this is a NIH_MGC Library."

ORIGIN

Query Match 6.9%; Score 114.4; DB 14; Length 467;
Best Local Similarity 75.5%; Pred. No. 1.4e-09;
Matches 142; Conservative 0; Mismatches 46; Indels 0; Gaps 0;
QY 4 CAACACTGAACATTTTCAGAGCTATGAGATGCTTCTGAAATTTGAGTTTGCTAGCTCTTG 63
DB |||||
DB 466 CAACCGAGACGTTTCAGAGCCATGAGGATGCTTCTGCAATTTGATTTGCTAGCTCTTG 407
QY 64 GGCTGCGCTATGTTTCTGCTTGCTGTAGAAAATCCCATGAATAGACTGGTGCGAGAGA 123
DB |||||
DB 406 GAGCTGCTACGTGTATGCCATCCACAGAAATTCACACAGTGCATTGGTGAAGAGA 347
QY 124 CTTTGACATGCTCTCCACTCAGCACTGGCTGATAGCGATGGGTAATTTCTTTT 183
DB |||||
DB 346 CTTTGGCACTGCTTTCTACTCATGCACTCTGCTGATAGCAATGAGACTCTGAGGATTC 287
QY 184 TGATTCCT 191
DB |||||
DB 286 CTGTTCCT 279

RESULT 4
CD559690/c
LOCUS
DEFINITION AGENCOURT 14496838 NIH_MGC_195 Homo sapiens cDNA clone
IMAGE:6971768 5', mRNA sequence.
ACCESSION CD559690
VERSION CD559690.2 GI:38453490
KEYWORDS EST.
SOURCE Homo sapiens (human)

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 467)

NIH-MGC http://mgs.nci.nih.gov/.

AUTHORS

National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL

Unpublished (1999)

On Jun 10, 2003 this sequence version replaced gi:31585758.

Contact: Daniela S. Gerhard, Ph.D.

Office of Cancer Genomics

National Cancer Institute / NIH

Bldg. 31 Rm10A07 Bethesda, MD 20892

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Narayan Bhat

cDNA Library Preparation: Bhat Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: IRBK1 row: g column: 07

High quality sequence stop: 467.

FEATURES

Location/Qualifiers
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/tissue_type="mixed"
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/clone_lib="NIH_MGC 195"
/notes="Vector: pDNR-Dual; Site 1: loxp-SalI; Site 2:
loxP-HindIII; Clones from this library have been
PCR-amplified using gene-specific primers to contain the
complete open reading frame (based on known gene sequences
available from NCBI's RefSeq). Template for PCR is cDNA
derived from either pooled cytoplasmic polyA RNA from 30
cells lines or pooled total RNA from 10 different tissues
(from BD Biosciences/Clontech and Washington University).
PCR products are directionally cloned into the loxp sites
of the pDNR-Dual vector. Library constructed by Dr.
Narayan Bhat, Earl Bere III and Hongling Liao (Gene
Expression Laboratory, Research Technology Program, SAIC
Frederick, NCI-Frederick, Frederick, MD 21702). For
information on which gene each clone represents, please
visit our anonymous ftp site at
ftp://image.llnl.gov/image/rearrayed_plates/IRBK.presv.dat
a Note: this is a NIH_MGC Library."

ORIGIN

Query Match 6.9%; Score 114.4; DB 14; Length 467;
Best Local Similarity 75.5%; Pred. No. 1.4e-09;
Matches 142; Conservative 0; Mismatches 46; Indels 0; Gaps 0;
QY 4 CAACACTGAACATTTTCAGAGCTATGAGATGCTTCTGAAATTTGAGTTTGCTAGCTCTTG 63
DB |||||
DB 466 CAACCGAGACGTTTCAGAGCCATGAGGATGCTTCTGCAATTTGATTTGCTAGCTCTTG 407
QY 64 GGCTGCGCTATGTTTCTGCTTGCTGTAGAAAATCCCATGAATAGACTGGTGCGAGAGA 123
DB |||||
DB 406 GAGCTGCTACGTGTATGCCATCCACAGAAATTCACACAGTGCATTGGTGAAGAGA 347
QY 124 CTTTGACATGCTCTCCACTCAGCACTGGCTGATAGCGATGGGTAATTTCTTTT 183
DB |||||
DB 346 CTTTGGCACTGCTTTCTACTCATGCACTCTGCTGATAGCAATGAGACTCTGAGGATTC 287
QY 184 TGATTCCT 191
DB |||||
DB 286 CTGTTCCT 279

RESULT 5
CD559687/c

LOCUS CD559687 470 bp mRNA linear EST 19-NOV-2003
 DEFINITION AGENCOURT 14497029 NIH_MGC_195 Homo sapiens cDNA clone
 IMAGE:6971771 5', mRNA sequence.
 ACCESSION CD559687
 VERSION CD559687.2 GI:38453484
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 470)
 NIH-MGC http://mgi.nci.nih.gov/.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 COMMENT On Jun 10, 2003 this sequence version replaced gi:31585755.
 Contact: Daniela S. Gerhard, Ph.D.
 Office of Cancer Genomics / NIH
 National Cancer Institute / NIH
 Bldg. 31 Rm10A07 Bethesda, MD 20892
 Email: cgabs-r@mail.nih.gov
 Tissue Procurement: Narayan Bhat
 cDNA Library Preparation: Bhat Laboratory
 DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: IRBK1 row: g column: 10
 High quality sequence start: 14
 High quality sequence stop: 470.
 High quality sequence stop: 470.
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 /db_xref="taxon:9606"
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 /clone_lib="NIH_MGC_195"
 /notes="Vector: pDNR-Dual; Site 1: loxp-SalI; Site 2:
 loxp-HindIII; Clones from this library have been
 PCR-amplified using gene-specific primers to contain the
 complete open reading frame (based on known gene sequences
 available from NCBI's RefSeq). Template for PCR is cDNA
 derived from either pooled cytoplasmic polyA RNA from 30
 cells lines or pooled total RNA from 10 different tissues
 (from BD Biosciences/Clontech and Washington University).
 PCR products are directionally cloned into the loxp sites
 of the pDNR-Dual vector. Library constructed by Dr.
 Narayan Bhat, Earl Bere III and Hongling Liao (Gene
 Expression Laboratory, Research Technology Program, SAIC
 Frederick, NCI-Frederick, Frederick, MD 21702). For
 information on which gene each clone represents, please
 visit our anonymous ftp site at
 ftp://image.llnl.gov/image/rearrayed_plates/IRBK.presv.dat
 a Note: this is a NIH_MGC Library."

ORIGIN
 Query Match 6.9%; Score 114.4; DB 14; Length 470;
 Best Local Similarity 75.5%; Pred. No. 1.4e-09;
 Matches 142; Conservative 0; Mismatches 46; Indels 0; Gaps 0;
 4 CAAACACTGAACATTTTCAGAGCTATGAGATGCTTCTGAATTTGAGTTTGTAGCTCTTG 63
 469 CAAACGAGAACTTTTCAGAGCCATGAGGATGCTTCTGCATTTGAGTTTGTAGCTCTTG 410
 64 GGGCTGCCTATGTTTCTGCTTGTGTAGAAATCCCATGATGACTGGTGGCAGAGA 123
 409 GAGCTGCCTACGTTGATGTCATCCACAGAAATCCCAAGATGCTTGGTGAAGAGA 350
 124 CCTTGACACTGCTCTCCACTCATCGAACTTGGCTGATAGCGATGGGTAAATTTCTTTT 183
 349 CCTTGGCACTGCTTTCTACTCATCGAACTTGTGTATAGCAATGAGACTCTGAGGATTC 290

LOCUS CD559689 473 bp mRNA linear EST 19-NOV-2003
 DEFINITION AGENCOURT 14496901 NIH_MGC_195 Homo sapiens cDNA clone
 IMAGE:6971769 5', mRNA sequence.
 ACCESSION CD559689
 VERSION CD559689.2 GI:38453487
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 473)
 NIH-MGC http://mgi.nci.nih.gov/.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 COMMENT On Jun 10, 2003 this sequence version replaced gi:31585757.
 Contact: Daniela S. Gerhard, Ph.D.
 Office of Cancer Genomics / NIH
 National Cancer Institute / NIH
 Bldg. 31 Rm10A07 Bethesda, MD 20892
 Email: cgabs-r@mail.nih.gov
 Tissue Procurement: Narayan Bhat
 cDNA Library Preparation: Bhat Laboratory
 DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: IRBK1 row: g column: 08
 High quality sequence start: 16
 High quality sequence stop: 473.
 High quality sequence stop: 473.
 Location/Qualifiers
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 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
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 /tissue_type="mixed"
 /lab_host="DH5A (T1 phage-resistant)"
 /clone_lib="NIH_MGC_195"
 /notes="Vector: pDNR-Dual; Site 1: loxp-SalI; Site 2:
 loxp-HindIII; Clones from this library have been
 PCR-amplified using gene-specific primers to contain the
 complete open reading frame (based on known gene sequences
 available from NCBI's RefSeq). Template for PCR is cDNA
 derived from either pooled cytoplasmic polyA RNA from 30
 cells lines or pooled total RNA from 10 different tissues
 (from BD Biosciences/Clontech and Washington University).
 PCR products are directionally cloned into the loxp sites
 of the pDNR-Dual vector. Library constructed by Dr.
 Narayan Bhat, Earl Bere III and Hongling Liao (Gene
 Expression Laboratory, Research Technology Program, SAIC
 Frederick, NCI-Frederick, Frederick, MD 21702). For
 information on which gene each clone represents, please
 visit our anonymous ftp site at
 ftp://image.llnl.gov/image/rearrayed_plates/IRBK.presv.dat
 a Note: this is a NIH_MGC Library."

ORIGIN
 Query Match 6.8%; Score 114.4; DB 14; Length 473;
 Best Local Similarity 75.5%; Pred. No. 1.4e-09;
 Matches 142; Conservative 0; Mismatches 46; Indels 0; Gaps 0;
 4 CAAACACTGAACATTTTCAGAGCTATGAGATGCTTCTGAATTTGAGTTTGTAGCTCTTG 63
 472 CAAACGAGAACTTTTCAGAGCCATGAGGATGCTTCTGCATTTGAGTTTGTAGCTCTTG 413

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QY 64 GGGTGCCTATGTTCTGCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGA 123
DB 412 GAGCTGCTACGTGTATGCTCCACAGAAAATCCCAAGTGCATTGGTGAAGAAGA 353
QY 124 CTTTGACACTGCTCTCCACTCATCGAACTTGGCTGATAGGCGATGGGGTAAATTTCTTTT 183
DB 352 CTTTGACACTGCTTCTACTCATCGAACTCTGCTGATAGCCATGAGACTCTGAGGATTC 293
QY 184 TGATTCCT 191
DB 292 CTGTTCT 285

RESULT 7
CD559534
LOCUS AGENCOURT_14496928 NIH_MGC_195 Homo sapiens cDNA clone
IMAGE:6971770 5', mRNA sequence.
CD559534
ACCESSION CD559534.2 GI:38558949
VERSION EST.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE NIH-MGC http://mgi.nci.nih.gov/
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished (1999)
JOURNAL On Jun 10, 2003 this sequence version replaced gi:31585602.
COMMENT Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-remail.nih.gov
Tissue Procurement: Narayan Bhat
cDNA Library Preparation: Bhat Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: IRBKI row: 9 column: 09
High quality sequence start: 3
High quality sequence stop: 478.
Location/Qualifiers
1. .478
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6971770"
/tissue_type="mixed"
/lab_host="DH5A (T1 phage-resistant)"
/clone_lib="NIH MGC 195"
/notes="vector: pDNR-Dual; Site 1: loxp-Sall; Site 2:
loxP-HindIII; Clones from this library have been
PCR-amplified using gene-specific primers to contain the
complete open reading frame (based on known gene sequences
available from NCBI's RefSeq). Template for PCR is cDNA
derived from either pooled cytoplasmic polyA RNA from 30
cells lines or pooled total RNA from 10 different tissues
(from BD Biosciences/Clontech and Washington University).
PCR products are directionally cloned into the loxp sites
of the pDNR-Dual vector. Library constructed by Dr.
Narayan Bhat, Earl Bere III and Hongling Liao (Gene
Expression Laboratory, Research Technology Program, SAIC
Frederick, NCI-Frederick, Frederick, MD 21702). For
information on which gene each clone represents, please
visit our anonymous ftp site at
ftp://image.llnl.gov/image/rearrayed_plates/IRBK.presv.dat
a Note: this is a NIH_MGC Library."

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ORIGIN

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Query Match 6.9%; Score 114.4; DB 14; Length 478;
Best Local Similarity 75.5%; Pred. No. 1.4e-09;
Matches 142; Conservative 0; Mismatches 46; Indels 0; Gaps 0;

QY 4 CAAACACTGAACATTTTCAGAGCTATGAGAAATGCTTCTGAATTTGAGTTGCTAGCTCTTG 63
DB 22 CAAACGAGAAAGCTTTTCAGAGCCATGAGAGTCTTCTGCAATTTGAGTTTGTAGCTCTTG 81
QY 64 GGGTGCCTATGTTCTGCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGA 123
DB 82 GAGCTGCTACGTGTATGCTCCACAGAAAATCCCAAGTGCATTGGTGAAGAAGA 141
QY 124 CTTTGACACTGCTCTCCACTCATCGAACTTGGCTGATAGGCGATGGGGTAAATTTCTTTT 183
DB 142 CTTTGACACTGCTTCTACTCATCGAACTCTGCTGATAGCCATGAGACTCTGAGGATTC 201
QY 184 TGATTCCT 191
DB 202 CTGTTCT 209

RESULT 8
CD559533
LOCUS AGENCOURT_14496993 NIH_MGC_195 Homo sapiens cDNA clone
IMAGE:6971771 5', mRNA sequence.
CD559533
ACCESSION CD559533.2 GI:38558947
VERSION EST.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE NIH-MGC http://mgi.nci.nih.gov/
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished (1999)
JOURNAL On Jun 10, 2003 this sequence version replaced gi:31585601.
COMMENT Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-remail.nih.gov
Tissue Procurement: Narayan Bhat
cDNA Library Preparation: Bhat Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: IRBKI row: 9 column: 10
High quality sequence start: 14
High quality sequence stop: 492.
Location/Qualifiers
1. .492
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6971771"
/tissue_type="mixed"
/lab_host="DH5A (T1 phage-resistant)"
/clone_lib="NIH MGC 195"
/notes="vector: pDNR-Dual; Site 1: loxp-Sall; Site 2:
loxP-HindIII; Clones from this library have been
PCR-amplified using gene-specific primers to contain the
complete open reading frame (based on known gene sequences
available from NCBI's RefSeq). Template for PCR is cDNA
derived from either pooled cytoplasmic polyA RNA from 30
cells lines or pooled total RNA from 10 different tissues
(from BD Biosciences/Clontech and Washington University).
PCR products are directionally cloned into the loxp sites
of the pDNR-Dual vector. Library constructed by Dr.

```

Narayan Bhat, Earl Bere III and Hongling Liao (Gene Expression Laboratory, Research Technology Program, SAIC Frederick, NCI-Frederick, Frederick, MD 21702). For information on which gene each clone represents, please visit our anonymous ftp site at
ftp://image.llnl.gov/image/rearrayed_plates/IRBK.presv.dat
a Note: this is a NIH_MGC Library."

ORIGIN

Query Match 6.9%; Score 114.4; DB 14; Length 492;
Best Local Similarity 75.5%; Pred. No. 1.3e-09;
Matches 142; Conservative 0; Mismatches 46; Indels 0; Gaps 0;

Qy 4 CAACACTGACATTTTCAGAGCTATGAGATGCTTCTGMAATTTGAGTTTGGCTAGCTCTTG 63
Db |||||
33 CAACCGAGAACGTTTCAGAGCCATGAGGATGCTTCTGCATTGAGTTTGGCTAGCTCTTG 92
Qy 64 GGGCTGCTATGTTTCTGCTTGTGCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGA 123
Db |||||
93 GAGCTGCTAGCTGATGCTATGCCATCCACACAGAAATCCACAGTGCATTGGTGAAGAGA 152
Qy 124 CTTGACACTGCTCTCCACTCATCGAATTTGGCTGATAGCGGATGGGTAAATTTTCTTTT 183
Db |||||
153 CTTGGGACGCTCTTCTACTCATCGAACTCTGCTGATAGCAATGAGACTCTGAGGATTC 212
Qy 184 TGATTTCT 191
Db |||||
213 CTGTTCT 220

RESULT 9

CD559536
LOCUS
DEFINITION AGENCOURT 14496804 NIH MGC 195 Homo sapiens cDNA clone
IMAGE:6971768 5', mRNA sequence.

CD559536
VERSION
CD559536.2 GI:38558953

EST.
KEYWORDS

SOURCE
Homo sapiens (human)

ORGANISM
Homo sapiens

REFERENCE
1 (bases 1 to 489)
Narayan Bhat, Earl Bere III and Hongling Liao (Gene Expression Laboratory, Research Technology Program, SAIC Frederick, NCI-Frederick, Frederick, MD 21702). For information on which gene each clone represents, please visit our anonymous ftp site at
ftp://image.llnl.gov/image/rearrayed_plates/IRBK.presv.dat
a Note: this is a NIH_MGC Library."

On Jun 10, 2003 this sequence version replaced gi:31585604.

Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgabs-r@mail.nih.gov

Tissue Procurement: Narayan Bhat
CDNA Library Preparation: Bhat Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov

Plate: IRBK1 row: 9 column: 07
High quality sequence start: 17
High quality sequence stop: 489.

Location/Qualifiers

1. .489
/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:6971768"

/issue_type="mixed"

/lab_host="DH5A (T1 phage-resistant)"

/clone_lib="NIH MGC 195"

/note="Vector: pDNR-Dual; Site 1: loxP-SalI; Site 2: loxP-HindIII; Clones from this library have been

features

source

PCR-amplified using gene-specific primers to contain the complete open reading frame (based on known gene sequences available from NCBI's RefSeq). Template for PCR is cDNA derived from either pooled cytoplasmic polyA RNA from 30 cells lines or pooled total RNA from 10 different tissues (from BD Biosciences/Clontech and Washington University). PCR products are directionally cloned into the loxP sites of the pDNR-Dual vector. Library constructed by Dr. Narayan Bhat, Earl Bere III and Hongling Liao (Gene Expression Laboratory, Research Technology Program, SAIC Frederick, NCI-Frederick, Frederick, MD 21702). For information on which gene each clone represents, please visit our anonymous ftp site at
ftp://image.llnl.gov/image/rearrayed_plates/IRBK.presv.dat
a Note: this is a NIH_MGC Library."

ORIGIN

Query Match 6.8%; Score 113.2; DB 14; Length 489;
Best Local Similarity 74.7%; Pred. No. 2.1e-09;
Matches 142; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

Qy 2 GGCAACACACTGACATTTTCAGAGCTATGAGATGCTTCTGMAATTTGAGTTTGGCTAGCTCT 61
Db |||||
29 GACCAACGAGAACGTTTCAGAGCCATGAGGATGCTTCTGCATTGAGTTTGGCTAGCTCT 88
Qy 62 TGGGGCTGCCCTATGTTTCTGCTTGTAGAAAATCCCATGAATAGACTGGTGGCAGA 121
Db |||||
89 TGGAGCTGCCCTACGTGTATGCCATCCACAGAAATCCCAAGTGCATTGGTGAAGA 148
Qy 122 GACCTTGACACTGCTCTCCACTCATCGAATTTGGCTGATAGCGGATGGGTAAATTTTCTT 181
Db |||||
149 GACCTTGGCACTGCTTCTTCTACTCATCGAATTTGCTGATAGCAATGAGACTCTGAGGAT 208
Qy 182 TTTGATTTCT 191
Db |||||
209 TCCTGTTCT 218

RESULT 10

CD559686/c

LOCUS

DEFINITION AGENCOURT 14497093 NIH MGC 195 Homo sapiens cDNA clone

IMAGE:6971772 3', mRNA sequence.

CD559686

VERSION

CD559686.1 GI:31585754

EST.

KEYWORDS

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

REFERENCE

1 (bases 1 to 456)

Narayan Bhat, Earl Bere III and Hongling Liao (Gene Expression Laboratory, Research Technology Program, SAIC Frederick, NCI-Frederick, Frederick, MD 21702). For information on which gene each clone represents, please visit our anonymous ftp site at
ftp://image.llnl.gov/image/rearrayed_plates/IRBK.presv.dat
a Note: this is a NIH_MGC Library."

On Jun 10, 2003 this sequence version replaced gi:31585604.

Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgabs-r@mail.nih.gov

Tissue Procurement: Narayan Bhat
CDNA Library Preparation: Bhat Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov

Plate: IRBK1 row: 9 column: 11

High quality sequence stop: 456.

Location/Qualifiers

1. .456
/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:6971772"

/issue_type="mixed"

/lab_host="DH5A (T1 phage-resistant)"

/clone_lib="NIH MGC 195"

/note="Vector: pDNR-Dual; Site 1: loxP-SalI; Site 2: loxP-HindIII; Clones from this library have been

features

source

/clone="IMAGE:6971772"
 /issue type="mixed"
 /lab host="DH5A (TI phage-resistant)"
 /clone lib="NIH_MGC_195"
 /note="vector: pDNR-Dual; Site 1: loxP-Sall; Site 2: loxP-HindIII; Clones from this library have been PCR-amplified using gene-specific primers to contain the complete open reading frame (based on known gene sequences available from NCBI's RefSeq). Template for PCR is cDNA derived from either pooled cytoplasmic polyA RNA from 30 calls lines or pooled total RNA from 10 different tissues (from BD Biosciences/Clontech and Washington University). PCR products are directionally cloned into the loxP sites of the pDNR-Dual vector. Library constructed by Dr. Narayan Bhat, Earl Bere III and Hongling Liao (Gene Expression Laboratory, Research Technology Program, SAIC Frederick, NCI-Frederick, Frederick, MD 21702). For information on which gene each clone represents, please visit our anonymous ftp site at
 ftp://image.llnl.gov/image/rearrayed_plates/IRBK.presv.dat
 a Note: this is a NIH_MGC Library."

ORIGIN
 Query Match 6.7%; Score 111.2; DB 14; Length 456;
 Best Local Similarity 74.5%; Pred. No. 4.8e-09;
 Matches 140; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

QY 4 CAAACACTGACATTTTCAGAGCTATGAGATGCTTCTGAATTTGAGTTTGTAGCTCTTG 63
 DB 456 CCAAGCAGAACGTTTCAGAGCCATGAGGATGCTTCTGCATTTGAGTTTGTAGCTCTTG 397
 QY 64 GGCCTGCTATGTTTCTGCTTGTAGAAATCCCATGATAGACTGCTGGCAGAGA 123
 DB 396 GAGCTGCTACGTTGATGCCATCCCAAGAAATCCCAAGTGCATTTGGTGAAGAGA 337
 QY 124 CTTGACACATGCTCTCCACTCACTGGAATTTGGCTGATAGCGATGGGGTAATTTCTTTT 183
 DB 336 CTTGGCAGCTCTTCTTACTCATCGAATCTGCTGATAGCAATGAGACTCTGAGGATTC 277
 QY 184 TGATTCCT 191
 DB 276 CTGTTCT 269

RESULT 11
 CD559532 456 bp mRNA linear EST 11-JUN-2003
 LOCUS AGENCOURT_14497057 NIH_MGC_195 Homo sapiens cDNA clone
 DEFINITION IMAGE:6971772 5', mRNA sequence.

ACCESSION CD559532
 VERSION CD559532.1 GI:31585600
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 AUTHORS NIH-MGC http://mgi.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)

COMMENT Contact: Daniela S. Gerhard, Ph.D.
 Office of Cancer Genomics
 National Cancer Institute / NIH
 Bldg. 31 Rm10A07 Bethesda, MD 20892
 Email: csaple-r@mail.nih.gov
 Tissue Procurement: Narayan Bhat
 cDNA Library Preparation: Bhat Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: IRBK1 row: 9 column: 11

FEATURES
 source High quality sequence stop: 456.
 Location/Qualifiers
 1..456

/organism="Homo sapiens"
 /mol type="mRNA"
 /db xref="taxon:9606"
 /clone="IMAGE:6971772"
 /tissue_type="mixed"
 /lab_host="DH5A (TI phage-resistant)"
 /clone lib="NIH_MGC_195"
 /note="vector: pDNR-Dual; Site 1: loxP-Sall; Site 2: loxP-HindIII; Clones from this library have been PCR-amplified using gene-specific primers to contain the complete open reading frame (based on known gene sequences available from NCBI's RefSeq). Template for PCR is cDNA derived from either pooled cytoplasmic polyA RNA from 30 cells lines or pooled total RNA from 10 different tissues (from BD Biosciences/Clontech and Washington University). PCR products are directionally cloned into the loxP sites of the pDNR-Dual vector. Library constructed by Dr. Narayan Bhat, Earl Bere III and Hongling Liao (Gene Expression Laboratory, Research Technology Program, SAIC Frederick, NCI-Frederick, Frederick, MD 21702). For information on which gene each clone represents, please visit our anonymous ftp site at
 ftp://image.llnl.gov/image/rearrayed_plates/IRBK.presv.dat
 a Note: this is a NIH_MGC Library."

ORIGIN
 Query Match 6.7%; Score 110.8; DB 14; Length 456;
 Best Local Similarity 74.7%; Pred. No. 5.6e-09;
 Matches 139; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

QY 6 AACACTGACATTTTCAGAGCTATGAGATGCTTCTGAATTTGAGTTTGTAGCTCTTG 65
 DB 1 AAAGCAGAACGTTTCAGAGCCATGAGGATGCTTCTGCATTTGAGTTTGTAGCTCTTG 60
 QY 66 GTCGCTATGTTTCTGCTTGTAGAAATCCCATGATAGACTGCTGGCAGAGACC 125
 DB 61 GCTGCTACGTTGATGCCATCCCAAGAAATCCCAAGTGCATTTGGTGAAGAGACC 120
 QY 126 TTGACATGCTCTCCACTCATCGAATCTGGCTGATAGCGATGGGGTAATTTCTTTTG 185
 DB 121 TTGGCACTGCTTTTCTACTCATCGAATCTGCTGATAGCAATGAGACTCTGAGGATTCCT 180
 QY 186 ATTCTCT 191
 DB 181 GTTCTCT 186

RESULT 12
 AY412020 405 bp DNA linear GSS 16-DEC-2003
 LOCUS Homo sapiens IL5 gene, VIRTUAL TRANSCRIPT, partial sequence,
 DEFINITION Genomic survey sequence.

ACCESSION AY412020
 VERSION AY412020.1 GI:39767985
 KEYWORDS GSS.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 AUTHORS Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.

TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios
 JOURNAL Science 302 (5652), 1960-1963 (2003)
 PUBMED 14671302
 REFERENCE 2 (bases 1 to 405)
 AUTHORS Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,

Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
 Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
 Adams,M.D. and Cargill,M.
 Direct Submission
 Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
 Rockville, MD 20850, USA
 This sequence was made by sequencing genomic exons and ordering
 them based on alignment.
 Location/Qualifiers
 1..405
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
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 /genes="IL5"
 /locus_tag="HCM4418"

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 Best Local Similarity 74.5%; Pred. No. 9e-07;
 Matches 123; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

QY 27 ATGAGATGCTTCTGCAATTTGAGTTTGTAGCTCTTGGGGCTGCCTATGTTCTGCTTT 86
 Db 1 ATGAGGATGCTTCTGCAATTTGAGTTTGTAGCTCTTGGGGCTGCCTATGTTCTGCTTT 60

QY 87 GCTGTAGAAAATCCCATGATAGTGGTGGCAGAGACCTTGACACTGCTTCCACTCAT 146
 Db 61 CCCACAGAAAATCCCATGATAGTGGTGGCAGAGACCTTGACACTGCTTCCACTCAT 120

QY 147 CGAACTGGCTGATAGCGATGGGTAAATTTCTTTTGTATTCCT 191
 Db 121 CGAACTGGCTGATAGCGATGGGTAAATTTCTTTTGTATTCCT 165

RESULT 13
 AY412021
 LOCUS 405 bp DNA linear GSS 16-DEC-2003
 DEFINITION Pan troglodytes IL5 gene, VIRTUAL TRANSCRIPT, partial sequence,
 genomic survey sequence.
 ACCESSION AY412021
 VERSION AY412021.1 GI:39767986
 KEYWORDS GSS.
 SOURCE Pan troglodytes (chimpanzee)
 ORGANISM Pan troglodytes
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
 1 (bases 1 to 405)
 Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,
 Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
 Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
 Adams,M.D. and Cargill,M.
 Infering nonneutral evolution from human-chimp-mouse orthologous
 gene trios
 Science 302 (5652), 1960-1963 (2003)
 14671302

2 (bases 1 to 405)
 Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,
 Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
 Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
 Adams,M.D. and Cargill,M.
 Direct Submission
 Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
 Rockville, MD 20850, USA
 This sequence was made by sequencing genomic exons and ordering
 them based on alignment.
 Location/Qualifiers
 1..405
 /organism="Pan troglodytes"
 /mol_type="genomic DNA"
 /db_xref="taxon:9598"
 <1..>405
 /genes="IL5"

gene

/locus_tag="HCM4418"

Query Match 5.8%; Score 96.2; DB 29; Length 405;
 Best Local Similarity 73.9%; Pred. No. 1.7e-06;
 Matches 122; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

QY 27 ATGAGATGCTTCTGCAATTTGAGTTTGTAGCTCTTGGGGCTGCCTATGTTCTGCTTT 86
 Db 1 ATGAGGATGCTTCTGCAATTTGAGTTTGTAGCTCTTGGGGCTGCCTATGTTCTGCTTT 60

QY 87 GCTGTAGAAAATCCCATGATAGTGGTGGCAGAGACCTTGACACTGCTTCCACTCAT 146
 Db 61 CCCACAGAAAATCCCATGATAGTGGTGGCAGAGACCTTGACACTGCTTCCACTCAT 120

QY 147 CGAACTGGCTGATAGCGATGGGTAAATTTCTTTTGTATTCCT 191
 Db 121 CGAACTGGCTGATAGCGATGGGTAAATTTCTTTTGTATTCCT 165

RESULT 14
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 LOCUS 477 bp mRNA linear EST 26-NOV-2003
 DEFINITION AGENCOURT 14496997 NIH MGC 195 Homo sapiens cDNA clone
 IMAGE:6971867 5', mRNA sequence.
 ACCESSION CD559608
 VERSION CD559608.2 GI:38558942
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 477)
 NIH-MGC <http://mgs.nci.nih.gov/>.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 On Jun 10, 2003 this sequence version replaced gi:31585676.
 Contact: Daniela S. Gerhard, Ph.D.
 Office of Cancer Genomics / NIH
 National Cancer Institute / NIH
 Bldg. 31 Rm10A07 Bethesda, MD 20892
 Email: cgabs-remail.nih.gov
 Tissue Procurement: Narayan Bhat
 CDNA Library Preparation: Bhat Laboratory
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 CDNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: IRBK2 row: g column: 10
 High quality sequence start: 107
 High quality sequence stop: 353.
 High quality sequence stop: 353.

FEATURES
 Location/Qualifiers
 1..477
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:6971867"
 /tissue_type="mixed"
 /lab_hosts="DH5A (T1 phage-resistant)"
 /clone_lib="NIH_MGC_195"
 /notes="Vector: pDNR-Dual; Site 1: loxP-Sall; Site 2:
 loxP-HindIII; Clones from this library have been
 PCR-amplified using gene-specific primers to contain the
 complete open reading frame (based on known gene sequences
 available from NCBI's RefSeq). Template for PCR is cDNA
 derived from either pooled cytoplasmic polyA RNA from 30
 cells lines or pooled total RNA from 10 different tissues
 (from BD Biosciences/Clontech and Washington University).
 PCR products are directionally cloned into the loxP sites
 of the pDNR-Dual vector. Library constructed by Dr.
 Narayan Bhat, Earl Bere III and Hongling Liao (Gene
 Expression Laboratory, Research Technology Program, SAIC

Frederick, NCI-Frederick, Frederick, MD 21702). For information on which gene each clone represents, please visit our anonymous ftp site at ftp://image.llnl.gov/image/rearrayed_plates/IRBK.presv.dat a Note: this is a NIH_MGC Library."

ORIGIN

Query Match 5.8%; Score 95.8; DB 14; Length 477;
Best Local Similarity 72.3%; Pred. No. 1.8e-06;
Matches 139; Conservative 0; Mismatches 52; Indels 1; Gaps 1;
QY 2 GCGAACAACATTCGAGCTATGAGA-ATGCTTCTGATTTGAGTTGCTAGCTC 60
Db 15 GACTAAGCGAGACGTTTACAGCCGCTGAGAGCGCTTCTGATTTGAGTTGCTAGCTC 74
QY 61 TTGGGGCTGCTATGTTTCTGCTGTGAGAAATCCCATGATAGACTGGTGCGAG 120
Db 75 TTGAGCTGCTACGTGTATGCCATCCCAAGAAATCCCAAGTGCATTGGTGAAG 134
QY 121 AGACCTTGACATGCTCTCCACTCATCGAATCTGGCTGATAGCGATGGGTAATTTCT 180
Db 135 AGACCTTGACATGCTCTTCTACTCGTGAACCTGCTGATAGCAATGAGACTCTGAGGA 194
QY 181 TTTTGATTCCT 191
Db 195 TTCTGTTCCT 205

RESULT 15

BQ598873/c
LOCUS BQ598873 503 bp mRNA linear EST 24-JUN-2002
DEFINITION MI-P-E4-ah-e-08-1-UM.s1 MI-P-E4 Sus scrofa cDNA clone
MI-P-E4-ah-e-08-1-UM 3', mRNA sequence.

ACCESSION

BQ598873

VERSION

BQ598873.1 GI:21545599

KEYWORDS

EST.

SOURCE

Sus scrofa (pig)

ORGANISM

Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

REFERENCE

1 (bases 1 to 503)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
discovery
Genome Res. 6 (9), 791-806 (1996)

JOURNAL

Genome Res. 6 (9), 791-806 (1996)

MEDLINE

97044477

PUBMED

8889548

COMMENT

Contact: Tuggle CK
Molecular Genetics Laboratory, Department of Animal Science
Iowa State University
201 Kildee Hall, Ames, IA 50011-3150, USA
Tel: 5152944252
Fax: 5152942401
Email: cktuggle@iastate.edu
Tissue Procurement: Dr. Chris Tuggle, Iowa State University
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com).
Seq primer: M13 FORWARD
POLYA=Yes.

FEATURES

source

1. 503
Location/Qualifiers
/organism="Sus scrofa"
/mol_type="mRNA"
/strain="crossbreed"
/db_xref="taxon:9823"
/clone="MI-P-E4-ah-e-08-1-UM"
/lab_host="DH10B (Life Technologies)"
/clone_lib="MI-P-E4"
/note="Vector: pMT3D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: EcoRI; The MI-P-E4

Library is derived from embryo at gestational day 14. For a detailed description of the library from which this clone was derived, please visit our web site at <http://pigest.genome.iastate.edu/>.
TAG_TISSUE=postelongation_d_14_conceptus
TAG_LIB=MI-P-E4
TAG_SEQ=ACTCAC"

ORIGIN

Query Match 5.7%; Score 95.2; DB 13; Length 503;
Best Local Similarity 80.0%; Pred. No. 2.2e-06;
Matches 112; Conservative 0; Mismatches 28; Indels 0; Gaps 0;
QY 1518 AACGAAAAGTGTCCAGGAGAAAGATGGAGTGCACAAAGTTCTAGACTTACCTGCAAG 1577
Db 502 AAAAAAATAATTTGGAGGGGAAAGATGGAGTGCACAAAGTTCTAGACTTACCTGCAAG 443
QY 1578 TATTCTTGGTGTATAATAAACACCGAGTGGACACCGGAAAGTTGAGAACAAACCGGCTTAT 1637
Db 442 TTTTCTTGGTGTGATAAATACCGAGTGGACACCGGAAAGTTGAGAACAAACCGGCTTAT 1637
QY 1638 TGTAGTGGAAAGATTTTGGAG 1657
Db 382 CGAAGCAAAAGATTTTTCAG 363

Search completed: August 31, 2004, 13:00:16
Job time : 5572.11 secs

Blank sheet

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 30, 2004, 16:21:12 ; Search time 7167.07 Seconds
(without alignments)
10026.797 Million cell updates/sec

Title: US-10-787-382-18
Perfect score: 1658
Sequence: 1 aggcacacactgaacatttc.....gtagtggagattttggaga 1658

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues
Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:
1: gb_ba.*
2: gb_hgt.*
3: gb_in.*
4: gb_om.*
5: gb_ov.*
6: gb_pat.*
7: gb_ph.*
8: gb_pl.*
9: gb_pr.*
10: gb_ro.*
11: gb_sts.*
12: gb_sy.*
13: gb_un.*
14: gb_vi.*
15: em_ba.*
16: em_fun.*
17: em_hum.*
18: em_in.*
19: em_mu.*
20: em_om.*
21: em_or.*
22: em_ov.*
23: em_pat.*
24: em_ph.*
25: em_pl.*
26: em_ro.*
27: em_sts.*
28: em_un.*
29: em_vi.*
30: em_htg_hum.*
31: em_htg_inv.*
32: em_htg_other.*
33: em_htg_mus.*
34: em_htg_pln.*
35: em_htg_rod.*
36: em_htg_mam.*
37: em_htg_vrt.*
38: em_sy.*
39: em_htgo_hum.*
40: em_htgo_mus.*
41: em_htgo_other.*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	1658	100.0	1658	4	AF331920	AF331920 Canis fam
2	634.6	38.3	3241	9	HUMIL5A	J02971 Human eosin
3	634.6	38.3	5186	9	AF353265	AF353265 Homo sapi
4	634.6	38.3	57186	9	AC004042	AC004042 Homo sapi
5	634.6	38.3	180042	9	AC079320	AC079320 Homo sapi
c	634.6	38.3	163665	9	AC116366	AC116366 Homo sapi
c	600.6	36.2	3230	6	AR136275	AR136275 Sequence
7	600.6	36.2	3230	6	BD247730	BD247730 Antisense
8	600.6	36.2	3230	6	E01640	E01640 gene for hu
9	600.6	36.2	3230	6	AR364536	AR364536 Sequence
10	600.6	36.2	3230	9	HSBCDIPFI	X12706 H. sapiens g
11	600.6	36.2	3230	9	HUMIL5	J03478 Human inter
12	600.6	36.2	3230	6	EL3592	EL3592 gDNA encodi
13	599	36.1	3230	6	EL3592	EL4878 Homo sapien
14	490.6	29.6	3507	9	HUM21DC94Z	U17052 Ovis aries
15	347.4	21.0	1140	4	OAILV1	U17052 Ovis aries
16	272.6	16.4	700	6	AX182851	AX182851 Sequence
17	245.2	14.8	450	4	OAILV2	U17053 Ovis aries
18	221.6	13.4	700	6	AX182853	AX182853 Sequence
19	216	13.0	700	6	AX182850	AX182850 Sequence
20	215.4	13.0	700	6	AX182852	AX182852 Sequence
21	205.2	12.4	1395	6	A21910	A21910 partial gen
22	171.8	10.4	610	4	AF331919	AF331919 Canis fam
23	171.8	10.4	610	6	AR241536	AR241536 Sequence
c	171.8	10.4	610	6	AR241537	AR241537 Sequence
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c	171.8	10.4	610	6	AR254493	AR254493 Sequence
c	171.8	10.4	610	6	BD211558	BD211558 Canine an
c	171.8	10.4	610	6	BD211559	BD211559 Canine an
29	163	9.8	3710	9	HUM21DC93Z	L48477 Homo sapien
30	150.6	9.1	5397	6	AX345946	AX345946 Sequence
31	149.4	9.0	838	4	AF025436	AF025436 Felis cat
32	145.8	8.8	402	6	AR241538	AR241538 Sequence
c	145.8	8.8	402	6	AR241539	AR241539 Sequence
c	145.8	8.8	402	6	AR254494	AR254494 Sequence
c	145.8	8.8	402	6	AR254495	AR254495 Sequence
c	145.8	8.8	402	6	BD211560	BD211560 Canine an
c	145.8	8.8	402	6	BD211561	BD211561 Canine an
37	145.8	8.8	405	6	AR300436	AR300436 Sequence
38	145.8	8.8	405	6	AX083939	AX083939 Sequence
39	145.8	8.8	405	6	AX083939	U35038 Ovis aries
c	138.2	8.3	520	4	OUJ35038	AX345947 Sequence
c	134.6	8.1	5397	6	AX345947	AX083948 Sequence
42	131.6	7.9	343	6	AX083948	AR241540 Sequence
c	131.6	7.9	345	6	AR241541	AR241541 Sequence
c	131.6	7.9	345	6	AR254496	AR254496 Sequence

ALIGNMENTS

RESULT 1
AF331920 1658 bp DNA linear NAM 04-OCT-2001
LOCUS AF331920
DEFINITION Canis familiaris interleukin-5 gene, complete cds.
ACCESSION AF331920
VERSION AF331920.1 GI:15919182
KEYWORDS
SOURCE Canis familiaris (dog)
ORGANISM Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE 1 (bases 1 to 1658)
AUTHORS Yang, S., Sellins, K.S., Weber, E. and McCall, C.
TITLE Canine interleukin-5; molecular characterization of the gene and expression of biologically active recombinant protein

Pred. No. is the number of results predicted by chance to have a

J. Interferon Cytokine Res. 21 (6), 361-367 (2001)
 J21334408
 MEDLINE
 PUBMED
 11440633
 2 (bases 1 to 1658)
 REFERENCE
 Yang, S.
 TITLE
 Direct Submission
 JOURNAL
 Submitted (22-DEC-2000) Immunology, Heska Corporation, 1613
 Prospect Parkway, Ft Collins, CO 80525, USA
 Location/Qualifiers
 1..1658
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 /db_xref="taxon:9615"
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 3'UTR
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 Best Local Similarity 100.0%; Pred. No. 7.5e-291;
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 QY 181 TTTTGATTCCTACAGTCTTTAAATATGATGGGTAATTTGGTGGTGGCTAGTTTTTAA 240
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 QY 241 GATCCATTAATCAATATGAAGTAATGAGTGTAAATATAATATAATGATGGGTAACATGTTAC 300
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 QY 301 TCAGAGAAATTAATTAAGATTTACAACTTACATATCAATTAATAAATCAATGTTGTTTC 360
 DB 301 TCAGAGAAATTAATTAAGATTTACAACTTACATATCAATTAATAAATCAATGTTGTTTC 360
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 DB 421 GATTTGATTAATGATTAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 480
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 DB 541 TTATGAATATTAGGAATGTTAGGAATGTTAGGAATGTTAGGAATGTTAGGAATGTTAG 600
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DB 601 CAAGTGGATCAGGCCCTTTTGTGATGTTGTCAGTTCTCCATCTCAAGAGCCTCGTGCA 660
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 QY 721 TCTGTGCTTGGCTTTCTCCTCACTCAACGTTTCTCTGAAAGTACTAGCAACTTGGGGTTAT 780
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 DB 1081 AATTTATTAACATCAATTTACTTATGTTAATTTAGTCTAGTAAAGTGGTTCACACC 1140
 QY 1141 TGGAAAAAGACACAGTAAAAACCTCTTGGGAGAGGAACTTGTGTAACCCCAACAAAC 1200
 DB 1141 TGGAAAAAGACACAGTAAAAACCTCTTGGGAGAGGAACTTGTGTAACCCCAACAAAC 1200
 QY 1201 AAAGTCTAACTTTTGGACCAAAATTTTATGCTTGTGTTTGTGATGAATTTATTTTAA 1260
 DB 1201 AAAGTCTAACTTTTGGACCAAAATTTTATGCTTGTGTTTGTGATGAATTTATTTTAA 1260
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RESULT 2

HUMIL5A 3241 bp DNA linear PRI 29-APR-1996
LOCUS Human eosinophil differentiation factor (interleukin 5) gene,
DEFINITION complete cds.
ACCESSION J02971.1 GI:186340
VERSION eosinophil differentiation factor; interleukin 5.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 3241)
AUTHORS Campbell,H.D., Tucker,W.Q., Hort,Y., Martinson,M.E., Mayo,G.,
Clutterbuck,E.J., Sanderson,C.J. and Young,I.G.
TITLE Molecular cloning, nucleotide sequence, and expression of the gene
encoding human eosinophil differentiation factor (interleukin 5)
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 84 (19), 5629-5633 (1987)
MEDLINE 88016145
PubMed 3498940
COMMENT Original source text: Homo sapiens (clone: beta-EDFH-1.) (clone
library: lambda-EDFH-1) DNA.
Draft entry and computer-readable sequence for [1] kindly provided
by H.D.Campbell, 09-SEP-1987.
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ORIGIN 1 bp upstream of BamHI site; chromosome 5q23.3-q32.
Query Match 38.3%; Score 634.6; DB 9; Length 3241;
Best Local Similarity 68.6%; Pred. No. 2.5e-105;
Matches 1226; Conservative 0; Mismatches 374; Indels 187; Gaps 18;
QY 1 AGGCAACACTGACATTTTCAGAGCTATGAGATGCTTCTGAATTTGAGTTTGCTAGCTC 60
DB 526 AGGCAACAGCAGACGTTTCAGACCAAGAGATGCTTCTGCATTTGAGTTTGCTAGCTC 585
QY 61 TTGGGGCTGCTCATTTTCTGCTTTCTGTAGAAAAATCCCATGAATAGACTGTGGCAG 120
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QY 121 AGACCTTGACACTGCTCTCCACTCATCGAATTTGGCTGATAGGCGATGGGTAAATTTCT 180
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DB 1228 TCTCGGTGCAAGTTCTGAC-----TCTTTCTCACTCAACGTTTCTTCTGAAAGTACTAGCA 1282
QY 769 ACTTGGGGTTATATTTTGTAGAAATTAAGTCAATAGCAATGAAATATATACAGTGAAGTCT 828
DB 1283 ACTCAGAAATTAATTTTGAACCAATGATCAGTAGACATTAATAATATATAACAAATGCC- 1341
QY 829 ATATTAATAGTCACTTCCACATATTTAATGATTTTAACTCTAATGAATCATATACAT 888
DB 1342 -CTATATTAATAATTTCTGCATACATAATAATAATTAATGACTATATGATGGTGTGTATGCA 1400
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Db 1401 TTTGAATATGCTCGGTGCATATTAATAATGTAATAATATATAGTTTATATAGTCTAAATAGA 1460
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 Db 1515 --TGCATATACACTTCCAAACATTTTTCAGTTACATATATATATATATATATATATATATAT 1572
 QY 1069 ACATCTCTCAGTAT 1127
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 DEFINITION Homo sapiens interleukin 5 (IL5) gene, complete cds.
 ACCESSION AF353265
 VERSION AF353265.1 GI:13346490
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 Rieder, M.J., Carrington, D.P., Chung, M.-W., Lee, K.L., Poel, C.L.,

Yi, Q. and Nickerson, D.A.
 Direct Submission
 Submitted (25-FEB-2001) Molecular Biotechnology, University of
 Washington, 1705 NE Pacific, Seattle, WA 98195, USA
 To cite this work please use: SeattleSNPs. NHUBI Program for
 Genomic Applications, UW-FHCRC, Seattle, WA (URL:
 http://pga.mbt.washington.edu).

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QY 61 TTGGGGCTGCTATGTTTCTGCTTCTGTAGAAATCCCATGATAGACTGGTGGCAG 120  
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Db 1948 ACATCACCAGCAACATTTCTGTTAAAGTTATGAATGCTGGTGTGCTGTAATAATGATG 2007  
  
QY 354 TTGTTTCTTTCTTTTCAGAACTGATGATTTCTACTCTCGTAAATATAAATGTAAGTT 413  
Db 2008 -TAUUTCTTTCTCTCCAGACTCTGAGGATTTCTGTTCTCTGTTACATAAATAATGTAAGTT 2066  
  
QY 414 AAATATGATTTGATAAATGATTTACATGATCACTG-----TTTCATATTTTAAGCTATAAA 469  
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DEFINITION AC116366
ACCESSION AC116366
VERSION AC116366.2 GI:21070669
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SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 169385)
AUTHORS DOE Joint Genome Institute and Stanford Human Genome Center.
TITLE Direct Submission
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 169385)
AUTHORS DOE Joint Genome Institute.
TITLE Direct Submission
JOURNAL Submitted (27-MAR-2002) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
REFERENCE 3 (bases 1 to 169385)
AUTHORS DOE Joint Genome Institute and Stanford Human Genome Center.
TITLE Direct Submission
JOURNAL Submitted (22-MAY-2002) DOE Joint Genome Institute, 2800 Mitchell
Drive, Walnut Creek, CA 94598, USA
COMMENT On May 22, 2002 this sequence version replaced gi:19745048.
Draft Sequence Produced by DOE Joint Genome Institute
www.jgi.doe.gov
Finishing Completed at Stanford Human Genome Center
www-shgc.stanford.edu
Quality: Phrap Quality >=40 99.9% of Sequence;
Estimated Total Number of Errors is 0.1.

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DEFINITION	Sequence 78 from patent US 6136603.	linear	PAT 16-JUN-2001
ACCESSION	AR136275		
VERSION	AR136275.1	GI:14476947	
KEYWORDS			
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	Unclassified.		
AUTHORS	1. (Bases 1 to 3230)		
TITLE	Dean, N.M., Karras, J.G. and McKay, R.		
JOURNAL	Antisense modulation of interleukin-5 signal transduction		
FEATURES	Patent: US 6136603-A 78 24-OCT-2000;		
source	Location/Qualifiers		
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Query Match	36.2%;	Score 600.6;	DB 6;
Best Local Similarity	67.8%;	Pred. No. 3.6e-99;	
Matches 1212;	Conservative	0; Mismatches 384;	Indels 191; Gaps 19;
Qy	1	AGGCAACACTGAACATTTGACAGCTATGAGAATGCTTCTGAAATTTGAGTTTGTAGCTC	60
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Qy	61	TTGGGGCTCGCTATGTTTCTGCCCTTTGCTGTAGAAAATCCCATGAATAGACTGGTGGAG	120
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Db	647	AGACCTTTGGCACTGCTTTCTACTCATCGAACTCTGCTATAGCCAAATGAGTAAATTTCT	706
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QY 1215 -----TGGACCAAAATTTTATGCCCTTTTGTGATGAATATATATTTT 1256
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RESULT 8

BD247730 3230 bp DNA linear PAT 17-JUL-2003
LOCUS Antisense modulation of interleukin-5 signal transduction.

DEFINITION BD247730

ACCESSION BD247730.1 GI:33057500

VERSION JP 2002539846-A/78.

KEYWORDS Homo sapiens (human)

SOURCE Homo sapiens

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 3230)

Dean,N.M., Karras,J.G. and McKay,R.

Antisense modulation of interleukin-5 signal transduction

Patent: JP-2002539846-A 78 26-NOV-2002;

ISIS PHARMACEUTICALS INC

OS Homo sapiens (human)

PN JP 2002539846-A/78

PF 17-MAR-2000 JP 2000608790

PR 26-MAR-1999 US 09/280799

PI NICHOLAS M DEAN, JAMES G KARRAS, ROBERT MCKAY

PC C12N15/09, A61K31/711, A61K48/00, A61P11/06, A61P29/00, A61P35/00,

PC A61P43/00,

PC A61P43/00, C12N5/02, C12N15/00

PC Antisense modulation of interleukin-5 signal transduction FH

CC Antisense modulation of interleukin-5 signal transduction FH

Key Location/Qualifiers

FT source 1..3230

FT Location/Qualifiers

1..3230

/organism="Homo sapiens"

/mol_type="genomic DNA"

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Query Match 36.2%; Score 600.6; DB 6; Length 3230;

Best Local Similarity 67.8%; Pred. No. 3.6e-99;

Matches 1212; Conservative 0; Mismatches 384; Indels 191; Gaps 19;

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QY 1215 -----TGGACCAAAATTTTATGCTTTTGGTATCAATTTATTTT 1256
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RESULT 9

E01640

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

E01640 3230 bp DNA linear PAT 29-SEP-1997

gene for human B cell differentiation Factor.

E01640

E01640.1 GI:2169893

JP 1988185387-A/2.

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 3230)

HONSHIYO YUJ

OS Human

PN JP 1988185387-A/2

PD 30-JUL-1988

PF 21-SEP-1987 JP 1987236842

PR 20-SEP-1986 JP 86P 223284

PI HONSHIYO YUJ TAKATSU KIYOSHI, EBA SEBERINSON PC

C12N15/00, C07K13/00, C12N5/00, C12P21/02, (C12N5/00, C12R1/91); CC

strandedness: Double;	
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CC hypothetical: No;	
CC anti-sense: No;	
CC *source: tissue_type=fetal liver;	
CC *source: clone=PKCR-hil-5gene;	
CC Feature is identified by similarity;	
FH Key	
Location/Qualifiers	
5' UTR	509..552
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FT intron	697..904
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FT exon	1883..2011
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ORIGIN	
Query Match	
Best Local Similarity 36.2%; Score 600.6; DB 6; Length 3230;	
Matches 1212; Conservative 0; Mismatches 384; Indels 191; Gaps 19;	
QY 1	AGGCAACACATGAACTTCAGAGCTATGAAATGCTTCGAAATTTGAGTTTCTAGCTC 60
DB 527	AGGCAACACGAGAACTTCAGAGCTATGAAATGCTTCGAAATTTGAGTTTCTAGCTC 586
QY 61	TTGGGCTGCTATGTTCTTCCTCTGCTGAGAAATCCATGATAGCTAGCTGCTGCGAG 120
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DEFINITION	Sequence 1 from patent US 5324640.		linear
ACCESSION	AR364536		
VERSION	AR364536.1	GI:34427297	
KEYWORDS	Unknown.		
SOURCE	Unknown.		
ORGANISM	Unclassified.		
REFERENCE	1 (bases 1 to 3230)		
AUTHORS	Honjo, T., Takatsu, K. and Severinson, E.		
TITLE	Human B-cell differentiation factor and process of producing said factor		
JOURNAL	Patent: US 5324640-A 1 28-JUN-1994;		
FEATURES	Location/Qualifiers		
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	Best Local Similarity	67.8%;	Pred. No. 3.6e-99;
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Qy	1	AGGCAACACTGACATTTCCAGAGCTATGAGAATGCTTCTGAATTTGAGTTTCTAGCTC	60
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Qy	61	TTGGGGTGCGTATGTTTCTGCTTTCCTGTAGAAAATCCCATGAATAGACTGGTGGCAG	120
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Qy	235	-----TTTAAAGATCCATATCAATAATGAAGTAATGAGTGTAAATAATAATAATGGTAACC	293
Db	767	ATATAGAGATCTGTTATATAATATAAGATTCGAG-CACATAGTACATGGGTGATAACT	825
Qy	294	ATGTTATCTCAGAGAATATATATTTAAAAGTTATGAACCTTACAATACATTTAAAATGAATG	353
Db	826	ACATCACCGCAACAACTTCTGTATAAGTTATGAATGCTGTGTGCTGTAAAAATGATTG	885
Qy	354	TTGTTTCCTTTCTTTTCAGAACCTGATGATCTCTACTCTCTGAAAATAAAAATGTAAGTT	413
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Qy	414	AAATTTATCATTTGTATATAATCATATACATGAATCAG-----TTTCATATTTTAAAGCTATAAA	469
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Qy	470	GTATCAGTTAAATGCGGATGATTAATTTTATCTATTTTGTGTTTTATGTGTGGGATGT	529
Db	1005	TCATTTAGTTATCATTTGGAACATATTTAATTTTCTATATTTTCTCATATGTTGGTGGCTGT	1064
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Dy 2044 TGTCCTGGCTG----- 1496
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RESULT 12

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HUMIL5
LOCUS HUMIL5 3230 bp DNA linear PRI 21-AUG-1995
DEFINITION Human interleukin 5 (IL-5) gene, complete cds.
ACCESSION J03478
VERSION J03478.1 GI:186338
KEYWORDS colony stimulating factor; interleukin 5.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 3230)
AUTHORS Tanabe,T., Konishi,M., Mizuta,T., Noma,T. and Honjo,T.
TITLE Molecular cloning and structure of the human interleukin-5 gene
JOURNAL J. Biol. Chem. 262 (34), 16580-16584 (1987)
MEDLINE 88059042
PUBMED 2824500
REFERENCE
2 (bases 1 to 3230)
AUTHORS Tanabe,T.
TITLE Direct Submission
JOURNAL Submitted (09-SEP-1987) T. Tanabe, Department of Medical Chemistry,
Kyoto University Faculty of Medicine, Japan
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LOCUS	E13592	3230 bp	DNA linear PAT 27-APR-1998
DEFINITION	gDNA encoding beta-cell differentiation factor, BCDF.		
ACCESSION	E13592		
VERSION	E13592.1	GI:3252397	
KEYWORDS	JP 1997215496-A/2.		
SOURCE	Homo sapiens		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
AUTHORS	Honshiyu, Y., Takatsu, K. and Eba, S.		
TITLE	PRODUCTION OF HUMAN B CELL DIFFERENTIATION FACTOR		
JOURNAL	Patent: JP 1997215496-A 2 19-AUG-1997;		
COMMENT	HONSHIYO YU		
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	PR	20-SEP-1986 JP 86P 223284	
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	C1	C12N15/09, A61K38/00, A61K38/00, A61K38/00, C07H21/04, C07K14/47, PC	
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QY	1069	ACACTTCTCAGTAATATATAAAACATCATTTAC--TTATGTGTAATATATAGCTTAGTATAAG	1127
Db	1569	AAACTCTCTCAGTAATCATATAAGCTTCACTACTCTTTTGAATTTTATCTTAAATATGTC	1628
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QY	1437	ATATTTGTCTGACTGCTGCTGTTTTTTTTTTTTTTTTTTTTTACAAGAAATGACAGTTTCCTA	1496
Db	2044	TGCTCTGGCTG-----TGCCCTATTTCTATGGAATGACAGTTTCCCTG	2085
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ACCESSION	L48478		
VERSION	L48478.1	GI:1032381	
KEYWORDS			interleukin gene cluster.
SOURCE			Homo sapiens (human)
ORGANISM			Homo sapiens
REFERENCE			Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS			Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
			1 (bases 1 to 3507)
			Martin,C.H., Bondoc,M.M., Chiang,A., Cloutier,T., Davis,C.A.,
			Ericsson,C.L., Jaklevic,M.A., Kim,R.J., Lee,M.T., Li,M.,
			Maveda,C.A., Steiert-El, Kheir,A. and Palazzolo,M.J.
			Sequencing of the interleukin gene cluster of homo sapiens
TITLE			Unpublished (1995)
COMMENT			Original source text: Homo sapiens (tissue library: Subclones in
			POT2 from pl clone H21) DNA.
			This subclone overlaps H21 6 b10 and H21 6 h1.

AUTHORS Bryson, C.E.
TITLE Direct Submission
JOURNAL Submitted (08-NOV-1994) Claire E. Bryson, Department of Veterinary
Science, University of Melbourne, Flemington Rd., Parkville,
Victoria, 3052, Australia

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Location/Qualifiers
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DB 498 TTGGAGCTGCTTAATGTTTGCCAACTGCTGTAAGATACCATGAATAGACTGGTGGGAG 557
QY 121 AGACCTTGACATGCTCTCCACTCATCGAACTTTGGCTGATAGCGGATGGGTAATTTCT 180
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QY 241 GATCCATTAATCAATAATGAAGTAATGAGTGTAAATAAT-----ATAAATG 286
DB 678 GATCTGCTATTAGTCAATGAATTTGAGTTAGTACATATATAATTTGTAACAATATAATT 737
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Qy 889 CTGGATGATGATGCTGATTAATAATGTTAAATAATGCTGATATCATTTAGTCTAAATAGA 948
Db 1401 TGAATATG---CCTGGTCTATATTAATGTTAAATAATATATAGTTT-ATTAGTCTAAATAGA 1456
Qy 949 ATAAATATACAGCTAGAACTATACGAGGAAATCTGAGGTAGGTAAATCAGTAAGGCA 1008
Db 1457 ATAAATATACAGCTAGAACTATGAAACACAT--TGATATGATTTTAAATGATATATGTC- 1513
Qy 1009 GTTGATTTATACCTGTAAGCATTTATTTTTCATTAATCATTTTCTATATATCATTTGTA 1068
Db 1514 -----ATTACACTTCCAAACATTTTTCAGTACATATAATTAAGTTATATCCTTTATA 1568
Qy 1069 ACACCTTCTCAGTAATATATAAATCATTTTAC-TTATGGTAAATATAGCTTAGTATAAG 1127
Db 1569 AAATCTCTCAGTAATCATATAGCTTCACTACTTTTGAATAATTTTATCTTAATATGTG 1628
Qy 1128 GTGGTTTCCACCTGGGAAAGACACAGTAAACCTCTCGGAGAGGGAACCTGTGTA 1187
Db 1629 GTGGTTTGTGCTAGAAA-----ACAAACAAAAAATCTTTTGGAGAGGGAACCTCATGTA 1684
Qy 1188 AACCCCAACAAACAAAGCTCACTTTT----- 1214
Db 1685 AATACCAACAAACAAAGCTCACTTTTGGACCAAAATGTTTAAATAATTTTAA 1744
Qy 1215 ----- 1214
Db 1745 TTGATGAATTAAGATATATATTTTATTTGTGTACAAATATGATCTTTTGAAGTATGTAT 1804
Qy 1215 -----TGGACCAAAATTTTATGCTTTTGTGTAATTTTATGTAATTTT 1256
Db 1805 ACATTCAGAAATGGCAATGGACCAAAATTTTATACCTTGCTTGATTTTGA-TTTT 1863
Qy 1257 TAAATCTTCTCATTTAGCAACCACTGTGCATTTAAAGAAATTTTTCAGGATATAGACAC 1316
Db 1864 AAAAAATTTCTCATTTAGCAACCACTGTGCATGAGAAATCTTTTCAGGGAATAGGCAC 1923
Qy 1317 ATTGAAGAACCAAACTGCCCGGAGGCTGTGGATAAATATTTTCCAAACTGTCTTT 1376

Db 1924 ACTGGAGAGTCAAACTGTGCAAGGGGTACTGTGGAAGAAGTATTCAAAAACCTTGTCCTT 1983
Qy 1377 AATAAAGAACACATAGAGCGCCAAAAGTAAGTAAAGACATTTGGCAAAAACCTTAAGT 1436
Db 1984 AATAAAGAAATACATTTGAGCGCCAAAAGTAAGTAAAGTACACATTTCAATGAAGCTATATT 2043
Qy 1437 ATATTTGTCTGACTGCTGCTGTTTTTTTTTTTTTTTTTTTACAGAAATGACAGTTTCTTA 1496
Db 2044 TGTCTCTGGCTG-----TGCTTATTTCTATGGAATGACAGTTTCTCTG 2085
Qy 1497 CAATATCT-----CCTCTGTTCTTTTAAACAGAAAGGTGTGAGGAGAAAGTGGAGAG 1550
Db 2086 TAATACCTTATTTGTCATTTTCTTTTTCACAGAAAGTGTGGAGAAAGACGGAGAG 2145
Qy 1551 TGACAAAGTTCTTAGACTACCTGCAAGTATTTCTTGTGTAAATAACACCGAGTGGACAC 1610
Db 2146 TAAACCAATTTCTAGACTTACCTGCAAGAGTTTCTTGTGTAAAGAACACCGAGTGGATA 2205
Qy 1611 CGAAAGTTGAGAACAAACCGCTTATGTAGTGAAGATTTTGGAG 1657
Db 2206 TAGAAAGTTGAGACTAAACTGGTTTGTGACCCAAAGATTTTGGAG 2252

RESULT 2
5324640-1
; Patent No. 5324640
; APPLICANT: Honjo, Tazuku, Takatsu, Kiyoshi, Severinson, Eva
; TITLE OF INVENTION: HUMAN B-CELL DIFFERENTIATION FACTOR AND
; PROCESS OF PRODUCING SAID FACTOR
; NUMBER OF SEQUENCES: 2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/99,467
; FILING DATE: 21-SEP-1987
; SEQ ID NO:1:
; LENGTH: 3230
5324640-1

Query Match 36.2%; Score 600.6; DB 6; Length 3230;
Best Local Similarity 67.8%; Pred No. 3e-130;
Matches 1212; Conservative 0; Mismatches 384; Indels 191; Gaps 19;

Qy 1 AGGCAAACTGAAACATTTAGAGCTATGAGAGTCTTCTGAAATTTGAGTTGTAGCTC 60
Db 527 AGGCAAACTGAAACATTTAGAGCTATGAGAGTCTTCTGCAATTTGAGTTGTAGCTC 586
Qy 61 TTGGGGCTGCTCTATCTTCTGCTTTGTAGAAAATCCCATGAATAGACTGGTGGCAG 120
Db 587 TTGGAGCTGCTCTACCTGTATGCTCCATCCCAACAGAAATTTCCACAGTGCATTTGGTGAAG 646
Qy 121 AGACCTTTGACACTGCTCTCCACTCATCGAACTTGGCTGATAGGCGATGGGTAAATTTCT 180
Db 647 AGACCTTTGACACTGCTCTCTCTCTCATCGAACTCTGCTGATAGCCAAATGAGGTAAATTTCT 706
Qy 181 TTTTGAATCTTACAGCTCTTAAATGCAATGGTAAATTTGGTGGTGGTGGTCTAGTT----- 234
Db 707 TTATGATTTCTTACAGCTGTTAAAGTGCATAGTAGTAATCATTTGTGAAGTTCTTTTACTAT 766
Qy 235 -TTTAAAGATCCATTTATCAATTAATGAAGTAAATGAGTGTAAATATATATATATATGGTAAAC 293
Db 767 ATATAGAGATCTGTTATTAATTAATTAAGATTTCTGAG-CACATTTAGTACATGGGTGATAACT 825
Qy 294 ATGTTTACTCAGAAAGTATTAATTAAGTATTAAGACCTTACATACATTAATAATGAATG 353
Db 826 ACATCCAGCAACATTTCTGTTAAAGTATTAAGTATGAGTGTGGTGTCTGTAAATAATGATTTG 885
Qy 354 TTGTTTCTTTTCTTTTTCAGAACTGATGATTTCTCTCTCTGAAATTAATAATGTAAGTT 413
Db 886 -TATTTCTTTCTCTCCAGACTCTGAGATTTCTTCTTCTGTAATAATAATGTAAGTT 944
Qy 414 AAATTAAGTTTGAATAAATGATTAAGTAAATGAGTAAATGAGTAAATGAGTAAATGAGTAA 469
Db 945 AAATTAAGTTTGAATAAATGATTAAGTAAATGAGTAAATGAGTAAATGAGTAAATGAGTAA 1004

;; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
;; FILE REFERENCE: IM-2-C1
;; CURRENT APPLICATION NUMBER: US/09/322,409
;; CURRENT FILING DATE: 1999-05-28
;; EARLIER APPLICATION NUMBER: 60/087,306
;; EARLIER FILING DATE: 1998-05-29
;; NUMBER OF SEQ ID NOS: 154
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 82
;; LENGTH: 610
;; TYPE: DNA
;; ORGANISM: Canis familiaris
US-09-322-409-82

Query Match 10.4%; Score 171.8; DB 4; Length 610;
Best Local Similarity 93.7%; Pred. No. 6.4e-31;
Matches 179; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Qy 1 AGGCAACACCTGAACATTTTCAGAGCTATGAGAAATGCTTCTGAAATTTGAGTTTGTAGCTC 60
Db 608 AGGCAACACCTGAACATTTTCAGAGCTATGAGAAATGCTTCTGAAATTTGAGTTTGTAGCTC 549

Qy 61 TTGGGGCTGCTATGTTTCTGCTTCCCTATGAGAAATCCCATGAATAGACTGGTGGCAG 120
Db 548 TTGGGGCTGCTATGTTTCTGCTTCCCTATGAGAAATCCCATGAATAGACTGGTGGCAG 489

Qy 121 AGACCTTGACACTGCTCTCCACTCATCGAACTTGGCTGATAGGCGATGGGAACTGATGA 180
Db 488 AGACCTTGACACTGCTCTCCACTCATCGAACTTGGCTGATAGGCGATGGGAACTGATGA 429

Qy 181 TTTTGATTCT 191
Db 428 TTCCTACTCT 418

RESULT 5
US-09-451-527-80
; Sequence 80, Application US/09451527
; Patent No. 6482403
; GENERAL INFORMATION:
; APPLICANT: Sim, Gek-Kee
; APPLICANT: Yang, Shumin
; APPLICANT: Dreitz, Matthew J.
; APPLICANT: Wonderling, Ramani S.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; FILE REFERENCE: IM-2-C2
; CURRENT APPLICATION NUMBER: US/09/451,527
; CURRENT FILING DATE: 1999-12-01
; EARLIER APPLICATION NUMBER: 09/322,409
; EARLIER FILING DATE: 1999-05-28
; EARLIER APPLICATION NUMBER: 60/087,306
; EARLIER FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 80
; LENGTH: 610
; TYPE: DNA
; ORGANISM: Canis familiaris
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (29)..(430)
US-09-451-527-80

Query Match 10.4%; Score 171.8; DB 4; Length 610;
Best Local Similarity 93.7%; Pred. No. 6.4e-31;
Matches 179; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Qy 1 AGGCAACACCTGAACATTTTCAGAGCTATGAGAAATGCTTCTGAAATTTGAGTTTGTAGCTC 60
Db 3 AGGCAACACCTGAACATTTTCAGAGCTATGAGAAATGCTTCTGAAATTTGAGTTTGTAGCTC 62

Qy 61 TTGGGGCTGCTATGTTTCTGCTTCCCTATGAGAAATCCCATGAATAGACTGGTGGCAG 120
Db 63 TTGGGGCTGCTATGTTTCTGCTTCCCTATGAGAAATCCCATGAATAGACTGGTGGCAG 122

Qy 121 AGACCTTGACACTGCTCTCCACTCATCGAACTTGGCTGATAGGCGATGGGAACTGATGA 180
Db 123 AGACCTTGACACTGCTCTCCACTCATCGAACTTGGCTGATAGGCGATGGGAACTGATGA 182

Qy 181 TTTTGATTCT 191
Db 183 TTCCTACTCT 193

RESULT 6
US-09-451-527-82/c
; Sequence 82, Application US/09451527
; Patent No. 6482403
; GENERAL INFORMATION:
; APPLICANT: Sim, Gek-Kee
; APPLICANT: Yang, Shumin
; APPLICANT: Dreitz, Matthew J.
; APPLICANT: Wonderling, Ramani S.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; FILE REFERENCE: IM-2-C2
; CURRENT APPLICATION NUMBER: US/09/451,527
; CURRENT FILING DATE: 1999-12-01
; EARLIER APPLICATION NUMBER: 09/322,409
; EARLIER FILING DATE: 1999-05-28
; EARLIER APPLICATION NUMBER: 60/087,306
; EARLIER FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 82
; LENGTH: 610
; TYPE: DNA
; ORGANISM: Canis familiaris
US-09-451-527-82

Query Match 10.4%; Score 171.8; DB 4; Length 610;
Best Local Similarity 93.7%; Pred. No. 6.4e-31;
Matches 179; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Qy 1 AGGCAACACCTGAACATTTTCAGAGCTATGAGAAATGCTTCTGAAATTTGAGTTTGTAGCTC 60
Db 608 AGGCAACACCTGAACATTTTCAGAGCTATGAGAAATGCTTCTGAAATTTGAGTTTGTAGCTC 549

Qy 61 TTGGGGCTGCTATGTTTCTGCTTCCCTATGAGAAATCCCATGAATAGACTGGTGGCAG 120
Db 548 TTGGGGCTGCTATGTTTCTGCTTCCCTATGAGAAATCCCATGAATAGACTGGTGGCAG 489

Qy 121 AGACCTTGACACTGCTCTCCACTCATCGAACTTGGCTGATAGGCGATGGGAACTGATGA 180
Db 488 AGACCTTGACACTGCTCTCCACTCATCGAACTTGGCTGATAGGCGATGGGAACTGATGA 429

Qy 181 TTTTGATTCT 191
Db 428 TTCCTACTCT 418

RESULT 7
US-09-322-409-83
; Sequence 83, Application US/09322409
; Patent No. 6471957
; GENERAL INFORMATION:
; APPLICANT: Sim, Gek-Kee
; APPLICANT: Yang, Shumin
; APPLICANT: Dreitz, Matthew J.
; APPLICANT: Wonderling, Ramani S.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; FILE REFERENCE: IM-2-C1
; CURRENT APPLICATION NUMBER: US/09/322,409

Qy 181 TTTTGATTCT 191
Db 428 TTCCTACTCT 418

```

; CURRENT FILING DATE: 1999-05-28
; EARLIER APPLICATION NUMBER: 60/087,306
; EARLIER FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 154
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 83
; LENGTH: 402
; TYPE: DNA
; ORGANISM: Canis familiaris
US-09-322-409-83

Query Match      8.8%; Score 145.8; DB 4; Length 402;
Best Local Similarity 92.7%; Pred. No. 6.1e-25;
Matches 153; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 27 ATGAGAATGCTTCTGAATTTGAGTTTGTAGCTCTTTGGGGCTGCTATGTTTCTGCTTT 86
Db 1 ATGAGAATGCTTCTGAATTTGAGTTTGTAGCTCTTTGGGGCTGCTATGTTTCTGCTTT 60

QY 87 GCTGTAGAAAATCCCATGATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACTCAT 146
Db 61 GCTGTAGAAAATCCCATGATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACTCAT 120

QY 147 CGAACTTGGCTGATAGCGGATGGGTAATTTCTTTTGTATTCCT 191
Db 121 CGAACTTGGCTGATAGCGGATGGGAACCTGATGATTCCTACTCT 165

RESULT 8
US-09-322-409-84/c
; Sequence 84, Application US/09322409
; Patent No. 6471957
; GENERAL INFORMATION:
; APPLICANT: Sim, Gek-Kee
; APPLICANT: Yang, Shumin
; APPLICANT: Dreitz, Matthew J.
; APPLICANT: Wonderling, Ramani S.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; FILE REFERENCE: IM-2-C1
; CURRENT APPLICATION NUMBER: US/09/322,409
; CURRENT FILING DATE: 1999-05-28
; EARLIER APPLICATION NUMBER: 60/087,306
; EARLIER FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 154
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 84
; LENGTH: 402
; TYPE: DNA
; ORGANISM: Canis familiaris
US-09-322-409-84.

Query Match      8.8%; Score 145.8; DB 4; Length 402;
Best Local Similarity 92.7%; Pred. No. 6.1e-25;
Matches 153; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 27 ATGAGAATGCTTCTGAATTTGAGTTTGTAGCTCTTTGGGGCTGCTATGTTTCTGCTTT 86
Db 402 ATGAGAATGCTTCTGAATTTGAGTTTGTAGCTCTTTGGGGCTGCTATGTTTCTGCTTT 343

QY 87 GCTGTAGAAAATCCCATGATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACTCAT 146
Db 342 GCTGTAGAAAATCCCATGATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACTCAT 283

QY 147 CGAACTTGGCTGATAGCGGATGGGTAATTTCTTTTGTATTCCT 191
Db 282 CGAACTTGGCTGATAGCGGATGGGAACCTGATGATTCCTACTCT 238

RESULT 9
US-09-451-527-83
; Sequence 83, Application US/09451527
; Patent No. 6482403
; GENERAL INFORMATION:
; APPLICANT: Sim, Gek-Kee
; APPLICANT: Yang, Shumin
; APPLICANT: Dreitz, Matthew J.
; APPLICANT: Wonderling, Ramani S.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; FILE REFERENCE: IM-2-C2
; CURRENT APPLICATION NUMBER: US/09/451,527
; CURRENT FILING DATE: 1999-12-01
; EARLIER APPLICATION NUMBER: 09/322,409
; EARLIER FILING DATE: 1999-05-28
; EARLIER APPLICATION NUMBER: 60/087,306
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 84
; LENGTH: 402
; TYPE: DNA
; ORGANISM: Canis familiaris
US-09-451-527-84.

Query Match      8.8%; Score 145.8; DB 4; Length 402;
Best Local Similarity 92.7%; Pred. No. 6.1e-25;
Matches 153; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 27 ATGAGAATGCTTCTGAATTTGAGTTTGTAGCTCTTTGGGGCTGCTATGTTTCTGCTTT 86
Db 402 ATGAGAATGCTTCTGAATTTGAGTTTGTAGCTCTTTGGGGCTGCTATGTTTCTGCTTT 343

; GENERAL INFORMATION:
; APPLICANT: Sim, Gek-Kee
; APPLICANT: Yang, Shumin
; APPLICANT: Dreitz, Matthew J.
; APPLICANT: Wonderling, Ramani S.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; FILE REFERENCE: IM-2-C2
; CURRENT APPLICATION NUMBER: US/09/451,527
; CURRENT FILING DATE: 1999-12-01
; EARLIER APPLICATION NUMBER: 09/322,409
; EARLIER FILING DATE: 1999-05-28
; EARLIER APPLICATION NUMBER: 60/087,306
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 84
; LENGTH: 402
; TYPE: DNA
; ORGANISM: Canis familiaris
US-09-451-527-83.

Query Match      8.8%; Score 145.8; DB 4; Length 402;
Best Local Similarity 92.7%; Pred. No. 6.1e-25;
Matches 153; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 27 ATGAGAATGCTTCTGAATTTGAGTTTGTAGCTCTTTGGGGCTGCTATGTTTCTGCTTT 86
Db 402 ATGAGAATGCTTCTGAATTTGAGTTTGTAGCTCTTTGGGGCTGCTATGTTTCTGCTTT 343
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QY 87 GCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACTCAT 146
Db 342 GCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACTCAT 283
QY 147 CGAAGTTGGCTGATAGCGGATGGGTAATTTCTTTTGATTCCT 191
Db 282 CGAAGTTGGCTGATAGCGGATGGGTAATTTCTTTTGATTCCT 238

RESULT 11

US-09-371-615A-1
; Sequence 1, Application US/09371615A
; Patent No. 6537781
; GENERAL INFORMATION:
; APPLICANT: IDEXX LABORATORIES
; TITLE OF INVENTION: METHODS AND COMPOSITIONS CONCERNING
; FILE REFERENCE: CANINE INTERLEUKIN 5
; FILE REFERENCE: 03604001700US00
; CURRENT APPLICATION NUMBER: US/09/371,615A
; CURRENT FILING DATE: 1999-08-10
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Fast-Seq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 405
; TYPE: DNA
; ORGANISM: Canis familiaris
US-09-371-615A-1

Query Match 8.8%; Score 145.8; DB 4; Length 405;
Best Local Similarity 92.7%; Pred. No. 6.1e-25;
Matches 153; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 27 ATGAGATGCTTCTGAAATTTGAGTTTGTGCTAGCTCTGGGCTGCCATGCTTCTGCTTT 86
Db 1 ATGAGATGCTTCTGAAATTTGAGTTTGTGCTAGCTCTGGGCTGCCATGCTTCTGCTTT 60

QY 87 GCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACTCAT 146
Db 61 GCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACTCAT 120

QY 147 CGAAGTTGGCTGATAGCGGATGGGTAATTTCTTTTGATTCCT 191

Db 121 CGAAGTTGGCTGATAGCGGATGGGTAATTTCTTTTGATTCCT 165

RESULT 12

US-09-322-409-85
; Sequence 85, Application US/09322409
; Patent No. 6471957
; GENERAL INFORMATION:
; APPLICANT: Sim, Gek-Ke
; APPLICANT: Yang, Shumin
; APPLICANT: Dreitz, Matthew J.
; APPLICANT: Wonderling, Ramani S.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; FILE REFERENCE: IM-2-C1
; CURRENT APPLICATION NUMBER: US/09/322,409
; CURRENT FILING DATE: 1999-05-28
; EARLIER APPLICATION NUMBER: 60/087,306
; EARLIER FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 154
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 85
; LENGTH: 345
; TYPE: DNA
; ORGANISM: Canis familiaris
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(345)
US-09-322-409-85

Query Match 7.9%; Score 131.6; DB 4; Length 345;

Best Local Similarity 97.1%; Pred. No. 1.1e-21;
Matches 134; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1274 AGCACCAACTGTGCATTAAAGAGCTTTTTCAGGGTATAGACACATTGCAAGAACCAAACTG 1333
Db 119 ATCACCAACTGTGCATTAAAGAGCTTTTTCAGGGTATAGACACATTGCAAGAACCAAACTG 178
QY 1334 CCCACGGGGAGGCTGTGATAAACTATTCACAAAACCTTGCTTTTAAATAAAGAACACATAG 1393
Db 179 CCCACGGGGAGGCTGTGATAAACTATTCACAAAACCTTGCTTTTAAATAAAGAACACATAG 238
QY 1394 AGCGCCAAAAGTAAGTT 1411
Db 239 AGCGCCAAAAGTAAGTT 256

RESULT 13

US-09-322-409-87/C
; Sequence 87, Application US/09322409
; Patent No. 6471957
; GENERAL INFORMATION:
; APPLICANT: Sim, Gek-Ke
; APPLICANT: Yang, Shumin
; APPLICANT: Dreitz, Matthew J.
; APPLICANT: Wonderling, Ramani S.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; FILE REFERENCE: IM-2-C1
; CURRENT APPLICATION NUMBER: US/09/322,409
; CURRENT FILING DATE: 1999-05-28
; EARLIER APPLICATION NUMBER: 60/087,306
; EARLIER FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 154
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 87
; LENGTH: 345
; TYPE: DNA
; ORGANISM: Canis familiaris
US-09-322-409-87

Query Match 7.9%; Score 131.6; DB 4; Length 345;

Best Local Similarity 97.1%; Pred. No. 1.1e-21;
Matches 134; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1274 AGCACCAACTGTGCATTAAAGAGCTTTTTCAGGGTATAGACACATTGCAAGAACCAAACTG 1333
Db 227 ATCACCAACTGTGCATTAAAGAGCTTTTTCAGGGTATAGACACATTGCAAGAACCAAACTG 168
QY 1334 CCCACGGGGAGGCTGTGATAAACTATTCACAAAACCTTGCTTTTAAATAAAGAACACATAG 1393
Db 167 CCCACGGGGAGGCTGTGATAAACTATTCACAAAACCTTGCTTTTAAATAAAGAACACATAG 108
QY 1394 AGCGCCAAAAGTAAGTT 1411
Db 107 AGCGCCAAAAGTAAGTT 90

RESULT 14

US-09-451-527-85
; Sequence 85, Application US/09451527
; Patent No. 6482403
; GENERAL INFORMATION:
; APPLICANT: Sim, Gek-Ke
; APPLICANT: Yang, Shumin
; APPLICANT: Dreitz, Matthew J.
; APPLICANT: Wonderling, Ramani S.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; FILE REFERENCE: IM-2-C2
; CURRENT APPLICATION NUMBER: US/09/451,527
; CURRENT FILING DATE: 1999-12-01
; EARLIER APPLICATION NUMBER: 09/322,409
; EARLIER FILING DATE: 1999-05-28

; EARLIER APPLICATION NUMBER: 60/087,306
; EARLIER FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 85
; LENGTH: 345
; TYPE: DNA
; ORGANISM: Canis familiaris
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(345)
US-09-451-527-85

Query Match 7.9%; Score 131.6; DB 4; Length 345;
Best Local Similarity 97.1%; Pred. No. 1.1e-21;
Matches 134; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1274 AGCACCACCTGTCATTAAAGAGTTTTCAGGGTATAGACACATTGAGAACCAACTG 1333
DB 119 ATCACCACCTGTCATTAAAGAGTTTTCAGGGTATAGACACATTGAGAACCAACTG 178
QY 1334 CCCACGGGGAGGCTGGGATAAACTATTCCAAAACCTGTCTTTAATAAAGAACACATAG 1393
DB 179 CCCACGGGGAGGCTGGGATAAACTATTCCAAAACCTGTCTTTAATAAAGAACACATAG 238
QY 1394 AGCGCCAAAAGTAAGTT 1411
DB 239 AGCGCCAAAAGTAAGTT 256

RESULT 15
US-09-451-527-87/c
; Sequence 87, Application US/09451527
; Patent No. 6482403
; GENERAL INFORMATION:
; APPLICANT: Sim, Gek-Ke
; APPLICANT: Yang, Shumin
; APPLICANT: Dreitz, Matthew J.
; APPLICANT: Wonderling, Ramani S.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; FILE REFERENCE: IM-2-C2
; CURRENT APPLICATION NUMBER: US/09/451,527
; EARLIER FILING DATE: 1999-12-01
; EARLIER APPLICATION NUMBER: 09/322,409
; EARLIER FILING DATE: 1999-05-28
; EARLIER APPLICATION NUMBER: 60/087,306
; EARLIER FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 87
; LENGTH: 345
; TYPE: DNA
; ORGANISM: Canis familiaris
US-09-451-527-87

Query Match 7.9%; Score 131.6; DB 4; Length 345;
Best Local Similarity 97.1%; Pred. No. 1.1e-21;
Matches 134; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1274 AGCACCACCTGTCATTAAAGAGTTTTCAGGGTATAGACACATTGAGAACCAACTG 1333
DB 227 ATCACCACCTGTCATTAAAGAGTTTTCAGGGTATAGACACATTGAGAACCAACTG 168
QY 1334 CCCACGGGGAGGCTGGGATAAACTATTCCAAAACCTGTCTTTAATAAAGAACACATAG 1393
DB 167 CCCACGGGGAGGCTGGGATAAACTATTCCAAAACCTGTCTTTAATAAAGAACACATAG 108
QY 1394 AGCGCCAAAAGTAAGTT 1411
DB 107 AGCGCCAAAAGTAAGTT 90

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Job time : 151.928 secs

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OM nucleic - nucleic search, using sw model

Run on: August 31, 2004, 13:00:28 ; Search time 4443 Seconds
(without alignments)
11143.708 Million cell updates/sec

Title: US-10-787-382-18
Perfect score: 1658
Sequence: 1 agcacaactgaacatttc.....gtagtgaagatttggaga 1658

Scoring table: OLIGO NUC
Gapop 60.0 , Gapext 60.0

Searched: 27513289 seqs, 14931090276 residues

Word size : 0
Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : EST*

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1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_man:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_phg:*
27: em_gss_vrl:*
28: gb_gssi:*
29: gb_gss2:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	389	23.5	622	29	CE331159 tigr-gss-
2	29	1.7	528	13	EX493336
3	28	1.7	556	13	EX467653
4	28	1.7	684	14	CB076419

5	28	1.7	915	10	BE897924
6	27	1.6	522	9	AL370520
7	27	1.6	534	9	AW102086
8	27	1.6	559	13	BU571592
9	27	1.6	614	14	CA429123
10	27	1.6	687	14	CB824053
11	27	1.6	720	14	CD038829
12	27	1.6	818	29	CNS04725
13	26	1.6	114	14	CB972911
14	26	1.6	114	14	CD407086
15	26	1.6	120	10	BE153390
16	26	1.6	140	12	BQ022057
17	26	1.6	145	12	BM710374
18	26	1.6	202	10	AW524394
19	26	1.6	206	9	AA475329
20	26	1.6	271	12	BG651868
21	26	1.6	273	13	BQ156344
22	26	1.6	287	12	BG157100
23	26	1.6	299	9	AL836569
24	26	1.6	299	9	AL836604
25	26	1.6	322	12	B1708412
26	26	1.6	352	10	BE474681
27	26	1.6	363	13	BU700148
28	26	1.6	371	12	B1299610
29	26	1.6	390	13	BU759812
30	26	1.6	411	9	A1274359
31	26	1.6	415	12	B1301007
32	26	1.6	418	14	CD424543
33	26	1.6	426	10	AW124901
34	26	1.6	426	10	BE687063
35	26	1.6	428	14	R68705
36	26	1.6	429	12	B1376645
37	26	1.6	431	10	BF465903
38	26	1.6	440	14	CA894542
39	26	1.6	441	9	AA028711
40	26	1.6	441	9	A1716899
41	26	1.6	441	14	CA830267
42	26	1.6	443	14	CB250412
43	26	1.6	446	9	AU183176
44	26	1.6	453	12	BG374060
45	26	1.6	455	12	BG377615

ALIGNMENTS

RESULT 1
CE331159
LOCUS tigr-gss-dog-17000333986568 Dog Library Canis familiaris genomic,
DEFINITION genomic survey sequence.
ACCESSION CE331159
VERSION CE331159.1 GI:36147469
KEYWORDS GSS:
SOURCE Canis familiaris (dog)
ORGANISM Canis familiaris
REFERENCE 1 (bases 1 to 622)
AUTHORS Kirksnes,E.F., Bafna,V., Halpern,A.L., Levy,S., Remington,K.,
Rusch,D.B., Delcher,A.L., Pop,M., Wang,M., Fraser,C.W. and
Venter,J.C.
TITLE The dog genome: survey sequencing and comparative analysis
JOURNAL science 301 (5641), 1898-1903 (2003)
MEDLINE 22875432
PUBMED 14512627
COMMENT Contact: Kirkness EF
The Institute for Genomic Research
Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
Rockville, MD 20850, USA
Tel: 301-838-0200
Fax: 301-838-0208
Email: ekirknes@tigr.org

CE331159 622 bp DNA linear GSS 26-SEP-2003
tigr-gss-dog-17000333986568 Dog Library Canis familiaris genomic,
genomic survey sequence.

CE331159
CE331159.1 GI:36147469
GSS:
Canis familiaris (dog)

Canis familiaris
Mammalia; Euthera; Chordata; Vertebrata; Euteleostomi;
Mammalia; Carnivora; Fissipedia; Canidae; Canis.

1 (bases 1 to 622)
Kirksnes,E.F., Bafna,V., Halpern,A.L., Levy,S., Remington,K.,
Rusch,D.B., Delcher,A.L., Pop,M., Wang,M., Fraser,C.W. and
Venter,J.C.

The dog genome: survey sequencing and comparative analysis
science 301 (5641), 1898-1903 (2003)
14512627

Contact: Kirkness EF
The Institute for Genomic Research
Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
Rockville, MD 20850, USA
Tel: 301-838-0200
Fax: 301-838-0208
Email: ekirknes@tigr.org

Class: shotgun.
 Location/Qualifiers
 1. 622
 /organism="Canis familiaris"
 /mol_type="genomic DNA"
 /strain="Standard Poodle"
 /db_xref="taxon:9615"
 /clone_lib="Dog Library"
 /note="Site 1: BstXI; Libraries were prepared from peripheral blood"

ORIGIN

Query Match 23.5%; Score 389; DB 29; Length 622;
 Best Local Similarity 100.0%; Pred. No. 2.3e-66;
 Matches 389; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1270 ATTTAGCACCACCTGTCATTAAAGAGTTTTCAGGGTATAGACACATTGAAGAACCAA 1329
 DB 36 ATTAGCACCACCTGTCATTAAAGAGTTTTCAGGGTATAGACACATTGAAGAACCAA 95
 QY 1330 ACTGCCACGGGGAGGCTGGATAACTATTCCTAAACTTGTCTTAATAAAGAACAC 1389
 DB 96 ACTGCCACGGGGAGGCTGGATAACTATTCCTAAACTTGTCTTAATAAAGAACAC 155
 QY 1390 ATAGAGCGCCAAAGTAAGTAAAGACATTTCGCAAAACTTAAGTATATTTGCTGAC 1449
 DB 156 ATAGAGCGCCAAAGTAAGTAAAGACATTTCGCAAAACTTAAGTATATTTGCTGAC 215
 QY 1450 TCTGCTGTTTTTTTTTTTTTTTACAAAGATTGACAGTTTCTTACAAATATCTCTCT 1509
 DB 216 TCTGCTGTTTTTTTTTTTTTTTACAAAGATTGACAGTTTCTTACAAATATCTCTCT 275
 QY 1510 GTTCTTTTACAGAAAAGGTGTGAGGAGAAAGATGAGAGTACAAAAGTTCTTACACTA 1569
 DB 276 GTTCTTTTACAGAAAAGGTGTGAGGAGAAAGATGAGAGTACAAAAGTTCTTACACTA 335
 QY 1570 CTTCAAGTATTTCTTGGTGTAAATAACACCGAGTGACACCGGAAAGTTGAGAACAAAC 1629
 DB 336 CTTCAAGTATTTCTTGGTGTAAATAACACCGAGTGACACCGGAAAGTTGAGAACAAAC 395
 QY 1630 CGGCTTATTTAGTGGAGAGATTTTGGAGA 1658
 DB 396 CGGCTTATTTAGTGGAGATTTTGGAGA 424

RESULT 2
 BX493336
 LOCUS
 DEFINITION DKFP7811243_s1 781 (synonym: hicc4) Homo sapiens cDNA clone
 DKFP7811243_3', mRNA sequence.
 ACCESSION BX493336
 VERSION BX493336.1 GI:32005734
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 528)
 Bloeker H., Boecker M., Mewes H.W., Weil B., Amid C., Osanger A.,
 Fobo G., Han M. and Wiemann S.
 EST (Bioecker, H., Boecker M., Mewes H.W., Weil B., Amid C., et al.)
 Unpublished (2003)
 Contact: MIPS
 MIPS
 Ingolstaedter Landstr. 1, D-85764 Neuherberg, Germany
 This is the 3' sequence of the clone insert.
 Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
 Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
 sequenced by GBF (National Research Centre for Biotechnology Ltd.,
 Braunschweig/Germany) within the cDNA sequencing consortium of the
 German Genome Project.
 r1 sequence also available.
 This clone (DKFP7811243) is available at the RZPD in Berlin.

Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.

FEATURES
 source
 Location/Qualifiers
 1. 528
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="DKFP7811243"
 /dev_stage="adult"
 /lab_host="DH10B"
 /clone_lib="781 (synonym: hicc4)"
 /note="Vector: pSport1_Sfi; Site_1: SfiI; Site_2: SfiI; CDNA-collection"

ORIGIN

Query Match 1.7%; Score 29; DB 13; Length 528;
 Best Local Similarity 100.0%; Pred. No. 6.1e+03;
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1456 TGTGTTTTTTTTTTTTTTTACAGAATT 1484
 DB 1 TGTGTTTTTTTTTTTTTTTACAGAATT 29

RESULT 3
 BX467653/c
 LOCUS
 DEFINITION BX467653 NAP1 Anopheles gambiae cDNA clone NAP1-P126-D-10-5, mRNA
 sequence.
 ACCESSION BX467653
 VERSION BX467653.1 GI:31658594
 KEYWORDS EST.
 SOURCE Anopheles gambiae (African malaria mosquito)
 ORGANISM Anopheles gambiae
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 Neoptera; Endopterygota; Diptera; Nematocera; Culicoides;
 Anopheles.
 1 (bases 1 to 556)
 Christophides G.K., Blass K., Zdobnov E.M., Carmouche R., Benes V.
 and Kafatos F.C.
 Anopheles gambiae EST, European Molecular Biology Laboratory
 Unpublished (2002)
 Contact: Christophides G.K.
 Fotis C. Kafatos Laboratory
 European Molecular Biology Laboratory
 Meyerhofstr. 1, 69117 Heidelberg, Germany.
 Tel: +49 6221 387-440
 Fax: +49 6221 387-440
 Email: christophe@ebi-heidelberg.de
 Plate: P126 row: D column: 10.
 Location/Qualifiers
 1. 556
 /organism="Anopheles gambiae"
 /mol_type="mRNA"
 /db_xref="taxon:7165"
 /clone="NAP1-P126-D-10-5"
 /lab_host="E. coli DH10B"
 /clone_lib="NAP1"
 /note="Vector: pT7T3D-Pac (Pharmacia); Site 1: NotI;
 Site 2: EcoRI; ESTs sequenced from the T7 priming site
 that reads from the 5' end of cDNA. The NAP1 is a
 directionally cloned and normalized, oligo-T primed cDNA
 library constructed from a mixture of Anopheles gambiae
 developmental stages according to: Bonaldo, Lennon &
 Soares (1996): Normalization and Subtraction: Two
 Approaches To Facilitate Gene Discovery, Genome Research
 6, 791-806."

FEATURES
 source
 Location/Qualifiers

```

ORIGIN
Query Match      1.7%; Score 28; DB 13; Length 556;
Best Local Similarity 100.0%; Pred. No. 9e+03;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1452 TGCGTGTGTTTTTTTTTTTTTTTTTACAA 1479
|||||
Db 552 TGCGTGTGTTTTTTTTTTTTTTTTTACAA 525

RESULT 4
CB076419/c
LOCUS      684 bp      mRNA      linear      EST 24-JAN-2003
DEFINITION h42h04.g1 Hedyotis terminalis flower - Stage 2 (NYBG) Hedyotis
terminalis cDNA clone h42h04, mRNA sequence.
ACCESSION  CB076419
VERSION     CB076419.1 GI:27899856
KEYWORDS   EST.
SOURCE     Hedyotis terminalis
ORGANISM   Hedyotis terminalis
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            asterids; lamids; Gentianales; Rubiaceae; Rubioideae;
            Spmacoceae; Hedyotis.
REFERENCE  1 (bases 1 to 684)
AUTHORS   Levesque,M.P., Twigg,R.W., Motley,T., Katari,M.S., Dedhia,N.N.,
            O'Shaughnessy,A.L., Balija,V., Martienssen,R.A., McCombie,R.W.,
            Benfey,P. and Stevenson,D.
TITLE     Expressed tag sequences from Hedyotis terminalis flower - Stage 2
            (NYBG)
JOURNAL   Unpublished (2003)
COMMENT   Contact: W. Richard McCombie
            Lita Annenberg Hazen Genome Sequencing Center
            Cold Spring Harbor Laboratory
            PO Box 100, Cold Spring Harbor, NY 11724, USA
            Tel: 516 367 8884
            Fax: 516 367 8874
            Email: mcombie@cshl.org
            Plate: h42 row: h column: 04
            Seg primer: -21M13UnivRev
            High quality sequence stop: 684.
FEATURES   Location/Qualifiers
            source          1..684
                        /organism="Hedyotis terminalis"
                        /mol_type="mRNA"
                        /db_xref="taxon:219667"
                        /clone="h42h04"
                        /dev_stage="pre-anthesis; Stage 2"
                        /clone_lib="Hedyotis terminalis flower - Stage 2 (NYBG)"
                        /note="Organ: flower; Vector: pBK-CMV; Site 1: XhoI;
                        Site 2: Eco RI; Date: Completed 12/18/01. Submitted to
                        CSHL 12/21/01 Library: Stratagene ZAP Express cDNA
                        Synthesis Kit. The library was size-fractionated to enrich
                        for large inserts. Sample: collected on the island of
                        Hawaii, Hawaii; NYBG herbarium voucher TM2562"

ORIGIN
Query Match      1.7%; Score 28; DB 14; Length 684;
Best Local Similarity 100.0%; Pred. No. 7.3e+03;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1458 TTTTITTTTTTTTTTTTTTACAGAAATTG 1485
|||||
Db 620 TTTTITTTTTTTTTTTTTTACAGAAATTG 593

RESULT 5
BE897924
LOCUS      915 bp      mRNA      linear      EST 20-OCT-2000
DEFINITION 601440409F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3925155 5',
mRNA sequence.
ACCESSION  BE897924

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VERSION BE897924.1 GI:10363875
KEYWORDS EST.
SOURCE   Homo sapiens (human)
ORGANISM Homo sapiens
Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 915)
AUTHORS   NIH-MGC http://mgi.nci.nih.gov/
TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
            Email: cgabbs-r@mail.nih.gov
            Tissue Procurement: ATCC/DCTD/DTF
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM9764 row: b column: 04
            High quality sequence stop: 418.
FEATURES   Location/Qualifiers
            source          1..915
                        /organism="Homo sapiens"
                        /mol_type="mRNA"
                        /db_xref="taxon:9606"
                        /clone="IMAGE:3925155"
                        /tissue_type="melanotic melanoma"
                        /lab_host="DH10B (phage-resistant)"
                        /clone_lib="NIH_MGC_72"
                        /note="Organ: skin; Vector: pCMV-SPORT6; Site 1: NotI;
                        Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
                        Average insert size 2 kb. Library constructed by Life
                        Technologies."

ORIGIN
Query Match      1.7%; Score 28; DB 10; Length 915;
Best Local Similarity 100.0%; Pred. No. 5.5e+03;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1458 TTTTITTTTTTTTTTTTTTACAGAAATTG 1485
|||||
Db 21 TTTTITTTTTTTTTTTTTTACAGAAATTG 48

RESULT 6
AL370520/c
LOCUS      522 bp      mRNA      linear      EST 03-AUG-2000
DEFINITION McBA38C10R1 McBA Medicago truncatula cDNA clone McBA38C10 T7, mRNA
sequence.
ACCESSION  AL370520
VERSION     AL370520.1 GI:9670273
KEYWORDS   EST.
SOURCE     Medicago truncatula (barrel medic)
ORGANISM   Medicago truncatula
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
            Medicago.
REFERENCE  1 (bases 1 to 522)
AUTHORS   Journet,E.P., Crespeau,H., van-Tuinen,D., Gouzy,J., Jaillon,O.,
            Niebel,A., Carreau,V., Chatagnier,O., Kahn,D.,
            Gianinazzi-Pearson,V. and Gamds,P.
TITLE     Medicago truncatula ESTs from nitrogen-starved roots
JOURNAL   Unpublished (2000)
COMMENT   Contact: Genoscope
            Genoscope - Centre National de Sequencage
            Bp 191 91006 EVRY cedex - France
            Email: sequef@genoscope.cns.fr, Web : www.genoscope.cns.fr
            Contact : Pascal Gamas and Etienne-Pascal Journet, Laboratoire de
            Biologie Moleculaire des Relations Plantes-Microorganismes,
            CNRS-INRA, BP 27 31326 Castanet-Tolosan Cedex, France (Email :
            Mt-est@toulouse.inra.fr Website :

```


FEATURES
source

Location/Qualifiers
1. .559
/organism="Zea mays"
/mol_type="mRNA"
/cultivar="OH43"
/db_xref="taxon:4577"
/tissue_type="tassels"
/dev_stage="just after the transition from vegetative to inflorescence development"
/lab_host="XLOLR"
/clone_lib="946 - tassels primordium prepared by Schmidt lab"
/note="organ: tassels; Vector: HybridZAP; Site 1: EcoRI; Site 2: XhoI; George Chuck dissected immature tassels between 1mm and 3mm. Sharon Stanfield prepared the cDNA library in HybridZAP. Sample insert size range was 350 bp to 3 Kb with a 1 Kb average."

ORIGIN

Query Match 1.6%; Score 27; DB 13; Length 559;
Best Local Similarity 100.0%; Pred. NO. 1.4e+04;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1458 TTTTITTTTTTTTTTTTACAGAATT 1484

DB 6 TTTTITTTTTTTTTTTTACAGAATT 32

RESULT 9

CA429123 614 bp mRNA linear EST 07-NOV-2002
LOCUS UI-H-FHI-bfh-i-16-0-UI-el NCI CGAP FHI Homo sapiens cDNA clone
DEFINITION UI-H-FHI-bfh-i-16-0-UI 3', mRNA sequence.
CA429123
ACCESSION CA429123.1 GI:24791849
VERSION
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
REFERENCE
AUTHORS
TITLE NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL
COMMENT Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapsb@email.nih.gov
Tissue Procurement: James Martin
cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained from Dr. M. Bento Soares, bento-soares@uiowa.edu
The following repetitive elements were found in this cDNA sequence: 1-45, >AT richLow_complexity 46-166, >ALU (matched complement) 500-595, >ALU
Seq primer: M13 FORWARD
POLYA=Yes

FEATURES
source

Location/Qualifiers
1. .614
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-H-FHI-bfh-i-16-0-UI"
/tissue_type="Cell Line"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI CGAP FHI"
/note="Organ: Chondrosarcoma; Vector: p7T3-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I; NCI CGAP FHI is a normalized cDNA library obtained from a cell line derived from grade I chondrosarcoma tissue. The library was constructed and

normalized according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into p7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is AGAATCCGGC. The cell line was provided by Dr. James Martin from the University of Iowa.
TAG TISSUE=Human Chondrosarcoma Cell Line CS8 - Grade 1
Chondrosarcoma
TAG LIB=UI-H-FHI
TAG_SEQ=AGAATCCGGC"

ORIGIN

Query Match 1.6%; Score 27; DB 14; Length 614;
Best Local Similarity 100.0%; Pred. NO. 1.3e+04;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1458 TTTTITTTTTTTTTTTTACAGAATT 1484

DB 1 TTTTITTTTTTTTTTTTACAGAATT 27

RESULT 10

CB824053 687 bp mRNA linear EST 16-MAY-2003
LOCUS EST 5277 Ripe Apricot Fruit Lambda Zap II Library Prunus armeniaca
DEFINITION cDNA clone bh02p09 3', mRNA sequence.
CB824053
ACCESSION CB824053.1 GI:29959806
VERSION
KEYWORDS
SOURCE Prunus armeniaca (apricot)
ORGANISM

Prunus armeniaca
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosids; eurosid1; Rosales; Rosaceae; Amygdaloideae; Prunus.
1 (bases 1 to 687)
Bouchet,J.P. and Terrier,N.
High throughput Detection of Isogenes among 5724 3' EST from Apricot Fruit (Prunus armeniaca)
Contact: Audergon JM
Unpublished (2003)
Contact: Audergon JM
Unite de genetique et amelioration des fruits et legumes
Institut National de la Recherche Agronomique
Domaine Saint-Maurice BP 94 84143 Montfavet cedex
Tel: 00-33-(0)4-32-72-26-68
Fax: 00-33-(0)4-32-72-26-62
Email: audergon@avignon.inra.fr
Seq primer: T7.

JOURNAL

COMMENT

FEATURES

source

Location/Qualifiers
1. .687
/organism="Prunus armeniaca"
/mol_type="mRNA"
/cultivar="Bergeron"
/db_xref="taxon:36596"
/clone="bh02p09"
/dev_stage="Ripe stage"
/clone_lib="Ripe Apricot Fruit Lambda Zap II Library"
/note="Organ: Fruit; Vector: Lambda Zap II; Site 1: Eco RI; Site 2: XhoI; Oriented library, construction described in Molecular cloning and expression of a cDNA encoding 1-aminocyclopropane-1-carboxylate (ACC) oxidase from apricot fruit (Prunus armeniaca cv. Bergeron) by Mbeugue-Mbeugue D, Chahine H, Gomez RM, Gouble B, Audergon JM, Souty M, Albagnac G, Fils-Lycaon B in Physiol Plant 105:294-303, 1999"

ORIGIN

Query Match 1.6%; Score 27; DB 14; Length 687;

Best Local Similarity 100.0%; Pred. No. 1.1e+04; Mismatches 0; Indels 0; Gaps 0;

Qy 1458 TTTT...TTTACAGAATT 1484

Db 3 TTTT...TTTACAGAATT 29

RESULT 11

CDS038829

LOCUS

DEFINITION

UTPPI012_G08 USDA-Tifton Peanut Immature Pod cDNA Library (UTPP)

Atachis hypogaea cDNA clone UTPPI012_G08 5', mRNA sequence.

ACCESSION

CDS038829

VERSION

CDS038829.1 GI:30420667

KEYWORDS

EST.

SOURCE

Arachis hypogaea (peanut)

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Ascyonomenae; Arachis.

REFERENCE

1 (bases 1 to 720)

AUTHORS

Luo, M., Dang, P., Guo, B.Z., Holbrook, C.C., Lee, R.D., Bausher, M.G. and Lynch, R.E.

TITLE

Generation and Analyses of ESTs for Arachis hypogaea

JOURNAL

Unpublished (2003)

COMMENT

Contact: Baozhu Guo

Molecular Genetics

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2747 Davis Rd., Tifton, GA 31794, USA

Tel: 229-387-2334

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Email: bguo@tifton.usda.gov

Seq primer: T3.

FEATURES

source

1. 720

/organism="Arachis hypogaea"

/mol_type="mRNA"

/cultivar="A13"

/db_xref="taxon:3818"

/clone="UTPPI012_G08"

/tissue_type="Immature pods"

/dev_stage="R6"

/lab_host="X11-blue"

/clone_lib="USDA-Tifton Peanut Immature Pod cDNA Library (UTPP)"

/notes="Vector: Uni-ZAP XR; Site 1: EcoRI; Site 2: XhoI; cDNA library was constructed from peanut cultivar A13 (NCV1XAR4). A13 has resistance to Aspergillus infection and drought tolerance. The immature pods that developed to R6 stage were collected from different plants, and placed into liquid N2 immediately and stored in -80°C freezer. Total RNA was isolated with TRIzol-Reagent ultrapure (GIBCOBRL). mRNA was extracted and purified from total RNA (Promega). cDNA synthesis and library construction followed the protocol of by ZAP-cDNA Gigapack III Gold cloning kit (Stratagene). The cDNA above 500bp were collected after size-fraction. The inserts were directionally cloned into Uni-ZAP XR vector using XhoI EcoRI sites adaptors. The lambda library was packed into phages using Gigapack III Gold (Stratagene). The un-amplified library was used to excise pBluescript phagemids from the Uni-ZAP XR vector, and the phagemids was used to transform the host bacteria SOLR. The library was constructed by Dr. Meng Luo and Dr. Phat Dang."

ORIGIN

Query Match 1.6%; Score 27; DB 14; Length 720;

Best Local Similarity 100.0%; Pred. No. 1.1e+04; Mismatches 0; Indels 0; Gaps 0;

Qy 1458 TTTT...TTTACAGAATT 1484

Db 11 TTTT...TTTACAGAATT 37

RESULT 12

CNS04725

LOCUS

DEFINITION

Tetraodon nigroviridis genome survey sequence PUC-Ori end of clone

089D09 of library G from Tetraodon nigroviridis, genomic survey

sequence.

ACCESSION

AL278618

VERSION

AL278618.1 GI:8014612

KEYWORDS

GSS; genome survey sequence.

SOURCE

Tetraodon nigroviridis

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;

Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;

Tetraodontidae; Tetraodontidae; Tetraodon.

REFERENCE

1

AUTHORS

Roest Crolius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C.,

Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F.,

Saurin, W., and Weissenbach, J.

Estimate of human gene number provided by genome-wide analysis

using Tetraodon nigroviridis DNA sequence

Nat. Genet. 25 (2), 235-238 (2000)

20296633

PUBMED

10835645

REFERENCE

2

AUTHORS

Roest Crolius, H., Jaillon, O., Dasilva, C., Ozouf-Costaz, C.,

Fizames, C., Fischer, C., Bouneau, L., Billault, A., Quetier, F.,

Saurin, W., Bernot, A., and Weissenbach, J.

Characterization and repeat analysis of the compact genome of the

freshwater pufferfish Tetraodon nigroviridis

Genome Res. 10 (7), 939-949 (2000)

20359837

PUBMED

10899143

REFERENCE

3 (bases 1 to 818)

AUTHORS

Genoscope.

Direct Submission

Submitted (12-APR-2000) Genoscope - Centre National de Sequencage :

BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr

- Web : www.genoscope.cns.fr)

This sequence is a single read and was generated as part of a large

scale clone-end sequencing project of the Tetraodon nigroviridis

genome. For more information, please take a look at

http://www.genoscope.cns.fr/Tetraodon.

FEATURES

source

1. 818

Location/Qualifiers

/organism="Tetraodon nigroviridis"

/mol_type="genomic DNA"

/db_xref="taxon:99863"

/clone="089D09"

/clone_lib="G"

/notes="Genoscope sequence ID : C0BG089CB05SP1-end ;

PUC-Ori"

ORIGIN

Query Match 1.6%; Score 27; DB 29; Length 818;

Best Local Similarity 100.0%; Pred. No. 9.5e+03;

Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1449 CTCTGCTGTTTTTTTTTTTTTTTTTTTTTTT 1475

Db 585 CTCTGCTGTTTTTTTTTTTTTTTTTTTTTTT 611

RESULT 13

CB972911/c

LOCUS

DEFINITION

vinifera cDNA clone CAB30001_ib_Fb_F11 5', mRNA sequence.

ACCESSION

CB972911

Query Match 1.6%; Score 27; DB 14; Length 720;

Best Local Similarity 100.0%; Pred. No. 1.1e+04;

Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1458 TTTT...TTTACAGAATT 1484


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VERSION      CB972911.1  GI:30296117
KEYWORDS     EST.
SOURCE       Vitis vinifera
ORGANISM     Vitis vinifera
             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
             Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
             rosids; Vitaceae; Vitis.

REFERENCE    1 (bases 1 to 114)
AUTHORS      Goes da Silva, F., Iandolino, A., Lim, H., Baek, J., Jones, K. and
             Cook, D.
             Expressed sequence tags from Vitis vinifera 'Cabernet sauvignon'
             berries at various developmental stages
             Unpublished (2003)
             Contact: Douglas Cook, PhD
             CAES Genome Facility
             UC Davis, Plant Pathology
             One Shields Ave, Davis, CA 95616, USA
             Tel: 530 754 6561
             Fax: 530 754 6617
             Email: drcook@ucdavis.edu
             Seq primer: ACGTACCGACATATGCC.
FEATURES     Location/Qualifiers
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             /organism="Vitis vinifera"
             /mol_type="RNA"
             /cultivar="Cabernet Sauvignon"
             /db_xref="taxon:29760"
             /clone="CAB30001_Ib_Fb_F11"
             /sex="Hermaphrodite"
             /dev_stage="Berry stage I"
             /lab_host="DH5alpha"
             /clone_lib="Cabernet Sauvignon Berry Stage I - CAB3"
             /note="Organ: Berry; Vector: pDMR; Site 1: Sfil; Site 2:
             Sfil; CAB3 is a cDNA library of Vitis vinifera 'Cabernet
             Sauvignon' Clone 8 berries. Samples were collected after
             berry set from field-grown vines during stage I of berry
             growth, 17 days after full bloom. The average berry size
             was 6 millimeters. Sampled vines were located at the
             University of California, Davis, Experimental Vineyard.
             cDNAs were made by oligo-dT priming and directionally
             cloned. 5' and 3' adaptors were used in cloning as follows:
             5'-AAGCAGTGGTATCAACGAGTGGCCATTACGCGGG-3' and
             5'-ATTCTAGAGCGGCGGCGGACATG-3' (30)NN-3'. Library was
             constructed using the Clontech Creator SMART kit and
             size-selected to contain the 0.5-3 kb size fraction."

ORIGIN
Query Match      1.6%; Score 26; DB 14; Length 114;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1458 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT
      |||||
Db 112 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT

RESULT 14
LOCUS      CD407086
DEFINITION Gm_cx32086 Soybean induced by Salicylic Acid Glycine max cDNA 3',
            mRNA sequence.
ACCESSION  CD407086
VERSION     CD407086.1  GI:31465058
KEYWORDS   EST.
SOURCE      Glycine max (soybean)
ORGANISM   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
            Glycine.
            1 (bases 1 to 114)
AUTHORS     Tian, A.-G., Wang, J., Qui, P., Han, Y.-J., Xu, H., Cong, L.-J.,
            Huang, X.-G., Wang, X.-L., Jiao, Y.-Z., Wang, B.-J., Wang, Y.-J.,

TITLE       CD407086
JOURNAL     Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE     20202663
PUBMED      10737800
COMMENT     Contact: Simpson A. J. G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil

TITLE       Soybean Expressed Sequence Tags Sequencing
JOURNAL     Unpublished (2003)
COMMENT     Contact: Chen S-Y
            Plant Biotechnology Laboratory
            Institute of Genetics and Developmental Biology, CAS, China
            Datun road, Beijing 100101, China
            Tel: 86-10-64868659
            Fax: 86-10-64873428
            Email: sychen@genetics.ac.cn
            Email: sychen@genetics.ac.cn
            Seq primer: T7 primer.
FEATURES     Location/Qualifiers
             1..114
             /organism="Glycine max"
             /mol_type="mRNA"
             /cultivar="Kefeng 1"
             /db_xref="taxon:3847"
             /tissue_type="Seedlings"
             /dev_stage="two-week seedlings"
             /lab_host="XLI-Blue MRF, strain"
             /clone_lib="Soybean induced by Salicylic Acid"
             /note="Vector: pluscript SK+; Site 1: EcoR I; Site 2:
             Xho I; The cDNA library was constructed by He, C-Y from
             mRNA isolated from two-week seedlings (cultivar Kefeng 1)
             treated by spraying 2.0mM salicylic acid for 24, 36, 48
             and 72 h. Complementary DNA was synthesized from mRNA
             using a primer consisting of a poly(GT) sequence with a
             XhoI restriction site. EcoRI adapters were ligated to the
             blunt-ended cDNA fragments followed by XhoI digestion. The
             cDNA fragments were directionally cloned into the
             EcoRI-XhoI restriction site of the pluscript vector. The
             ligated cDNA fragments were transformed into XLI-Blue MRF.
             host cells (Stratagene)."

```

Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the FAPESP/LICR Human Cancer Genome
 Project. This entry can be seen in the following URL
 (<http://www.ludwig.org.br/scripts/gethtml2.pl?tl=st2=PM1-HT0350-270>)
 300-010-d06&t3=2000-03-27&t4=1)
 Seq primer: puc 18 forward
 High quality sequence start: 4
 High quality sequence stop: 68.

FEATURES

Location/Qualifiers
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 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /dev_stage="Adult"
 /clone_lib="HT0350"

/note="Organ: head neck; Vector: puc18; Site: 1: SmaI;
 Site 2: SmaI; A mini-library was made by cloning products
 derived from ORESYS PCR (U.S. Letters Patent application
 No. 196,716 - Ludwig Institute for Cancer Research)
 profiles into the pUC 18 vector. Reverse transcription of
 tissue mRNA and cDNA amplification were performed under
 low stringency conditions."

ORIGIN

Query Match 1..68; Score 26; DB 10; Length 120;
 Best Local Similarity 100.0%; Pred. NO. 1e-05;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1453 GCCTGTTTTTTTTTTTTTTTAC 1478
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 Db 112 GCCGTTTTTTTTTTTTTTTACA 87

Search completed: August 31, 2004, 17:42:19
 Job time : 4449 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 31, 2004, 14:34:40 ; Search time 770 Seconds
(without alignments)
10597.045 Million cell updates/sec

Title: US-10-787-382-18
Perfect score: 1658
Sequence: 1 aggcacactgaacatttc.....gtagtggaagatttggaga 1658

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 3237270 seqs, 2460713050 residues

Word size : 0
Total number of hits satisfying chosen parameters: 6474540

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published Applications NA:
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2: /cgn2_6/prodata/1/pubpna/PCT_NEW_PUB.seq:
3: /cgn2_6/prodata/1/pubpna/US06_NEW_PUB.seq:
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5: /cgn2_6/prodata/1/pubpna/US07_NEW_PUB.seq:
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9: /cgn2_6/prodata/1/pubpna/US09A_PUBCOMB.seq:
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11: /cgn2_6/prodata/1/pubpna/US09C_PUBCOMB.seq:
12: /cgn2_6/prodata/1/pubpna/US09_NEW_PUB.seq:
13: /cgn2_6/prodata/1/pubpna/US09_PUBCOMB.seq:
14: /cgn2_6/prodata/1/pubpna/US10A_PUBCOMB.seq:
15: /cgn2_6/prodata/1/pubpna/US10B_PUBCOMB.seq:
16: /cgn2_6/prodata/1/pubpna/US10C_PUBCOMB.seq:
17: /cgn2_6/prodata/1/pubpna/US10_NEW_PUB.seq:
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19: /cgn2_6/prodata/1/pubpna/US60_PUBCOMB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1658	100.0	1658	9	US-09-755-633-18
2	1335	80.5	1658	9	US-09-755-633-19
3	406	24.5	671	9	US-09-755-633-21
4	170	10.3	610	9	US-09-755-633-4
5	170	10.3	610	9	US-09-755-633-6
6	170	10.3	610	15	US-10-218-654-80
7	170	10.3	610	15	US-10-218-654-82
8	170	10.3	610	15	US-10-262-439-80
9	170	10.3	610	15	US-10-262-439-82
10	144	8.7	402	9	US-09-755-633-7
11	144	8.7	402	9	US-09-755-633-8
12	144	8.7	402	15	US-10-218-654-83
13	144	8.7	402	15	US-10-218-654-84
14	144	8.7	402	15	US-10-262-439-83

C 15	144	8.7	402	15	US-10-262-439-84	Sequence 84, Appl
C 16	129	7.8	345	9	US-09-755-633-9	Sequence 9, Appl
C 17	129	7.8	345	9	US-09-755-633-11	Sequence 11, Appl
C 18	129	7.8	345	15	US-10-218-654-85	Sequence 85, Appl
C 19	129	7.8	345	15	US-10-218-654-87	Sequence 87, Appl
C 20	129	7.8	345	15	US-10-262-439-85	Sequence 85, Appl
C 21	129	7.8	345	15	US-10-262-439-87	Sequence 87, Appl
C 22	28	1.7	2122	13	US-10-424-599-35126	Sequence 35126, A
C 23	26	1.6	394	17	US-10-437-963-99632	Sequence 99632, A
C 24	26	1.6	2235	15	US-10-318-780-20	Sequence 20, Appl
C 25	26	1.6	3230	9	US-09-800-623A-78	Sequence 78, Appl
C 26	26	1.6	3230	17	US-10-679-532-78	Sequence 78, Appl
C 27	25	1.5	407	15	US-10-198-846-13075	Sequence 13075, A
C 28	25	1.5	461	15	US-10-198-846-6011	Sequence 6011, Ap
C 29	25	1.5	512	13	US-10-621-901-295	Sequence 295, App
C 30	25	1.5	516	17	US-10-437-963-51964	Sequence 51964, A
C 31	25	1.5	586	13	US-10-027-632-220494	Sequence 220494, A
C 32	25	1.5	586	16	US-10-027-632-220494	Sequence 220494, A
C 33	25	1.5	596	13	US-09-770-152-6	Sequence 6, Appl
C 34	25	1.5	608	17	US-10-437-963-40666	Sequence 40666, A
C 35	25	1.5	824	9	US-09-770-445-715	Sequence 715, App
C 36	25	1.5	850	17	US-10-437-963-31566	Sequence 31566, A
C 37	25	1.5	859	17	US-10-437-963-48530	Sequence 48530, A
C 38	25	1.5	937	17	US-10-437-963-5140	Sequence 5140, Ap
C 39	25	1.5	970	10	US-09-934-455-293	Sequence 293, App
C 40	25	1.5	970	13	US-10-225-066A-691	Sequence 691, App
C 41	25	1.5	970	16	US-10-374-780A-2213	Sequence 2213, Ap
C 42	25	1.5	1475	17	US-10-437-963-18375	Sequence 18375, A
C 43	25	1.5	1607	17	US-10-437-963-9407	Sequence 9407, Ap
C 44	25	1.5	1740	15	US-10-260-046-19	Sequence 19, Appl
C 45	25	1.5	3018	17	US-10-332-406A-5	Sequence 5, Appl

ALIGNMENTS

RESULT 1

US-09-755-633-18
Sequence 18, Application US/09755633
Patent No. US20020127200A1
GENERAL INFORMATION:
APPLICANT: Yang, Shumin
APPLICANT: McCall, Catherine A.
APPLICANT: Weber, Eric R.
TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
FILE REFERENCE: IM-2-C1-C1
CURRENT APPLICATION NUMBER: US/09755,633
CURRENT FILING DATE: 2001-01-05
PRIOR APPLICATION NUMBER: 09/322,409
PRIOR FILING DATE: 1999-05-28
PRIOR APPLICATION NUMBER: 60/087,306
PRIOR FILING DATE: 1998-05-29
NUMBER OF SEQ ID NOS: 21
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 18
LENGTH: 1658
TYPE: DNA
ORGANISM: Canis familiaris
FEATURE:
NAME/KEY: Intron
LOCATION: (171)..(373)
NAME/KEY: Intron
LOCATION: (407)..(1275)
NAME/KEY: Intron
LOCATION: (1405)..(1522)
US-09-755-633-18

Query Match 100.0%; Score 1658; DB 9; Length 1658;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1658; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGGCAACACTGAACATTTCAGAGCTATGAGAGTCCTCTGAAATTGAGTTGCTAGCTC 60

Db 1 AGGCAACACTGACATTTTCAGAGCTATGAGATGCTTCGAAATTTGAGTTTGTCTAGCTC 60
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Db 61 TTGGGGCTGCTATGTTTTCGCTTTCGCTGTAGAAAATCCATGAATAGACATGGTGGCAG 120
Qy 121 AGACCTTGACACTGCTCTCACTCATCGAATTTGGCTGTAGCGGATGGGTAATTTTCT 180
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Qy 541 TTATGAATATAGGAATGGTGTAGGAATGGTGTAGGAATGGTGTAGGAATGGTGTAGGAAT 600
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Qy 601 CAAGTGATCAGGCTCTTTTGAATGTTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 660
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Db 661 GGCATCTCTTCCAAAAGAAATCCATATTTGGGTGAGAGATCTTCTAGGCTCCATTCACC 720
Qy 721 TCTGCTGCTGCTTCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTC 780
Db 721 TCTGCTGCTGCTTCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTC 780
Qy 781 ATTTTGAATATAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGT 840
Db 781 ATTTTGAATATAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGT 840
Qy 841 ACTTCCACATATTTAAATGATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTT 900
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Qy 1201 AAAGTCTAACTTTTGGACCAAAATTTTATGCTCTGTTTGTGATGAATATATTTTAAA 1260
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Qy 1261 ATCTCTCTCAATTTAGACCAACTGTGATTAAGAAATTTTTCAGGTAATAGACATTTG 1320
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Qy 1321 AAGAACCAAACTGCCACGGGAGCTGTGATAACTATTTCACAAAATTTTCTTAAATA 1380
Db 1321 AAGAACCAAACTGCCACGGGAGCTGTGATAACTATTTCACAAAATTTTCTTAAATA 1380
Qy 1381 AAAGAACACATAGAGCGCCAAAAAGTAAAGTAAAGACATTTGGCAAAACTTAAAGTATAT 1440
Db 1381 AAAGAACACATAGAGCGCCAAAAAGTAAAGTAAAGACATTTGGCAAAACTTAAAGTATAT 1440
Qy 1441 TTGCTGACTCTGCTGCTGTTTTTTTTTTTTTTTTTTTTTTTACAGAAATGACAGTTTCTTACAAT 1500
Db 1441 TTGCTGACTCTGCTGCTGTTTTTTTTTTTTTTTTTTTTTTTACAGAAATGACAGTTTCTTACAAT 1500
Qy 1501 ATCTCTCTGTTCTTTTAAACAGAAAAGTGTGAGGAGAAAGATGGAGAGTGCACAAAGTT 1560
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Db 1561 CTTAGACTACTGCAAGTATTTCTGTTGTAAATAAACACCGAGTGGACACCGGAAAGTTG 1620
Qy 1621 AGAACAAACCGGCTTATTGTAGTGAAGATTTTGGAGA 1658
Db 1621 AGAACAAACCGGCTTATTGTAGTGAAGATTTTGGAGA 1658

RESULT 2

US-09-755-633-19/c
; Sequence 19, Application US/09755633
; Patent No. US20202127200A1
; GENERAL INFORMATION:
; APPLICANT: Yang, Shumin
; APPLICANT: McCall, Catherine A.
; APPLICANT: Weber, Eric R.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; FILE OF INVENTION: ACID MOLECULES, AND USES THEREOF
; FILE REFERENCE: IM-2-C1-C1
; CURRENT APPLICATION NUMBER: US/09/755,633
; CURRENT FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: 09/322,409
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/087,306
; PRIOR FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 19
; LENGTH: 1658
; TYPE: DNA
; ORGANISM: Canis familiaris
US-09-755-633-19

Query Match 80.5%; Score 1335; DB 9; Length 1658;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1625; Conservative 0; Mismatches 1; Indels 2; Gaps 2;
Qy 32 AATGCTTCTGAATTTGAGTTTGTAGCTCTTGGGGCTGCTATGTTTCTGCTTTGCTGT 91
Db 1627 AATGCTTCTGAATTTGAGTTTGTAGCTCTTGGGGCTGCTATGTTTCTGCTTTGCTGT 1568
Qy 92 AGAAATCCCATGAATAGTAGTGGGAGAGACCTTGACACTGCTCTCCACTCATCGAAC 151

Db 63 TTGGGGCTGCTATGTTTCTGCTTGTGAGAAAATCCATGAATAGACTGGTGGCAG 122
QY 121 AGACTTGACACTGCTTCCGACTCATCGAATCTTGGCTGATAGGCGATGGG 170
Db 123 AGACCTTGACACTGCTTCCACTCATCGAATCTGGCTGATAGGCGATGGG 172

RESULT 7

US-10-218-654-82/c
; Sequence 82, Application US/10218654
; Publication No. US20030099609A1
; GENERAL INFORMATION:
; APPLICANT: Sim, Gek-Kee
; APPLICANT: Yang, Shumin
; APPLICANT: Dreitz, Matthew J.
; APPLICANT: Wonderling, Ramani S.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; FILE REFERENCE: IM-2-C1
; CURRENT APPLICATION NUMBER: US/10/218,654
; PRIOR FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: US/09/322,409
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/087,306
; PRIOR FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 154
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 82
; LENGTH: 610
; TYPE: DNA
; ORGANISM: Canis familiaris
US-10-218-654-82

Query Match 10.3%; Score 170; DB 15; Length 610;
Best Local Similarity 100.0%; Pred. No. 1.3e-70;
Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AGGCAAACTGAACATTTGAGACTATGAGAAATCTTCTGAATTTGAGTTTGTAGCTC 60
Db 608 AGGCAAACTGAACATTTGAGACTATGAGAAATCTTCTGAATTTGAGTTTGTAGCTC 549
QY 61 TTGGGGCTGCTATGTTTCTGCTTGTGAGAAAATCCATGAATAGACTGGTGGCAG 120
Db 548 TTGGGGCTGCTATGTTTCTGCTTGTGAGAAAATCCATGAATAGACTGGTGGCAG 489
QY 121 AGACCTTGACACTGCTTCCACTCATCGAATCTGGCTGATAGGCGATGGG 170
Db 488 AGACCTTGACACTGCTTCCACTCATCGAATCTGGCTGATAGGCGATGGG 439

RESULT 8

US-10-262-439-80
; Sequence 80, Application US/10262439
; Publication No. US20030143196A1
; GENERAL INFORMATION:
; APPLICANT: Sim, Gek-Kee
; APPLICANT: Yang, Shumin
; APPLICANT: Dreitz, Matthew J.
; APPLICANT: Wonderling, Ramani S.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; FILE REFERENCE: IM-2-C2
; CURRENT APPLICATION NUMBER: US/10/262,439
; PRIOR FILING DATE: 2002-09-30
; PRIOR APPLICATION NUMBER: US/09/451,527
; PRIOR FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: 09/322,409
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/087,306
; PRIOR FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 80

; LENGTH: 610
; TYPE: DNA
; ORGANISM: Canis familiaris
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (29)..(430)
US-10-262-439-80

Query Match 10.3%; Score 170; DB 15; Length 610;
Best Local Similarity 100.0%; Pred. No. 1.3e-70;
Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AGGCAAACTGAACATTTGAGACTATGAGAAATCTTCTGAATTTGAGTTTGTAGCTC 60
Db 3 AGGCAAACTGAACATTTGAGACTATGAGAAATCTTCTGAATTTGAGTTTGTAGCTC 62
QY 61 TTGGGGCTGCTATGTTTCTGCTTGTGAGAAAATCCATGAATAGACTGGTGGCAG 120
Db 63 TTGGGGCTGCTATGTTTCTGCTTGTGAGAAAATCCATGAATAGACTGGTGGCAG 122
QY 121 AGACCTTGACACTGCTTCCACTCATCGAATCTGGCTGATAGGCGATGGG 170
Db 123 AGACCTTGACACTGCTTCCACTCATCGAATCTGGCTGATAGGCGATGGG 172

RESULT 9

US-10-262-439-82/c
; Sequence 82, Application US/10262439
; Publication No. US20030143196A1
; GENERAL INFORMATION:
; APPLICANT: Sim, Gek-Kee
; APPLICANT: Yang, Shumin
; APPLICANT: Dreitz, Matthew J.
; APPLICANT: Wonderling, Ramani S.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; FILE REFERENCE: IM-2-C2
; CURRENT APPLICATION NUMBER: US/10/262,439
; PRIOR FILING DATE: 2002-09-30
; PRIOR APPLICATION NUMBER: US/09/451,527
; PRIOR FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: 09/322,409
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/087,306
; PRIOR FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 82
; LENGTH: 610
; TYPE: DNA
; ORGANISM: Canis familiaris
US-10-262-439-82

Query Match 10.3%; Score 170; DB 15; Length 610;
Best Local Similarity 100.0%; Pred. No. 1.3e-70;
Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AGGCAAACTGAACATTTGAGACTATGAGAAATCTTCTGAATTTGAGTTTGTAGCTC 60
Db 608 AGGCAAACTGAACATTTGAGACTATGAGAAATCTTCTGAATTTGAGTTTGTAGCTC 549
QY 61 TTGGGGCTGCTATGTTTCTGCTTGTGAGAAAATCCATGAATAGACTGGTGGCAG 120
Db 548 TTGGGGCTGCTATGTTTCTGCTTGTGAGAAAATCCATGAATAGACTGGTGGCAG 489
QY 121 AGACCTTGACACTGCTTCCACTCATCGAATCTGGCTGATAGGCGATGGG 170
Db 488 AGACCTTGACACTGCTTCCACTCATCGAATCTGGCTGATAGGCGATGGG 439

RESULT 10

US-09-755-633-7
; Sequence 7, Application US/09755633

Patent No. US20020127200A1
; GENERAL INFORMATION:
; APPLICANT: Yang, Shumin
; APPLICANT: McCall, Catherine A.
; APPLICANT: Weber, Eric R.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF
; FILE REFERENCE: IM-2-C1-C1
; CURRENT APPLICATION NUMBER: US/09/755,633
; CURRENT FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: 09/322,409
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/087,306
; PRIOR FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 402
; TYPE: DNA
; ORGANISM: Canis familiaris
US-09-755-633-7

Query Match 8.7%; Score 144; DB 9; Length 402;
Best Local Similarity 100.0%; Pred. No. 3.6e-58;
Matches 144; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 27 ATGAGAATGCTTCTGAATTCGATTGCTAGCTCTTGGGGCTGCTATGTTCTTGCCTTT 86
DB 1 ATGAGAATGCTTCTGAATTCGATTGCTAGCTCTTGGGGCTGCTATGTTCTTGCCTTT 60

QY 87 GCTGTAGAAAATCCCATGAATAGACTGTGGCAGAGACCTTGACACTGCTCTCCACTCAT 146
DB 61 GCTGTAGAAAATCCCATGAATAGACTGTGGCAGAGACCTTGACACTGCTCTCCACTCAT 120

QY 147 CGAACTTGGCTGATAGGCGATGGG 170
DB 121 CGAACTTGGCTGATAGGCGATGGG 144

RESULT 11
US-09-755-633-8/c
; Sequence 8, Application US/09755633
; Patent No. US20020127200A1
; GENERAL INFORMATION:
; APPLICANT: Yang, Shumin
; APPLICANT: McCall, Catherine A.
; APPLICANT: Weber, Eric R.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF
; FILE REFERENCE: IM-2-C1-C1
; CURRENT APPLICATION NUMBER: US/09/755,633
; CURRENT FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: 09/322,409
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/087,306
; PRIOR FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 402
; TYPE: DNA
; ORGANISM: Canis familiaris
US-09-755-633-8

Query Match 8.7%; Score 144; DB 9; Length 402;
Best Local Similarity 100.0%; Pred. No. 3.6e-58;
Matches 144; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 27 ATGAGAATGCTTCTGAATTCGATTGCTAGCTCTTGGGGCTGCTATGTTCTTGCCTTT 86
DB 402 ATGAGAATGCTTCTGAATTCGATTGCTAGCTCTTGGGGCTGCTATGTTCTTGCCTTT 343

QY 87 GCTGTAGAAAATCCCATGAATAGACTGTGGCAGAGACCTTGACACTGCTCTCCACTCAT 146

DB 342 GCTGTAGAAAATCCCATGAATAGACTGTGGCAGAGACCTTGACACTGCTCTCCACTCAT 283

QY 147 CGAACTTGGCTGATAGGCGATGGG 170

DB 282 CGAACTTGGCTGATAGGCGATGGG 259

RESULT 12
US-10-218-654-83
; Sequence 83, Application US/10218654
; Publication No. US20030099609A1
; GENERAL INFORMATION:
; APPLICANT: Sim, Gek-Kee
; APPLICANT: Yang, Shumin
; APPLICANT: Dretz, Matthew J.
; APPLICANT: Wonderling, Ramani S.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF
; FILE REFERENCE: IM-2-C1
; CURRENT APPLICATION NUMBER: US/10/218,654
; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: US/09/322,409
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/087,306
; PRIOR FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 154
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 83
; LENGTH: 402
; TYPE: DNA
; ORGANISM: Canis familiaris
US-10-218-654-83

Query Match 8.7%; Score 144; DB 15; Length 402;
Best Local Similarity 100.0%; Pred. No. 3.6e-58;
Matches 144; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 27 ATGAGAATGCTTCTGAATTCGATTGCTAGCTCTTGGGGCTGCTATGTTCTTGCCTTT 86
DB 1 ATGAGAATGCTTCTGAATTCGATTGCTAGCTCTTGGGGCTGCTATGTTCTTGCCTTT 60

QY 87 GCTGTAGAAAATCCCATGAATAGACTGTGGCAGAGACCTTGACACTGCTCTCCACTCAT 146
DB 61 GCTGTAGAAAATCCCATGAATAGACTGTGGCAGAGACCTTGACACTGCTCTCCACTCAT 120

QY 147 CGAACTTGGCTGATAGGCGATGGG 170
DB 121 CGAACTTGGCTGATAGGCGATGGG 144

RESULT 13
US-10-218-654-84/c
; Sequence 84, Application US/10218654
; Publication No. US20030099609A1
; GENERAL INFORMATION:
; APPLICANT: Sim, Gek-Kee
; APPLICANT: Yang, Shumin
; APPLICANT: Dretz, Matthew J.
; APPLICANT: Wonderling, Ramani S.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF
; FILE REFERENCE: IM-2-C1
; CURRENT APPLICATION NUMBER: US/10/218,654
; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: US/09/322,409
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/087,306
; PRIOR FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 154
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 84
; LENGTH: 402


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; TYPE: DNA
; ORGANISM: Canis familiaris
US-10-218-654-84

Query Match
Best Local Similarity 8.7%; Score 144; DB 15; Length 402;
Matches 144; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 27 ATGAGAAATGCTTCTGAATTGAGTTGCTAGCTTTGGGGCTGCCCTATGTTTCTGCCTTT 86
Db 402 ATGAGAAATGCTTCTGAATTGAGTTGCTAGCTTTGGGGCTGCCCTATGTTTCTGCCTTT 343

QY 87 GCTGTAGAAAATCCCATGATAGACTGTTGGGAGACCTTGACACTGCTCTCCACTCAT 146
Db 342 GCTGTAGAAAATCCCATGATAGACTGTTGGGAGACCTTGACACTGCTCTCCACTCAT 283

QY 147 CGAACTTGGCTGATAGCGGATGGG 170
Db 282 CGAACTTGGCTGATAGCGGATGGG 259

; LENGTH: 402
; TYPE: DNA
; ORGANISM: Canis familiaris
US-10-262-439-84
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Query Match
Best Local Similarity 8.7%; Score 144; DB 15; Length 402;
Matches 144; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 27 ATGAGAAATGCTTCTGAATTGAGTTGCTAGCTTTGGGGCTGCCCTATGTTTCTGCCTTT 86
Db 402 ATGAGAAATGCTTCTGAATTGAGTTGCTAGCTTTGGGGCTGCCCTATGTTTCTGCCTTT 343

QY 87 GCTGTAGAAAATCCCATGATAGACTGTTGGGAGACCTTGACACTGCTCTCCACTCAT 146
Db 342 GCTGTAGAAAATCCCATGATAGACTGTTGGGAGACCTTGACACTGCTCTCCACTCAT 283

QY 147 CGAACTTGGCTGATAGCGGATGGG 170
Db 282 CGAACTTGGCTGATAGCGGATGGG 259

; LENGTH: 402
; TYPE: DNA
; ORGANISM: Canis familiaris
US-10-262-439-84
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; TYPE: DNA
; ORGANISM: Canis familiaris
US-10-218-654-84

Query Match
Best Local Similarity 8.7%; Score 144; DB 15; Length 402;
Matches 144; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 27 ATGAGAAATGCTTCTGAATTGAGTTGCTAGCTTTGGGGCTGCCCTATGTTTCTGCCTTT 86
Db 402 ATGAGAAATGCTTCTGAATTGAGTTGCTAGCTTTGGGGCTGCCCTATGTTTCTGCCTTT 343

QY 87 GCTGTAGAAAATCCCATGATAGACTGTTGGGAGACCTTGACACTGCTCTCCACTCAT 146
Db 342 GCTGTAGAAAATCCCATGATAGACTGTTGGGAGACCTTGACACTGCTCTCCACTCAT 283

QY 147 CGAACTTGGCTGATAGCGGATGGG 170
Db 282 CGAACTTGGCTGATAGCGGATGGG 259

; LENGTH: 402
; TYPE: DNA
; ORGANISM: Canis familiaris
US-10-262-439-84
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RESULT 14
US-10-262-439-83
; Sequence 83, Application US/10262439
; Publication No. US20030143196A1
; GENERAL INFORMATION:
; APPLICANT: Sim, Gek-Kee
; APPLICANT: Yang, Shumin
; APPLICANT: Dreitz, Matthew J.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; FILE REFERENCE: IN-2-C2
; CURRENT APPLICATION NUMBER: US/10/262,439
; PRIOR FILING DATE: 2002-09-30
; PRIOR FILING DATE: 1999-05-28
; PRIOR FILING DATE: 1999-12-01
; PRIOR FILING DATE: 1999-05-28
; PRIOR FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 83
; LENGTH: 402
; TYPE: DNA
; ORGANISM: Canis familiaris
US-10-262-439-83
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Query Match
Best Local Similarity 8.7%; Score 144; DB 15; Length 402;
Matches 144; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 27 ATGAGAAATGCTTCTGAATTGAGTTGCTAGCTTTGGGGCTGCCCTATGTTTCTGCCTTT 86
Db 1 ATGAGAAATGCTTCTGAATTGAGTTGCTAGCTTTGGGGCTGCCCTATGTTTCTGCCTTT 60

QY 87 GCTGTAGAAAATCCCATGATAGACTGTTGGGAGACCTTGACACTGCTCTCCACTCAT 146
Db 61 GCTGTAGAAAATCCCATGATAGACTGTTGGGAGACCTTGACACTGCTCTCCACTCAT 120

QY 147 CGAACTTGGCTGATAGCGGATGGG 170
Db 121 CGAACTTGGCTGATAGCGGATGGG 144

; LENGTH: 402
; TYPE: DNA
; ORGANISM: Canis familiaris
US-10-262-439-83
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RESULT 15
US-10-262-439-84/c
; Sequence 84, Application US/10262439
; Publication No. US20030143196A1
; GENERAL INFORMATION:
; APPLICANT: Sim, Gek-Kee
; APPLICANT: Yang, Shumin
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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7244.949 Million cell updates/sec

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Perfect score: 1658
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Scoring table: OLIGO_NUC
Gapop_60.0 , Gapext 60.0

Searched: 682709 seqs, 277475446 residues

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Minimum DB seq length: 0
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Post-processing: Listing first 45 summaries

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5: /cgn2_6/ptodata/2/ina/PGTUS_COMB.seq.*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	170	10.3	610	4	US-09-322-409-80
2	170	10.3	610	4	US-09-322-409-82
3	170	10.3	610	4	US-09-451-527-80
4	170	10.3	610	4	US-09-451-527-82
5	144	8.7	402	4	US-09-322-409-83
6	144	8.7	402	4	US-09-322-409-84
7	144	8.7	402	4	US-09-451-527-83
8	144	8.7	402	4	US-09-451-527-84
9	144	8.7	405	4	US-09-371-615A-1
10	129	7.8	345	4	US-09-322-409-85
11	129	7.8	345	4	US-09-322-409-87
12	129	7.8	345	4	US-09-451-527-85
13	129	7.8	345	4	US-09-451-527-87
14	26	1.6	2235	4	US-09-569-804-20
15	26	1.6	3230	3	US-09-280-799-78
16	26	1.6	3230	6	5324640-1
17	25	1.5	29485	4	US-09-785-381-6
18	24	1.4	3182	1	US-08-188-582-12
19	24	1.4	3182	1	US-08-646-715-12
20	23	1.4	40	3	US-09-306-290-11
21	23	1.4	442	4	US-09-372-422A-35
22	23	1.4	1017	3	US-08-849-751-1
23	23	1.4	1017	4	US-09-478-816-1
24	23	1.4	2082	4	US-09-149-476-257
25	23	1.4	31571	1	US-08-323-443B-1
26	23	1.4	53526	3	US-08-658-136-2
27	23	1.4	53577	3	US-08-658-136-1

28	22	1.3	27	1	US-08-434-503-41	Sequence 41, Appl
C 29	22	1.3	32	4	US-09-322-409-138	Sequence 138, App
C 30	22	1.3	32	4	US-09-451-527-138	Sequence 138, App
31	22	1.3	40	3	US-09-306-290-16	Sequence 16, Appl
C 32	22	1.3	47	1	US-08-466-852-2	Sequence 2, Appl
33	22	1.3	127	3	US-09-014-416-59	Sequence 59, Appl
34	22	1.3	176	3	US-09-014-416-63	Sequence 63, Appl
35	22	1.3	183	3	US-09-014-416-60	Sequence 60, Appl
C 36	22	1.3	183	4	US-09-621-976-13606	Sequence 13606, A
37	22	1.3	200	3	US-09-014-416-64	Sequence 64, Appl
38	22	1.3	227	2	US-08-520-678A-28	Sequence 28, Appl
39	22	1.3	227	3	US-08-897-126-28	Sequence 28, Appl
40	22	1.3	253	2	US-08-520-678A-25	Sequence 25, Appl
41	22	1.3	253	3	US-08-897-126-25	Sequence 25, Appl
C 42	22	1.3	255	4	US-09-621-976-9406	Sequence 9406, Ap
C 43	22	1.3	255	4	US-09-621-976-18743	Sequence 18743, A
44	22	1.3	257	2	US-08-520-678A-24	Sequence 24, Appl
45	22	1.3	257	3	US-08-897-126-24	Sequence 24, Appl

ALIGNMENTS

RESULT 1
US-09-322-409-80
; Sequence 80, Application US/09322409
; Patent No. 6471957
; GENERAL INFORMATION:
; APPLICANT: Sim, Gek-Kee
; APPLICANT: Yang, Shumin
; APPLICANT: Drelitz, Matthew J.
; APPLICANT: Wonderling, Ramani S.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF
; FILE REFERENCE: IM-2-CI
; CURRENT APPLICATION NUMBER: US/09/322,409
; CURRENT FILING DATE: 1999-05-28
; EARLIER APPLICATION NUMBER: 60/087,306
; EARLIER FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 154
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 80
; LENGTH: 610
; TYPE: DNA
; ORGANISM: Canis familiaris
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (29)..(430)
US-09-322-409-80
Query Match 10.3%; Score 170; DB 4; Length 610;
Best Local Similarity 100.0%; Pred. No. 3.6e-61;
Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AGGCAAACTGAACTTCAGAGCTATGAGATGCTTCTGAAATTTGAGTTGCTAGCTC 60
Db 3 AGGCAAACTGAACTTCAGAGCTATGAGATGCTTCTGAAATTTGAGTTGCTAGCTC 62
QY 61 TTGGGGCTGCCCTATCTTTCTGCTTTGCTAGAAAATCCCATGAAATAGACTGTGGCAG 120
Db 63 TTGGGGCTGCCCTATCTTTCTGCTTTGCTAGAAAATCCCATGAAATAGACTGTGGCAG 122
QY 121 AGACCTTGACACTGCTCTCCACTCATCGAACTTGCTGATAGCGCATGGG 170
Db 123 AGACCTTGACACTGCTCTCCACTCATCGAACTTGCTGATAGCGCATGGG 172
RESULT 2
US-09-322-409-82/c
; Sequence 82, Application US/09322409
; Patent No. 6471957
; GENERAL INFORMATION:
; APPLICANT: Sim, Gek-Kee

APPLICANT: Yang, Shumin
APPLICANT: Dreitz, Matthew J.
TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
FILE REFERENCE: IM-2-C1
CURRENT APPLICATION NUMBER: US/09/322,409
EARLIER FILING DATE: 1999-05-28
EARLIER APPLICATION NUMBER: 60/087,306
NUMBER OF SEQ ID NOS: 154
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 82
LENGTH: 610
TYPE: DNA
ORGANISM: Canis familiaris
US-09-322-409-82

Query Match 10.3%; Score 170; DB 4; Length 610;
Best Local Similarity 100.0%; Pred. No. 3.6e-61;
Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGGCAACACCTGACACTCTCCACTATGAGCTATGAGATGCTTCTGAAATTTGAGTTTCTAGCTC 60
Db 608 AGGCAACACCTGACACTCTCCACTATGAGCTATGAGATGCTTCTGAAATTTGAGTTTCTAGCTC 549

Qy 61 TTGGGGCTGCTATGTTTCTGCTTTCCTGCTGAGAAATCCCATGAAATAGACTGGTGGCAG 120
Db 548 TTGGGGCTGCTATGTTTCTGCTTTCCTGCTGAGAAATCCCATGAAATAGACTGGTGGCAG 489

Qy 121 AGACTTGACACTGCTCTCCACTCATCGAACTTGCTGATAGCGATGGG 170
Db 488 AGACTTGACACTGCTCTCCACTCATCGAACTTGCTGATAGCGATGGG 439

RESULT 3
US-09-451-527-80
Sequence 80, Application US/09451527
Patent No. 6482403
GENERAL INFORMATION:
APPLICANT: Yang, Shumin
APPLICANT: Dreitz, Matthew J.
APPLICANT: Wonderling, Ramani S.
TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
FILE REFERENCE: IM-2-C2
CURRENT APPLICATION NUMBER: US/09/451,527
CURRENT FILING DATE: 1999-12-01
EARLIER FILING DATE: 1999-05-28
EARLIER APPLICATION NUMBER: 60/087,306
NUMBER OF SEQ ID NOS: 174
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 80
LENGTH: 610
TYPE: DNA
ORGANISM: Canis familiaris
FEATURE:
NAME/KEY: CDS
LOCATION: (29)..(430)
US-09-451-527-80

Query Match 10.3%; Score 170; DB 4; Length 610;
Best Local Similarity 100.0%; Pred. No. 3.6e-61;
Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGGCAACACCTGACACTCTCCACTATGAGCTATGAGATGCTTCTGAAATTTGAGTTTCTAGCTC 60
Db 3 AGGCAACACCTGACACTCTCCACTATGAGCTATGAGATGCTTCTGAAATTTGAGTTTCTAGCTC 62

Qy 61 TTGGGGCTGCTATGTTTCTGCTTTCCTGCTGAGAAATCCCATGAAATAGACTGGTGGCAG 120

Query Match 10.3%; Score 170; DB 4; Length 610;
Best Local Similarity 100.0%; Pred. No. 3.6e-61;
Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGGCAACACCTGACACTCTCCACTATGAGCTATGAGATGCTTCTGAAATTTGAGTTTCTAGCTC 60
Db 3 AGGCAACACCTGACACTCTCCACTATGAGCTATGAGATGCTTCTGAAATTTGAGTTTCTAGCTC 62

Qy 61 TTGGGGCTGCTATGTTTCTGCTTTCCTGCTGAGAAATCCCATGAAATAGACTGGTGGCAG 120

Db 63 TTGGGGCTGCTATGTTTCTGCTTTCCTGCTGAGAAATCCCATGAAATAGACTGGTGGCAG 122

Qy 121 AGACTTGACACTGCTCTCCACTCATCGAACTTGCTGATAGCGATGGG 170
Db 123 AGACTTGACACTGCTCTCCACTCATCGAACTTGCTGATAGCGATGGG 172

RESULT 4
US-09-451-527-82/c
Sequence 82, Application US/09451527
Patent No. 6482403
GENERAL INFORMATION:
APPLICANT: Yang, Shumin
APPLICANT: Dreitz, Matthew J.
APPLICANT: Wonderling, Ramani S.
TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
FILE REFERENCE: IM-2-C2
CURRENT APPLICATION NUMBER: US/09/451,527
CURRENT FILING DATE: 1999-12-01
EARLIER APPLICATION NUMBER: 09/322,409
EARLIER FILING DATE: 1999-05-28
EARLIER APPLICATION NUMBER: 60/087,306
NUMBER OF SEQ ID NOS: 174
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 82
LENGTH: 610
TYPE: DNA
ORGANISM: Canis familiaris
US-09-451-527-82

Query Match 10.3%; Score 170; DB 4; Length 610;
Best Local Similarity 100.0%; Pred. No. 3.6e-61;
Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGGCAACACCTGACACTCTCCACTATGAGCTATGAGATGCTTCTGAAATTTGAGTTTCTAGCTC 60
Db 608 AGGCAACACCTGACACTCTCCACTATGAGCTATGAGATGCTTCTGAAATTTGAGTTTCTAGCTC 549

Qy 61 TTGGGGCTGCTATGTTTCTGCTTTCCTGCTGAGAAATCCCATGAAATAGACTGGTGGCAG 120
Db 548 TTGGGGCTGCTATGTTTCTGCTTTCCTGCTGAGAAATCCCATGAAATAGACTGGTGGCAG 489

Qy 121 AGACTTGACACTGCTCTCCACTCATCGAACTTGCTGATAGCGATGGG 170
Db 488 AGACTTGACACTGCTCTCCACTCATCGAACTTGCTGATAGCGATGGG 439

RESULT 5
US-09-322-409-83
Sequence 83, Application US/09322409
Patent No. 6471957
GENERAL INFORMATION:
APPLICANT: Yang, Shumin
APPLICANT: Dreitz, Matthew J.
APPLICANT: Wonderling, Ramani S.
TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
FILE REFERENCE: IM-2-C1
CURRENT APPLICATION NUMBER: US/09/322,409
CURRENT FILING DATE: 1999-05-28
EARLIER APPLICATION NUMBER: 60/087,306
EARLIER FILING DATE: 1998-05-29
NUMBER OF SEQ ID NOS: 154
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 83
LENGTH: 402
TYPE: DNA
ORGANISM: Canis familiaris

Query Match 10.3%; Score 170; DB 4; Length 610;
Best Local Similarity 100.0%; Pred. No. 3.6e-61;
Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGGCAACACCTGACACTCTCCACTATGAGCTATGAGATGCTTCTGAAATTTGAGTTTCTAGCTC 60
Db 608 AGGCAACACCTGACACTCTCCACTATGAGCTATGAGATGCTTCTGAAATTTGAGTTTCTAGCTC 549

Qy 61 TTGGGGCTGCTATGTTTCTGCTTTCCTGCTGAGAAATCCCATGAAATAGACTGGTGGCAG 120
Db 548 TTGGGGCTGCTATGTTTCTGCTTTCCTGCTGAGAAATCCCATGAAATAGACTGGTGGCAG 489

Qy 121 AGACTTGACACTGCTCTCCACTCATCGAACTTGCTGATAGCGATGGG 170
Db 488 AGACTTGACACTGCTCTCCACTCATCGAACTTGCTGATAGCGATGGG 439

US-09-322-409-83

Query Match 8.7%; Score 144; DB 4; Length 402;
Best Local Similarity 100.0%; Pred. No. 2.1e-50;
Matches 144; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 27 ATGAGAATGCTTCTGAATTTGAGTTTCTAGCTCTTGGGGCTGCCTATGTTTCTGCCTTT 86
DB 1 ATGAGAATGCTTCTGAATTTGAGTTTCTAGCTCTTGGGGCTGCCTATGTTTCTGCCTTT 60

QY 87 GCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACTCAT 146
DB 61 GCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACTCAT 120

QY 147 CGAACTTGGCTGATAGCGGATGGG 170
DB 121 CGAACTTGGCTGATAGCGGATGGG 144

RESULT 6

US-09-322-409-84/c
; Sequence 84, Application US/09322409
; Patent No. 6471957
; GENERAL INFORMATION:
; APPLICANT: Sim, Gek-Kee
; APPLICANT: Yang, Shumin
; APPLICANT: Dreitz, Matthew J.
; APPLICANT: Wonderling, Ramani S.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; FILE REFERENCE: IM-2-C1
; CURRENT APPLICATION NUMBER: US/09/322,409
; EARLIER FILING DATE: 1999-05-28
; EARLIER APPLICATION NUMBER: 60/087,306
; EARLIER FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 154
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 84
; LENGTH: 402
; TYPE: DNA
; ORGANISM: Canis familiaris
US-09-322-409-84

Query Match 8.7%; Score 144; DB 4; Length 402;
Best Local Similarity 100.0%; Pred. No. 2.1e-50;
Matches 144; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 27 ATGAGAATGCTTCTGAATTTGAGTTTCTAGCTCTTGGGGCTGCCTATGTTTCTGCCTTT 86
DB 402 ATGAGAATGCTTCTGAATTTGAGTTTCTAGCTCTTGGGGCTGCCTATGTTTCTGCCTTT 343

QY 87 GCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACTCAT 146
DB 342 GCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACTCAT 283

QY 147 CGAACTTGGCTGATAGCGGATGGG 170
DB 282 CGAACTTGGCTGATAGCGGATGGG 259

RESULT 7

US-09-451-527-83
; Sequence 83, Application US/09451527
; Patent No. 6482403
; GENERAL INFORMATION:
; APPLICANT: Sim, Gek-Kee
; APPLICANT: Yang, Shumin
; APPLICANT: Dreitz, Matthew J.
; APPLICANT: Wonderling, Ramani S.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; FILE REFERENCE: IM-2-C2
; CURRENT APPLICATION NUMBER: US/09/451,527

; CURRENT FILING DATE: 1999-12-01
; EARLIER APPLICATION NUMBER: 09/322,409
; EARLIER FILING DATE: 1999-05-28
; EARLIER APPLICATION NUMBER: 60/087,306
; EARLIER FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 83
; LENGTH: 402
; TYPE: DNA
; ORGANISM: Canis familiaris
US-09-451-527-83

Query Match 8.7%; Score 144; DB 4; Length 402;
Best Local Similarity 100.0%; Pred. No. 2.1e-50;
Matches 144; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 27 ATGAGAATGCTTCTGAATTTGAGTTTCTAGCTCTTGGGGCTGCCTATGTTTCTGCCTTT 86
DB 1 ATGAGAATGCTTCTGAATTTGAGTTTCTAGCTCTTGGGGCTGCCTATGTTTCTGCCTTT 60

QY 87 GCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACTCAT 146
DB 61 GCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACTCAT 120

QY 147 CGAACTTGGCTGATAGCGGATGGG 170
DB 121 CGAACTTGGCTGATAGCGGATGGG 144

RESULT 8

US-09-451-527-84/c
; Sequence 84, Application US/09451527.
; Patent No. 6482403
; GENERAL INFORMATION:
; APPLICANT: Sim, Gek-Kee
; APPLICANT: Yang, Shumin
; APPLICANT: Dreitz, Matthew J.
; APPLICANT: Wonderling, Ramani S.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; FILE REFERENCE: IM-2-C2
; CURRENT APPLICATION NUMBER: US/09/451,527
; CURRENT FILING DATE: 1999-12-01
; EARLIER APPLICATION NUMBER: 09/322,409
; EARLIER FILING DATE: 1999-05-28
; EARLIER APPLICATION NUMBER: 60/087,306
; EARLIER FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 84
; LENGTH: 402
; TYPE: DNA
; ORGANISM: Canis familiaris
US-09-451-527-84

Query Match 8.7%; Score 144; DB 4; Length 402;
Best Local Similarity 100.0%; Pred. No. 2.1e-50;
Matches 144; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 27 ATGAGAATGCTTCTGAATTTGAGTTTCTAGCTCTTGGGGCTGCCTATGTTTCTGCCTTT 86
DB 402 ATGAGAATGCTTCTGAATTTGAGTTTCTAGCTCTTGGGGCTGCCTATGTTTCTGCCTTT 343

QY 87 GCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACTCAT 146
DB 342 GCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACTCAT 283

QY 147 CGAACTTGGCTGATAGCGGATGGG 170
DB 282 CGAACTTGGCTGATAGCGGATGGG 259

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RESULT 9
US-09-371-615A-1
; Sequence 1, Application US/09371615A
; Patent No. 6537781
; GENERAL INFORMATION:
; APPLICANT: IDEXX LABORATORIES
; TITLE OF INVENTION: METHODS AND COMPOSITIONS CONCERNING
; FILE OF INVENTION: CANINE INTERLEUKIN 5
; FILE REFERENCE: 03604001700US00
; CURRENT APPLICATION NUMBER: US/09/371.615A
; CURRENT FILING DATE: 1999-08-10
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 405
; TYPE: DNA
; ORGANISM: Canis familiaris
US-09-371-615A-1
Query Match      8.7%; Score 144; DB 4; Length 405;
Best Local Similarity 100.0%; Pred. No. 2e-50;
Matches 144; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 27 ATGAGATGCTTCTGAATTTGCTAGCTCTTGGGCTGCTGCTATGTTCTGCTTT 86
DB 1 ATGAGATGCTTCTGAATTTGCTAGCTCTTGGGCTGCTGCTATGTTCTGCTTT 60
QY 87 GCTGTAGAAATCCCATGATAGACTGCTGCAGAGACCTTGACACTGCTCCACTCAT 146
DB 61 GCTGTAGAAATCCCATGATAGACTGCTGCAGAGACCTTGACACTGCTCTCATCAT 120
QY 147 CGAACTTGGCTGATAGCGATGGG 170
DB 121 CGAACTTGGCTGATAGCGATGGG 144
RESULT 10
US-09-322-409-85
; Sequence 85, Application US/09322409
; Patent No. 6471957
; GENERAL INFORMATION:
; APPLICANT: Sim, Gek-kee
; APPLICANT: Yang, Shumin
; APPLICANT: Dreitz, Matthew J.
; APPLICANT: Wonderling, Ramani S.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; FILE REFERENCE: IM-2-C1
; CURRENT APPLICATION NUMBER: US/09/322.409
; CURRENT FILING DATE: 1999-05-28
; EARLIER APPLICATION NUMBER: 60/087,306
; EARLIER FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 154
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 85
; LENGTH: 345
; TYPE: DNA
; ORGANISM: Canis familiaris
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(345)
US-09-322-409-85
Query Match      7.8%; Score 129; DB 4; Length 345;
Best Local Similarity 100.0%; Pred. No. 3.3e-44;
Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1276 CACCACTGTGCATTAAGAAGTTTTTCAGGGTATAGACATTTGAAGAACCAACTGCC 1335
DB 121 CACCACTGTGCATTAAGAAGTTTTTCAGGGTATAGACATTTGAAGAACCAACTGCC 180
QY 1336 CACGGGAGGCTGGTAAACTTTCCAAACTTGCTTTTAAATAAAGAACACATAGAG 1395
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Db 181 CACGGGAGGCTGTGATAAACTATTCCAAACTTGCTTTTAAATAAAGAACACATAGAG 240
QY 1396 CGCCAAAAA 1404
DB 241 CGCCAAAAA 249
RESULT 11
US-09-322-409-87/c
; Sequence 87, Application US/09322409
; Patent No. 6471957
; GENERAL INFORMATION:
; APPLICANT: Sim, Gek-kee
; APPLICANT: Yang, Shumin
; APPLICANT: Dreitz, Matthew J.
; APPLICANT: Wonderling, Ramani S.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; FILE REFERENCE: IM-2-C1
; CURRENT APPLICATION NUMBER: US/09/322.409
; CURRENT FILING DATE: 1999-05-28
; EARLIER APPLICATION NUMBER: 60/087,306
; EARLIER FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 154
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 87
; LENGTH: 345
; TYPE: DNA
; ORGANISM: Canis familiaris
US-09-322-409-87
Query Match      7.8%; Score 129; DB 4; Length 345;
Best Local Similarity 100.0%; Pred. No. 3.3e-44;
Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1276 CACCACTGTGCATTAAGAAGTTTTTCAGGGTATAGACATTTGAAGAACCAACTGCC 1335
DB 225 CACCACTGTGCATTAAGAAGTTTTTCAGGGTATAGACATTTGAAGAACCAACTGCC 166
QY 1336 CACGGGAGGCTGTGATAAACTATTCCAAACTTGCTTTTAAATAAAGAACACATAGAG 1395
DB 165 CACGGGAGGCTGTGATAAACTATTCCAAACTTGCTTTTAAATAAAGAACACATAGAG 106
QY 1396 CGCCAAAAA 1404
DB 105 CGCCAAAAA 97
RESULT 12
US-09-451-527-85
; Sequence 85, Application US/09451527
; Patent No. 6482403
; GENERAL INFORMATION:
; APPLICANT: Sim, Gek-kee
; APPLICANT: Yang, Shumin
; APPLICANT: Dreitz, Matthew J.
; APPLICANT: Wonderling, Ramani S.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; FILE REFERENCE: IM-2-C2
; CURRENT APPLICATION NUMBER: US/09/451.527
; CURRENT FILING DATE: 1999-12-01
; EARLIER APPLICATION NUMBER: 09/322.409
; EARLIER FILING DATE: 1999-05-28
; EARLIER APPLICATION NUMBER: 60/087,306
; EARLIER FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 85
; LENGTH: 345
; TYPE: DNA
; ORGANISM: Canis familiaris
; FEATURE:
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; NAME/KEY: CDS
; LOCATION: (1)..(345)
US-09-451-527-85

              7.8%;   Score 129;  DB 4;  Length 345;
Best Local Similarity 100.0%;  Pred. No. 3 3e-44;
Matches 129;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

Query Match
1276  CACCAACTGTCATTAAAGAAGTTTTTCAGGGTATAGACACATTGGAAGAACCAAACTGCC 1335
      |||||
121  CACCAACTGTCATTAAAGAAGTTTTTCAGGGTATAGACACATTGGAAGAACCAAACTGCC 180
      |||||

1336  CACGGGAGGCTGTGGATAAACAATTCCAAAACCTTGCTTTAATAAAGAACACATAGAG 1395
      |||||
181  CACGGGAGGCTGTGGATAAACAATTCCAAAACCTTGCTTTAATAAAGAACACATAGAG 240
      |||||

Qy      1396  CGCCAAAAA 1404
      |||||
Db      241  CGCCAAAAA 249
      |||||

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RESULT 13
 US-09-451-527-87/c
 ; Sequence 87, Application US/09451527
 ; Patent No. 6482403
 ; GENERAL INFORMATION:
 ; APPLICANT: Sim, Gek-Keo
 ; APPLICANT: Yang, Shumin
 ; APPLICANT: Dreitz, Matthew J.
 ; APPLICANT: Wonderling, Ramani S.
 ; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
 ; TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF
 ; FILE REFERENCE: IM-2-C2
 ; CURRENT APPLICATION NUMBER: US/09/451,527
 ; CURRENT FILING DATE: 1999-12-01
 ; EARLIER APPLICATION NUMBER: 09/322,409
 ; EARLIER FILING DATE: 1999-05-28
 ; EARLIER APPLICATION NUMBER: 60/087,306
 ; EARLIER FILING DATE: 1998-05-29
 ; NUMBER OF SEQ ID NOS: 174
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 87
 ; LENGTH: 345
 ; TYPE: DNA
 ; ORGANISM: Canis familiaris
 US-09-451-527-87

	Query Match	7.8%; Score 129; DB 4; Length 345;	
	Best Local Similarity 100.0%; Pred. No. 3.3e-44;		
	Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	1276	CACCACTGTCATTAAAGAAAGTTTTTCAGGGTATAGACACATTGAAGAACCAAACTGCC	1335
Db	225	CACCAACTGTCATTAAAGAAAGTTTTTCAGGGTATAGACACATTGAAGAACCAAACTGCC	156
QY	1336	CACGGGAGGCGCTGGGATAAACTATTCCAAAACTTGTCCTTTAATAAAGAACACATAGAG	1395
Db	165	CACGGGAGGCGCTGGGATAAACTATTCCAAAACTTGTCCTTTAATAAAGAACACATAGAG	106
QY	1396	CGCAAAAAA 1404	
Db	105	CGCAAAAAA 97	

RESULT 14
US-09-563-804-20/c
; Sequence 20, Application US/09569804
; Patent No. 6503662
; GENERAL INFORMATION:
; APPLICANT: Bougri, Oleg
; APPLICANT: Rommens, Caius
; APPLICANT: Srivastava, Neelam
; APPLICANT: Swords, Kathleen M

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; TITLE OF INVENTION: Acquired Resistance Genes in Plants
; FILE REFERENCE: 38-21(15415)
; CURRENT APPLICATION NUMBER: US/09/569,804
; CURRENT FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: 60/133,965
; PRIOR FILING DATE: 1999-05-13
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 2235
; TYPE: DNA
; ORGANISM: Zea mays
US-09-569-804-20

Query Match      1.6%; Score 26; DB 4; Length 2235;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 26; Conservative 0; Mismatches 0; Indels 0;

Qy    1458 TTTTTCATTTTTTTTTTTTACAGAAT 1483
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Db    2196 TTTTTCATTTTTTTTTTTTACAGAAT 2171

RESULT 15
US-09-280-799-78
; Sequence 78, Application US/09280799
; Patent No. 6136603
; GENERAL INFORMATION:
; APPLICANT: Dean, Nicholas M.
; APPLICANT: Karras, James G
; APPLICANT: McKay, Robert
; TITLE OF INVENTION: ANTISENSE MODULATION OF INTERLEUKIN-5 SIGNAL
; TITLE OF INVENTION: TRANSDUCTION
; FILE REFERENCE: ISPH-0340
; CURRENT APPLICATION NUMBER: US/09/280,799
; CURRENT FILING DATE: 1999-03-26
; NUMBER OF SEQ ID NOS: 208
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 78
; LENGTH: 3230
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-280-799-78

Query Match      1.6%; Score 26; DB 3; Length 3230;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 26; Conservative 0; Mismatches 0; Indels 0;

Qy    399 ATAAAAATGTAAGTTAAATTATGATT 424
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Db    930 ATAAAAATGTAAGTTAAATTATGATT 955

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Job time : 129 secs
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Search completed: August 31, 2004, 19:19:27
Job time : 129 secs

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OM nucleic - nucleic search, using sw model

Run on: August 31, 2004, 06:34:55 ; Search time 670 Seconds
(without alignments)
10512.705 Million cell updates/sec

Title: US-10-787-382-18
Perfect score: 1658
Sequence: 1 aggaacactgaacatttc.....gtatggagattttggaga 1658

Scoring table: OLIGO NUC
Gapop 60.0 , Gapext 60.0

Searched: 3373863 seqs, 2124099041 residues

Word size : 0

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

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- 2: Geneseq1990s.*
- 3: Geneseq2000s.*
- 4: Geneseq2001as.*
- 5: Geneseq2001bs.*
- 6: Geneseq2002s.*
- 7: Geneseq2003as.*
- 8: Geneseq2003bs.*
- 9: Geneseq2003cs.*
- 10: Geneseq2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	ID	Description
1	170	10.3	610	3 AAZ55546	Aaz55546 Canine in
2	170	10.3	610	3 AAZ55547	Aaz55547 Canine in
3	144	8.7	252	4 AAF74305	Aaf74305 Canine in
4	144	8.7	402	3 AAZ55548	Aaz55548 Canine in
5	144	8.7	402	3 AAZ55549	Aaz55549 Canine in
6	144	8.7	405	4 AAF74300	Aaf74300 Canine in
7	129	7.8	345	3 AAZ55550	Aaz55550 Canine in
8	129	7.8	345	3 AAZ55551	Aaz55551 Canine in
9	129	7.8	393	4 AAF74306	Aaf74306 Canine in
10	43	2.6	399	2 AAT50756	Aat50756 Canine in
11	43	2.6	520	2 AAT50755	Aat50755 Canine in
12	41	2.5	838	3 AAZ44265	Aaz44265 Porcine I
13	26	1.6	357	5 ABV56577	Abv56577 Human pro
14	26	1.6	700	4 AAH92592	Aah92592 Human inf
15	26	1.6	2235	4 AAC84351	Aac84351 Corn clon
16	26	1.6	3230	1 AAN81381	Aan81381 Entire nu
17	26	1.6	3230	2 AAQ74056	Aaq74056 Human int
18	26	1.6	3230	3 AAC73725	Aac73725 Human int
19	26	1.6	3230	7 ABX04379	Abx04379 Human int
20	26	1.6	3241	3 AAA34856	Aaa34856 Human ade
21	26	1.6	3241	3 AAF20978	Aaf20978 Human low
22	26	1.6	3241	7 ABZ96672	Abz96672 Human nuc
23	26	1.6	4057	3 AAA34858	Aaa34858 Human ade

24	26	1.6	4057	3 AAF20980	Aaf20980 Human low
25	26	1.6	4057	7 ABZ96674	Abz96674 Human nuc
26	26	1.6	9738	6 AAS15002	Aas15002 DNA encod
27	25	1.5	274	7 ABZ73094	Abz73094 Rice leaf
28	25	1.5	368	7 ACC55526	Acc55526 Rice endo
29	25	1.5	403	4 AAL14836	Aal14836 Human bre
30	25	1.5	423	4 AAL23698	Aal23698 Human bre
31	25	1.5	512	8 ACC73216	Acc73216 Cat flea
32	25	1.5	596	7 ABX56654	Abx56654 Arabidops
33	25	1.5	700	4 AAH92593	Aah92593 Human inf
34	25	1.5	700	4 AAH92594	Aah92594 Human inf
35	25	1.5	824	6 ABN98947	Abn98947 Arabidops
36	25	1.5	970	9 ADD30659	Add30659 Plant vie
37	25	1.5	1395	1 AAN71243	Aan71243 Sequence
38	25	1.5	1740	7 ACC47166	Acc47166 Z. mays p
39	25	1.5	3018	6 ABK15653	Abk15653 Rice lipo
40	25	1.5	6375	6 ABK15200	Abk15200 Human CDN
41	25	1.5	6410	7 ABZ33706	Abz33706 Human col
42	25	1.5	8443	9 ADC27428	Adc27428 cDNA enco
43	25	1.5	29485	10 ADE86101	Ade86101 BAC clone
44	25	1.5	96599	8 ADA02747	Ada02747 Mouse lrf
45	25	1.5	96599	9 ADB72485	Adb72485 Mouse lrf

ALIGNMENTS

RESULT 1

AAZ55546
ID AAZ55546 standard; cDNA; 610 BP.
XX
AC AAZ55546;
XX
DT 14-MAR-2000 (first entry)
XX
DE Canine interleukin-5 (IL-5) cDNA.
XX
KW Interleukin-5; IL-5; antibody; canine; inhibitor; immune response;
KW immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.
XX
OS Canis familiaris.
FH Key Location/Qualifiers
CDS 29..433
FT /*tag= a
FT /product= "Canine IL-5"
XX
XX WO961618-A2.
XX
XX 02-DEC-1999.
XX
XX 28-MAY-1999; 99WO-US011942.
XX
XX 29-MAY-1998; 98US-0087306P.
XX
XX (HESK-) HESKA CORP.
XX
XX Sim G, Yang S, Dreitz MJ, Wonderling RS;
XX
XX WPI; 2000-072623/06.
XX
XX P-PSDB; AAY58219.

Nucleic acids encoding immunoregulatory proteins from cats or dogs, useful for treating or preventing e.g. tumors or autoimmune disease.
Claim 1h; Page 233-224; 264pp; English.

Sequences AAZ55546-255551 represent cDNA sequences encoding canine interleukin-5 (IL-5). The invention relates to canine IL-4, canine or feline Flt-3 ligand, canine or feline CD40, canine or feline CD154 (CD40 ligand), canine IL-5, canine IL-13, feline interferon-alpha (IFN-alpha), and feline granulocyte macrophage colony-stimulating factor (GM-CSF), and nucleotides which encode these immunoregulatory proteins. The proteins,

CC their associated nucleic acids, specific antibodies and inhibitors may be
 CC used as vaccines for therapeutic or prophylactic regulation of an immune
 CC response in animals (particularly cats, dogs, horses and humans). They
 CC may be used to treat autoimmune or infectious diseases including
 CC allergies, tumours, inflammation and graft rejection, and to increase the
 CC response from a co-administered antigen. The nucleotide sequences can
 CC also be used for the recombinant production of a protein, while
 CC nucleotide fragments are useful as probes, as amplification primers and
 CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).
 CC The proteins may be used to raise antibodies and to screen for modulators
 CC of activity, while the antibodies may be used in detection, and in drug
 CC targeting

XX
 SQ Sequence 610 BP; 202 A; 114 C; 139 G; 155 T; 0 U; 0 Other;
 Query Match 10.3%; Score 170; DB 3; Length 610;
 Best Local Similarity 100.0%; Pred. No. 6.3e-52;
 Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGGCAACACTGACATTTTCAGAGCTATGAGATGCTTCTGAATTTGAGTTGCTAGCTC 60
 DB 3 AGGCAACACTGACATTTTCAGAGCTATGAGATGCTTCTGAATTTGAGTTGCTAGCTC 62
 QY 61 TTGGGGCTGCTATGTTTCTGCTTTGCTGTAGAAAATCCCATGAATAGACTGTTGGCAG 120
 DB 63 TTGGGGCTGCTATGTTTCTGCTTTGCTGTAGAAAATCCCATGAATAGACTGTTGGCAG 122
 QY 121 AGACCTTGACACTGCTCTCCACTCATCGAATGCTGCTAGAGCGGATGGG 170
 DB 123 AGACCTTGACACTGCTCTCCACTCATCGAATGCTGCTAGAGCGGATGGG 172

RESULT 2
 AAZ55547/c
 ID AAZ55547 standard; cDNA; 610 BP.
 AC AAZ55547;
 XX
 DT 14-MAR-2000 (first entry)
 XX
 DE Canine interleukin-5 (IL-5) cDNA complement.
 XX
 KW Interleukin-5; IL-5; antibody; canine; inhibitor; immune response;
 KW immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.
 XX
 OS Canis familiaris.

XX Key Location/Qualifiers
 FH complement(178..582)
 FT /*tag= a
 FT /product= "Canine IL-5"
 XX
 PN WO9961618-A2.
 XX
 XX
 PD 02-DEC-1999.
 XX
 XX 28-MAY-1999; 99WO-US011942.
 XX
 XX 29-MAY-1998; 98US-0087306P.
 XX
 XX (HESK-) HESKA CORP.
 XX
 XX Sim G, Yang S, Dreitz MJ, Wonderling RS;
 XX
 XX WPI; 2000-072623/06.
 DR P-PSDB; AAY58219.
 XX
 XX Nucleic acids encoding immunoregulatory proteins from cats or dogs,
 PT useful for treating or preventing e.g. tumors or autoimmune disease.
 XX
 XX Claim 1b; Page 224-225; 264pp; English.
 PS
 XX Sequences AAZ55546-255551 represent cDNA sequences encoding canine

CC interleukin-5 (IL-5). The invention relates to canine IL-4, canine or
 CC feline Flt-3 ligand, canine or feline CD40, canine or feline CD154 (CD40
 CC ligand), canine IL-5, canine IL-13, feline interferon-alpha (IFN-alpha)
 CC and feline granulocyte macrophage colony-stimulating factor (GM-CSF), and
 CC nucleotides which encode these immunoregulatory proteins. The proteins,
 CC their associated nucleic acids, specific antibodies and inhibitors may be
 CC used as vaccines for therapeutic or prophylactic regulation of an immune
 CC response in animals (particularly cats, dogs, horses and humans). They
 CC may be used to treat autoimmune or infectious diseases including
 CC allergies, tumours, inflammation and graft rejection, and to increase the
 CC response from a co-administered antigen. The nucleotide sequences can
 CC also be used for the recombinant production of a protein, while
 CC nucleotide fragments are useful as probes, as amplification primers and
 CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).
 CC The proteins may be used to raise antibodies and to screen for modulators
 CC of activity, while the antibodies may be used in detection, and in drug
 CC targeting

XX
 SQ Sequence 610 BP; 155 A; 139 C; 114 G; 202 T; 0 U; 0 Other;
 Query Match 10.3%; Score 170; DB 3; Length 610;
 Best Local Similarity 100.0%; Pred. No. 6.3e-52;
 Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGGCAACACTGACATTTTCAGAGCTATGAGATGCTTCTGAATTTGAGTTGCTAGCTC 60
 DB 608 AGGCAACACTGACATTTTCAGAGCTATGAGATGCTTCTGAATTTGAGTTGCTAGCTC 549
 QY 61 TTGGGGCTGCTATGTTTCTGCTTTGCTGTAGAAAATCCCATGAATAGACTGTTGGCAG 120
 DB 548 TTGGGGCTGCTATGTTTCTGCTTTGCTGTAGAAAATCCCATGAATAGACTGTTGGCAG 489
 QY 121 AGACCTTGACACTGCTCTCCACTCATCGAATGCTGCTAGAGCGGATGGG 170
 DB 488 AGACCTTGACACTGCTCTCCACTCATCGAATGCTGCTAGAGCGGATGGG 439

RESULT 3
 AAF74305
 ID AAF74305 standard; DNA; 252 BP.
 AC AAF74305;
 XX
 DT 04-MAY-2001 (first entry)
 XX
 DE Canine interleukin-5 coding sequence #2.
 XX
 KW Dog; interleukin-5; IL-5; allergy; cancer; gene therapy;
 KW inflammatory reaction; ds.
 XX
 OS Canis sp.
 XX
 PN WO200111049-A2.
 XX
 XX
 PD 15-FEB-2001.
 XX
 XX 09-AUG-2000; 2000WO-US021651.
 XX
 XX 10-AUG-1999; 99US-00371615.
 XX
 XX (IDEX-) IDEX LAB INC.
 XX
 XX Guo H, Lawton R, Mermer B, Aiyappa AP;
 PI
 XX WPI; 2001-191542/19.
 DR P-PSDB; AAB72616.
 XX
 XX Novel canine interleukin 5 polynucleotide and polypeptides are used for
 PT generating antibodies which are useful in treating allergies in dogs.
 XX
 XX Example 1; Fig 1; 48pp; English.
 PS
 XX The present invention provides the protein and coding sequences of the

CC canine interleukin-5 (IL-5) protein. This can be used to treat allergies,
 CC cancer and inflammatory reactions in dogs. The present sequence is one
 CC version of the IL-5 coding sequence shown in the specification

XX
 SQ Sequence 252 BP; 69 A; 54 C; 60 G; 69 T; 0 U; 0 Other;

Query Match 8.7%; Score 144; DB 4; Length 252;
 Best Local Similarity 100.0%; Pred. No. 1.8e-42;
 Matches 144; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 27 ATGAGAATGCTTCTGGAATTTGAGTTTCTAGCTTCTTGGGCTGCGCTATGTTTCTGCTTTT 86
 Db 1 ATGAGAATGCTTCTGGAATTTGAGTTTCTAGCTTCTTGGGCTGCGCTATGTTTCTGCTTTT 60

QY 87 GCTGTAGAAAATCCCATGAATAGACTGGTGGCAGACCTTGACATGCTCTCCACTCAT 146
 Db 61 GCTGTAGAAAATCCCATGAATAGACTGGTGGCAGACCTTGACATGCTCTCCACTCAT 120

QY 147 CGAACTTGGCTGATAGCGATGGG 170
 Db 121 CGAACTTGGCTGATAGCGATGGG 144

RESULT 4
 AAZ55548
 ID AAZ55548 standard; cDNA; 402 BP.

XX AC AAZ55548;
 XX DT 14-MAR-2000 (first entry)

XX DE Canine interleukin-5 (IL-5) cDNA coding region.

XX KW Interleukin-5; IL-5; antibody; canine; inhibitor; immune response;
 XX KW immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.

XX OS Canis familiaris.

XX PN WO9961618-A2.

XX PD 02-DEC-1999.

XX PF 28-MAY-1999; 99WO-US011942.

XX PR 29-MAY-1998; 98US-0087306P.

XX PA (HESK-) HESKA CORP.

XX PI Sim G, Yang S, Dreitz MJ, Wonderling RS;

XX DR WPI; 2000-072623/06.

XX DR P-PSDB; AAY58219.

XX PT Nucleic acids encoding immunoregulatory proteins from cats or dogs,
 XX PT useful for treating or preventing e.g. tumors or autoimmune disease.

XX PS Claim 1h; Page 225; 264pp; English.

XX CC Sequences AAZ55546-255551 represent cDNA sequences encoding canine
 CC interleukin-5 (IL-5). The invention relates to canine IL-4, canine or
 CC feline Flt-3 ligand, canine or feline CD40, canine or feline CD154 (CD40
 CC ligand), canine IL-5, canine IL-13, feline interferon-alpha (IFN-alpha)
 CC and feline granulocyte macrophage colony-stimulating factor (GM-CSF), and
 CC nucleotides which encode these immunoregulatory proteins. The proteins,
 CC their associated nucleic acids, specific antibodies and inhibitors may be
 CC used as vaccines for therapeutic or prophylactic regulation of an immune
 CC response in animals (particularly cats, dogs, horses and humans). They
 CC may be used to treat autoimmune or infectious diseases including
 CC allergies, tumours, inflammation and graft rejection, and to increase the
 CC response from a co-administered antigen. The nucleotide sequences can
 CC also be used for the recombinant production of a protein, while
 CC nucleotide fragments are useful as probes, as amplification primers and
 CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).

CC The proteins may be used to raise antibodies and to screen for modulators
 CC of activity, while the antibodies may be used in detection, and in drug
 CC targeting

XX SQ Sequence 402 BP; 129 A; 79 C; 93 G; 101 T; 0 U; 0 Other;

Query Match 8.7%; Score 144; DB 3; Length 402;
 Best Local Similarity 100.0%; Pred. No. 1.7e-42;
 Matches 144; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 27 ATGAGAATGCTTCTGGAATTTGAGTTTCTAGCTTCTTGGGCTGCGCTATGTTTCTGCTTTT 86
 Db 1 ATGAGAATGCTTCTGGAATTTGAGTTTCTAGCTTCTTGGGCTGCGCTATGTTTCTGCTTTT 60

QY 87 GCTGTAGAAAATCCCATGAATAGACTGGTGGCAGACCTTGACATGCTCTCCACTCAT 146
 Db 61 GCTGTAGAAAATCCCATGAATAGACTGGTGGCAGACCTTGACATGCTCTCCACTCAT 120

QY 147 CGAACTTGGCTGATAGCGATGGG 170
 Db 121 CGAACTTGGCTGATAGCGATGGG 144

RESULT 5
 AAZ55549/c
 ID AAZ55549 standard; cDNA; 402 BP.

XX AC AAZ55549;

XX DT 14-MAR-2000 (first entry)

XX DE Canine interleukin-5 (IL-5) cDNA coding region complement.

XX KW Interleukin-5; IL-5; antibody; canine; inhibitor; immune response;
 XX KW immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.

XX OS Canis familiaris.

XX PN WO9961618-A2.

XX PD 02-DEC-1999.

XX PF 28-MAY-1999; 99WO-US011942.

XX PR 29-MAY-1998; 98US-0087306P.

XX PA (HESK-) HESKA CORP.

XX PI Sim G, Yang S, Dreitz MJ, Wonderling RS;

XX DR WPI; 2000-072623/06.

XX DR P-PSDB; AAY58219.

XX PT Nucleic acids encoding immunoregulatory proteins from cats or dogs,
 XX PT useful for treating or preventing e.g. tumors or autoimmune disease.

XX PS Claim 1h; Page 226; 264pp; English.

XX CC Sequences AAZ55546-255551 represent cDNA sequences encoding canine
 CC interleukin-5 (IL-5). The invention relates to canine IL-4, canine or
 CC feline Flt-3 ligand, canine or feline CD40, canine or feline CD154 (CD40
 CC ligand), canine IL-5, canine IL-13, feline interferon-alpha (IFN-alpha)
 CC and feline granulocyte macrophage colony-stimulating factor (GM-CSF), and
 CC nucleotides which encode these immunoregulatory proteins. The proteins,
 CC their associated nucleic acids, specific antibodies and inhibitors may be
 CC used as vaccines for therapeutic or prophylactic regulation of an immune
 CC response in animals (particularly cats, dogs, horses and humans). They
 CC may be used to treat autoimmune or infectious diseases including
 CC allergies, tumours, inflammation and graft rejection, and to increase the
 CC response from a co-administered antigen. The nucleotide sequences can
 CC also be used for the recombinant production of a protein, while
 CC nucleotide fragments are useful as probes, as amplification primers and
 CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).

CC The proteins may be used to raise antibodies and to screen for modulators
 CC of activity, while the antibodies may be used in detection, and in drug
 CC targetting

SQ Sequence 402 BP; 101 A; 93 C; 79 G; 129 T; 0 U; 0 Other;

Query Match 8.7%; Score 144; DB 3; Length 402;
 Best Local Similarity 100.0%; Pred. No. 1.7e-42;
 Matches 144; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 27 ATGAGATGCTTCTGAATTCGATTGCTAGCTTTGCTAGCTTTGGGGCTGCTAGTTTCTGCTTT 86
 DB 402 ATGAGATGCTTCTGAATTCGATTGCTAGCTTTGCTAGCTTTGGGGCTGCTAGTTTCTGCTTT 343
 QY 87 GCTGTAGAAAATCCCATGATAGACTGTGGCAGAGACCTTGACACGCTCTCCACTCAT 146
 DB 342 GCTGTAGAAAATCCCATGATAGACTGTGGCAGAGACCTTGACACGCTCTCCACTCAT 283
 QY 147 CGAACTTGGCTGATAGCGATGGG 170
 DB 282 CGAACTTGGCTGATAGCGATGGG 259

RESULT 6

AAF74300
 ID AAF74300 standard; DNA; 405 BP.

AC AAF74300;

DT 04-MAY-2001 (first entry)

DE Canine interleukin-5 coding sequence #1.

KW Dog; interleukin-5; IL-5; allergy; cancer; gene therapy;
 KW inflammatory reaction; ds.

OS Canis sp.

PN WO20011049-A2.

XX 15-FEB-2001.

XX 09-AUG-2000; 2000WO-US021651.

XX 10-AUG-1999; 99US-00371615.

XX (INDEX-) IDEXX LAB INC.

PI Guo H, Lawton R, Mermer B, Aliyappa AP;

DR WPI; 2001-191542/19.

DR P-PSDB; AAB72615.

XX Novel canine interleukin 5 polynucleotide and polypeptides are used for
 XX generating antibodies which are useful in treating allergies in dogs.

PS Claim 31; Page 46; 48pp; English.

XX The present invention provides the protein and coding sequences of the
 CC canine interleukin-5 (IL-5) protein. This can be used to treat allergies,
 CC cancer and inflammatory reactions in dogs. The present sequence is one
 CC version of the IL-5 coding sequence shown in the specification

SQ Sequence 405 BP; 131 A; 77 C; 94 G; 103 T; 0 U; 0 Other;

Query Match 8.7%; Score 144; DB 4; Length 405;
 Best Local Similarity 100.0%; Pred. No. 1.7e-42;
 Matches 144; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 27 ATGAGATGCTTCTGAATTCGATTGCTAGCTTTGGGGCTGCTAGTTTCTGCTTT 86
 DB .1 ATGAGATGCTTCTGAATTCGATTGCTAGCTTTGGGGCTGCTAGTTTCTGCTTT 60

QY 87 GCTGTAGAAAATCCCATGATAGACTGTGGCAGAGACCTTGACACGCTCTCCACTCAT 146
 DB 61 GCTGTAGAAAATCCCATGATAGACTGTGGCAGAGACCTTGACACGCTCTCCACTCAT 120

QY 147 CGAACTTGGCTGATAGCGATGGG 170

DB 121 CGAACTTGGCTGATAGCGATGGG 144

RESULT 7

AAZ55550

ID AAZ55550 standard; cDNA; 345 BP.

XX AAZ55550;

XX 14-MAR-2000 (first entry)

XX Canine mature interleukin-5 (IL-5) cDNA.

XX Interleukin-5; IL-5; antibody; canine; inhibitor; immune response;
 KW immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.

OS Canis familiaris.

XX WO9961618-A2.

XX 02-DEC-1999.

XX 28-MAY-1999; 99WO-US011942.

XX 29-MAY-1998; 98US-0087306P.

XX (HESK-) HESKA CORP.

PI Sim G, Yang S, Dreitz MJ, Wonderling RS;

DR WPI; 2000-072623/06.

DR P-PSDB; AAY58220.

XX Nucleic acids encoding immunoregulatory proteins from cats or dogs,
 XX useful for treating or preventing e.g. tumors or autoimmune disease.

PS Claim 1h; Page 226-227; 264pp; English.

XX Sequences AAZ55546-Z55551 represent cDNA sequences encoding canine
 CC interleukin-5 (IL-5). The invention relates to canine IL-4, canine or
 CC feline Flt-3 ligand, canine or feline CD40, canine or feline CD154 (CD40
 CC ligand), canine IL-5, canine IL-13, feline interferon-alpha (IFN-alpha)
 CC and feline granulocyte macrophage colony-stimulating factor (GM-CSF), and
 CC nucleotides which encode these immunoregulatory proteins. The proteins,
 CC their associated nucleic acids, specific antibodies and inhibitors may be
 CC used as vaccines for therapeutic or prophylactic regulation of an immune
 CC response in animals (particularly cats, dogs, horses and humans). They
 CC may be used to treat autoimmune or infectious diseases including
 CC allergies, tumours, inflammation and graft rejection, and to increase the
 CC response from a co-administered antigen. The nucleotide sequences can
 CC also be used for the recombinant production of a protein, while
 CC nucleotide fragments are useful as probes, as amplification primers and
 CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).
 CC The proteins may be used to raise antibodies and to screen for modulators
 CC of activity, while the antibodies may be used in detection, and in drug
 CC targetting

XX Sequence 345 BP; 120 A; 68 C; 78 G; 79 T; 0 U; 0 Other;

Query Match 7.8%; Score 129; DB 3; Length 345;
 Best Local Similarity 100.0%; Pred. No. 4.6e-37;
 Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1276 CACCACTGTCATTAAAGAGTTTTTCAGGCTATAGACACATTGAGACCAACTGCC 1335
 DB 121 CACCACTGTCATTAAAGAGTTTTTCAGGCTATAGACACATTGAGACCAACTGCC 180

QY	1336	CACGGGAGGCTGTGGATAAACTATTCCAAACCTTCTTTAATAAAGAACACATAGAG	1395		
DB	181	CACGGGAGGCTGTGGATAAACTATTCCAAACCTTCTTTAATAAAGAACACATAGAG	240		
QY	1396	CGCCAAAAA 1404			
DB	241	CGCCAAAAA 249			
RESULT 8					
ID	AAZ5551/c	AAZ5551 standard; cDNA; 345 BP.			
XX	AAZ5551;				
DT	14-MAR-2000	(first entry)			
DE	Canine mature interleukin-5 (IL-5) cDNA complement.				
KW	Interleukin-5; IL-5; antibody; canine; inhibitor; immune response;				
KW	immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.				
OS	Canis familiaris.				
XX	WO9961618-A2.				
XX	02-DEC-1999.				
XX	28-MAY-1999;	99WO-US011942.			
XX	29-MAY-1998;	98US-0087306P.			
PA	(HESK-) HESKA CORP.				
PI	Sim G, Yang S, Dreitz MJ, Wonderling RS;				
DR	WPI; 2000-072623/06.				
DR	P-PSDB; AAY59220.				
PT	Nucleic acids encoding immunoregulatory proteins from cats or dogs,				
PT	useful for treating or preventing e.g. tumors or autoimmune disease.				
XX	Claim 1h; Page 228; 264pp; English.				
XX	Sequences AAZ55546-255551 represent cDNA sequences encoding canine				
CC	interleukin-5 (IL-5). The invention relates to canine IL-4, canine or				
CC	feline Flt-3 ligand, canine or feline CD40, canine or feline CD154 (CD40				
CC	ligand), canine IL-5, canine IL-13, feline interferon-alpha (IFN-alpha)				
CC	and feline granulocyte macrophage colony-stimulating factor (GM-CSF), and				
CC	nucleotides which encode these immunoregulatory proteins. The proteins,				
CC	their associated nucleic acids, specific antibodies and inhibitors may be				
CC	used as vaccines for therapeutic or prophylactic regulation of an immune				
CC	response in animals (particularly cats, dogs, horses and humans). They				
CC	may be used to treat autoimmune or infectious diseases including				
CC	allergies, tumours, inflammation and graft rejection, and to increase the				
CC	response from a co-administered antigen. The nucleotide sequences can				
CC	also be used for the recombinant production of a protein, while				
CC	nucleotide fragments are useful as probes, as amplification primers and				
CC	as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).				
CC	The proteins may be used to raise antibodies and to screen for modulators				
CC	of activity, while the antibodies may be used in detection, and in drug				
CC	targeting				
XX	Sequence 345 BP; 79 A; 78 C; 68 G; 120 T; 0 U; 0 Other;				
Query Match					
Best Local Similarity 7.8%; Score 129; DB 3; Length 345;					
Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
QY	1276	CACCAACTGTGCATTAAAGAGTTTTCAGGGTATAGACATTCAGAACCAAACTGCC	1335		
DB	225	CACCAACTGTGCATTAAAGAGTTTTCAGGGTATAGACATTCAGAACCAAACTGCC	166		

QY	1336	CACGGGAGGCTGTGGATAAACTATTCCAAACCTTCTTTAATAAAGAACACATAGAG	1395		
DB	165	CACGGGAGGCTGTGGATAAACTATTCCAAACCTTCTTTAATAAAGAACACATAGAG	106		
QY	1396	CGCCAAAAA 1404			
DB	105	CGCCAAAAA 97			
RESULT 9					
ID	AAF74306	AAF74306 standard; DNA; 393 BP.			
XX	AAF74306;				
DT	04-MAY-2001	(first entry)			
XX	Canine interleukin-5 coding sequence #3.				
KW	Dog; interleukin-5; IL-5; allergy; cancer; gene therapy;				
KW	inflammatory reaction; ds.				
OS	Canis sp.				
XX	WO200111049-A2.				
XX	15-FEB-2001.				
XX	09-AUG-2000;	2000WO-US021651.			
XX	10-AUG-1999;	99US-00371615.			
PA	(IDEX-) IDEXX LAB INC.				
XX	Guo H, Lawton R, Mermer B, Aiyappa AP;				
XX	WPI; 2001-191542/19.				
XX	Novel canine interleukin 5 polynucleotide and polypeptides are used for				
PT	generating antibodies which are useful in treating allergies in dogs.				
XX	Claim 1; Page 35; 48pp; English.				
XX	The present invention provides the protein and coding sequences of the				
CC	canine interleukin-5 (IL-5) protein. This can be used to treat allergies,				
CC	cancer and inflammatory reactions in dogs. The present sequence is one				
CC	version of the IL-5 coding sequence shown in the specification				
XX	Sequence 393 BP; 128 A; 82 C; 86 G; 97 T; 0 U; 0 Other;				
Query Match					
Best Local Similarity 7.8%; Score 129; DB 4; Length 393;					
Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
QY	1276	CACCAACTGTGCATTAAAGAGTTTTCAGGGTATAGACATTCAGAACCAAACTGCC	1335		
DB	76	CACCAACTGTGCATTAAAGAGTTTTCAGGGTATAGACATTCAGAACCAAACTGCC	135		
QY	1336	CACGGGAGGCTGTGGATAAACTATTCCAAACCTTCTTTAATAAAGAACACATAGAG	1395		
DB	136	CACGGGAGGCTGTGGATAAACTATTCCAAACCTTCTTTAATAAAGAACACATAGAG	195		
QY	1396	CGCCAAAAA 1404			
DB	196	CGCCAAAAA 204			
RESULT 10					
ID	AAT50756	AAT50756 standard; cDNA; 399 BP.			
XX	AAT50756;				
XX					

Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 100 CCATGAATAGACTGGTGCAGAGACCTTGACACTGCTCCAC 142
 DB 113 CCATGAATAGACTGGTGCAGAGACCTTGACACTGCTCCAC 155

RESULT 12
 AAZ44265
 ID AAZ44265 standard; DNA; 838 BP.
 XX
 AC AAZ44265;
 XX
 DT 31-MAR-2000 (first entry)
 XX
 DE Porcine IL-5 DNA.
 XX
 XX Pig; vaccine; cysticercosis; protective antigen; cC1; cC3; cC4;
 KW tenial cysticercus; gamma interferon; IFN-gamma; interleukin 5; IL-5; ss.
 XX
 OS Sus scrofa.
 XX
 PN CN1231339-A.
 XX
 PD 13-OCT-1999.
 XX
 XX 29-JAN-1999; 99CN-00113447.
 PF
 XX 29-JAN-1999; 99CN-00113447.
 PR
 XX (UYIW-) UNIV NO 2 MILITARY MEDICAL PLA.
 PA
 XX Sun S, Dai J;
 PI
 DR WPI; 2000-087904/08.
 XX
 PT Nucleic acid vaccine for cysticercosis co-contracted by human and pig.
 XX
 PS Claim 3; Page 9; 21pp; Chinese.
 XX
 CC This invention describes a novel nucleic acid vaccine for preventing and
 CC curing human and pork cysticercosis. The invention involves the formation
 CC of a eukaryotic expression plasmid from fusion transcript expression unit
 CC consisting of three protective antigen genes (cC1, cC3 and cC4) of pig
 CC tenial cysticercus and coexpression unit of related cell factor gamma
 CC interferon (IFN-gamma) and pork interleukin 5 (IL-5) genes. The
 CC production and purification process of said nucleic acid vaccine is
 CC simple and convenient, the physical and chemical properties of the
 CC vaccine are stable, and the vaccine is easy to store and transport, and
 CC possesses effective immunological protective function for human and pig
 CC cysticercosis. This sequence represents the pig IL-5 gene used in the
 CC method of the invention
 XX
 SQ Sequence 838 BP; 280 A; 148 C; 171 G; 239 T; 0 U; 0 Other;

Query Match 2.5%; Score 41; DB 3; Length 838;
 Best Local Similarity 100.0%; Pred. No. 2.5e-05;
 Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 43 ATTGAGTTGCTAGCTCTTGGGCTGCTATGTTCTGCC 83
 DB 61 ATTGAGTTGCTAGCTCTTGGGCTGCTATGTTCTGCC 101

RESULT 13
 ABV56577/c
 ID ABV56577 standard; cDNA; 357 BP.
 XX
 AC ABV56577;
 XX
 XX 17-SEP-2002 (first entry)
 DT
 XX Human prostate expression marker cDNA 56568.
 DE

XX Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
 KW pharmacogenomic marker; gene; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200160860-A2.
 XX
 PD 23-AUG-2001.
 XX
 PF 20-FEB-2001; 2001WO-US005171.
 XX
 PR 17-FEB-2000; 2000US-0183319P.
 PR 16-MAR-2000; 2000US-0189862P.
 PR 25-MAY-2000; 2000US-0207454P.
 PR 09-JUN-2000; 2000US-0211314P.
 PR 18-JUL-2000; 2000US-0219007P.
 PR 13-DEC-2000; 2000US-0255281P.
 XX
 XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 PA
 XX Schlegel R, Endege WO, Monahan JE;
 PI
 XX WPI; 2001-662795/76.
 DR
 XX
 PT Novel isolated nucleic acid molecule associated with cancerous state of
 PT prostate cells and correlating with presence of prostate cancer, useful
 PT for detecting presence of prostate cancer, stage of prostate cancer.
 XX
 PS Claim 1; Page 10911; 11750pp; English.
 XX
 CC The invention relates to an isolated nucleic acid molecule (I) comprising
 CC a nucleotide sequence given in Tables 1-9 (ABY00010-ABY62213) of the
 CC specification or its complement. (I) is useful for: (a) assessing whether
 CC a patient is afflicted with prostate cancer; (b) monitoring the
 CC progression of prostate cancer in a patient; (c) assessing the efficacy
 CC of a test compound to inhibit prostate cancer in a patient; (d) assessing
 CC the efficacy of a therapy for inhibiting prostate cancer in a patient;
 CC (e) selecting a composition for inhibiting prostate cancer in a patient;
 CC (f) assessing the prostate cell carcinogenic potential of a compound; (g)
 CC determining whether prostate cancer has metastasized in a patient; (h)
 CC assessing the aggressiveness or indolence of prostate cancer in a patient
 CC ; (i) is also useful as a pharmacodynamic or pharmacogenomic marker
 XX
 SQ Sequence 357 BP; 104 A; 93 C; 90 G; 69 T; 0 U; 1 Other;

Query Match 1.6%; Score 26; DB 5; Length 357;
 Best Local Similarity 100.0%; Pred. No. 7.7;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1458 TTTTITTTTTTTTTTTTACAGAAAT 1483
 DB 69 TTTTITTTTTTTTTTTTACAGAAAT 44

RESULT 14
 AAH92592
 ID AAH92592 standard; DNA; 700 BP.
 XX
 AC AAH92592;
 XX
 DT 09-OCT-2001 (first entry)
 XX
 DE Human inflammatory bowel disease related gene fragment IGR1292a.
 XX
 KW Human; inflammatory bowel disease; Crohn's disease; ulcerative colitis;
 KW single nucleotide polymorphism; SNP; chromosome 19p13; paternity test;
 KW chromosome 5q31-33; forensic test; gene therapy; ds.
 XX
 OS Homo sapiens.
 XX
 PN WO200142511-A2.
 XX

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OM nucleic - nucleic search, using sw model

Run on: August 30, 2004, 15:56:41 ; Search time 790.781 Seconds
(without alignments)
8907.036 Million cell updates/sec

Title: US-10-787-382-18
Perfect score: 1658
Sequence: 1 agcaaacactgacatttc.....gtagtgaagatttgaga 1658

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 212409041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N Geneseq_29Jan04:*

- 1: Geneseqn1980s:*
- 2: Geneseqn1980s:*
- 3: Geneseqn2000s:*
- 4: Geneseqn2001as:*
- 5: Geneseqn2001bs:*
- 6: Geneseqn2002s:*
- 7: Geneseqn2003as:*
- 8: Geneseqn2003bs:*
- 9: Geneseqn2003cs:*
- 10: Geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	634.6	38.3	3241	3 AAA34856	Aaa34856 Human ade
2	634.6	38.3	3241	3 AAF20978	Aaf20978 Human low
3	634.6	38.3	3241	7 ABZ96672	Abz96672 Human nuc
4	634.6	38.3	4057	3 AAA34858	Aaa34858 Human ade
5	634.6	38.3	4057	3 AAF20980	Aaf20980 Human low
6	634.6	38.3	4057	7 ABZ96674	Abz96674 Human nuc
7	634.6	38.3	9738	6 AAS15002	Aas15002 DNA encod
8	600.6	36.2	3230	1 AAN81381	Aan81381 Entire nu
9	600.6	36.2	3230	2 AAQ74056	Aaq74056 Human int
10	600.6	36.2	3230	3 AAC73725	Aac73725 Human IL-
11	600.6	36.2	3230	7 ABX04379	Abx04379 Human int
12	272.6	16.4	700	4 AAH92592	Aah92592 Human inf
13	221.6	13.4	700	4 AAH92594	Aah92594 Human inf
14	216	13.0	700	4 AAH92591	Aah92591 Human inf
15	215.4	13.0	700	4 AAH92593	Aah92593 Human inf
16	205.2	12.4	1395	1 AAN71243	Aan71243 Sequence
17	171.8	10.4	610	3 AAZ55546	Aaz55546 Canine in
18	171.8	10.4	610	3 AAZ55547	Aaz55547 Canine in
19	150.8	9.1	5397	6 ABL33044	AbL33044 Human imm
20	149.4	9.0	838	3 AAZ44265	Aaz44265 Porcine I
21	145.8	8.8	252	4 AAF74305	Aaf74305 Canine in
22	145.8	8.8	402	3 AAZ55548	Aaz55548 Canine in
23	145.8	8.8	402	3 AAZ55549	Aaz55549 Canine in

24	145.8	8.8	405	4 AAF74300	Aaf74300 Canine in
25	138.2	8.3	520	3 AAT50755	Aat50755 Ovine IL-
c 26	134.6	8.1	5397	6 ABL33045	AbL33045 Human imm
27	131.6	7.9	345	3 AAZ55550	Aaz55550 Canine ma
c 28	131.6	7.9	345	3 AAZ55551	Aaz55551 Canine ma
29	131.6	7.9	393	4 AAF74306	Aaf74306 Canine in
30	117.4	7.1	385	3 AAA43842	Aaa43842 Human sec
31	117.4	7.1	816	3 AAA34857	Aaa34857 Human ade
32	117.4	7.1	816	3 AAA13338	Aaa13338 Human int
33	117.4	7.1	816	3 AAL20979	Aal20979 Human low
34	117.4	7.1	816	7 ABZ96673	Abz96673 Human nuc
35	117.4	7.1	816	7 ACF63368	Acf63368 Human int
36	112.6	6.8	399	2 AAT50756	Aat50756 Ovine IL-
37	108	6.5	6727	2 AAT88014	Aat88014 Murine IL
38	108	6.5	6727	3 ACX73648	Acx73648 Murine IL
39	108	6.5	6727	7 ACX04302	Acx04302 Mouse int
40	99.4	6.0	402	1 AAN81390	Aan81390 A human B
41	97.2	5.9	444	3 AAC68875	Aac68875 Modified
42	96.2	5.8	858	8 AAL61293	Aal61293 hIL5-P2-P
43	96.2	5.8	858	8 AAL61294	Aal61294 hIL5-P30-
44	89.4	5.4	381	3 AAC68867	Aac68867 Modified
45	89	5.4	864	8 AAL61296	Aal61296 hIL5.37 v

ALIGNMENTS

RESULT 1
AAA34856
ID AAA34856 standard; DNA; 3241 BP.
XX
AC AAA34856;
XX
DT 28-JUL-2000 (first entry)
XX
DE Human adenosine receptor related polynucleotide SEQ ID NO:2545.
XX
KW Human; adenosine receptor; low adenosine antisense oligonucleotide;
KW phosphothicinate; impaired respiration; inflammation; allergy;
KW allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
KW antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway;
KW lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;
KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
KW cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.
XX
OS Homo sapiens.
XX
PN WO200009525-A2.
XX
PD 24-FEB-2000.
XX
PF 03-AUG-1999; 99WO-US017712.
XX
PR 03-AUG-1998; 98US-0095212P.
XX
PA (UYEC-) UNIV EAST CAROLINA.
XX
PI Nyce JW;
XX
DR WPI; 2000-205971/18.
XX
PT New antisense oligonucleotides useful for treating e.g. pulmonary
PT vasoconstriction, inflammation, allergies, asthma, hypertension, or
PT bronchitis, emphysema, respiratory distress syndrome, ischemia or
PS cancers.
PS Disclosure; Page 715-716; 1343pp; English.
XX
CC The present invention describes a new composition comprising an antisense
CC oligonucleotide (ON) with low adenosine (up to 15%), which targets
CC nucleic acids involved in bronchoconstriction, allergies, and/or
CC inflammation. The ON can have antiinflammatory, antiallergic,

antiasthmatic, cytostatic and analgesic activities. The compositions are useful for the treatment of diseases associated with inflammation, impaired airways, including lung disease and diseases whose secondary effects afflict the lungs of a subject. They can be used for treating e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma, CC impeded respiration, respiratory distress syndrome, pain, cystic fibrosis, pulmonary hypertension, emphysema, chronic obstructive pulmonary disease (COPD), and cancers such as leukaemias, lymphomas, CC carcinomas, and cancers which may metastasise to the lungs, including breast and prostate cancer. The reduction of the adenosine content of the CC ONs reduces side effects. The A-containing ONs break down with the release of deoxyadenosine which activates adenosine receptors causing bronchoconstriction and inflammation. AAA32313 to AAA35312 represent the nucleotide sequences given in the sequence listing from the present invention, which correspond to SEQ ID NO:1 to 2815, and then the last 185 sequences are also called SEQ ID NO:1 to 185, but the sequences differ from the previously named sequences. SEQ ID NO:11 to 1680 (AAA32323 to AAA33992) are specifically claimed ONs from the present invention. N.B. Sequences given in the disclosure of the present invention do not match up with their corresponding SEQ ID NO: sequences given in the sequence listing

XX
SQ Sequence 3241 BP; 1026 A; 546 C; 632 G; 1037 T; 0 U; 0 Other;

Query Match 38.3%; Score 634.6; DB 3; Length 3241;
Best Local Similarity 68.6%; Pred. No. 1e-115;
Matches 1226; Conservative 0; Mismatches 374; Indels 187; Gaps 18;

1 AGGCAACACATGAACTTCAGAGCTATGAGATGCTTCGAAATTCAGATTGCTAGCTC 60
526 AGGCAACGAGACGTTTCAGAGCCATGAGATGCTTCGAAATTCAGATTGCTAGCTC 595
61 TTGGGCTGCTATGTTTCGCTTTGCTGTGAGAAATCCCATGAAATGAGCTGGTGCAG 120
586 TTGGAGTGCCTAGCTGTATGCCATCCCAAGAAATCCCAAGTGCATGGTGAAG 645
121 AGACCTTGACACTGCTCCCACTCATCGAACTTGGCTGATGAGGATGGGTAAATTTCT 180
646 AGACCTTGGCACTGCTTCTACTCATCGAACTTGGCTGATGAGCAATGAGGTAAATTTCT 705
181 TTTTGAATCTACAGTCTTTAAATGTCATGGTAAATTTGGTGGTGGCTAGTT----- 234
706 TTATGATCTTACAGTCTGTAAGTGCATAGGTAATCATTTGATGTTCCCTTACTAT 765
235 -TTTAAAGATCCATATCAATATCAAGTATGAGTGTATTAATATATATATATATATATAT 293
766 ATATAGAGATCTGTATATAATATATATATATATATATATATATATATATATATATAT 824
294 ATGTTACTCAGAGAAATATATATAAAGTTATGAACCTTACATAATATAAATAAATGAATG 353
825 ACATCACCAGCAACATTCGTTAAAGTTATGAATGCTGGTGTCTGTAATAATGATG 884
354 TTGTTTCTTTTTCAGAACTGATGATGCTTCTACTCTGAAATATAAATAAATGTAAGTT 413
885 -TATTTCTTTCTCTCCAGACTCTGAGGATTCCTGTCTGTACATAAATAAATGTAAGTT 943
414 AAATATGATTTGATAAATGATTTACATGATCAGT-----TTCATATTTTAAGCTATAA 469
944 AAATATGATTCAGTAAATATGATGGAATGATGATGATGATGATGATGATGATGATGAT 1003
470 GTATCAGTTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 529
1004 TCATTAGTATATATGGAAT 1063
530 AAAT-TATGTCCTTATCAATATATAGGATGCTGTAGGATGCTCTACATATATATAT 588
1064 GAATGCTGCTACTTATATAATATAGGATGACTTT-----TATCAAGTA 1108
589 GAATCCATTAAGCAAGTGGATCAGGCCCTTTTGTGATGTTGTCAGTCTCCATCTCAAA 648
1109 GAATCCCTTAAACAAGTGGATAGGCTCTTTGGTGAATGTTGTTAGTT-TGCCTCCCAAG 1167
649 AGCTCTGTCAGGCATCTTTTCCAAAGAAATTCATATATGAGTGGTACAGATATCTCTAG 708

1168 AGCATCGTGTAGGATCTTTCCAGAGAGGATCCCACTGAGTGAGAGGTCGCTGCTAG 1227
709 GCTCATTCACCTCTGTGTGGTGGCTTCTCTACCTCAACGTTTCTGAAAGTACTAGCA 768
1228 TCTCCGTGCAAGTCTGAC-----TCTTTCTCACTCAACGTTTCTGAAAGTACTAGCA 1282
769 ACTTGGGGTTATATTTTAGAATATATGTCAGTACATGAAATATATACAGTGAAGTCT 828
1283 ACTGAAATATATTTTAGAACCAATGATCAGTAGACATTAATATATATACAAATGCC- 1341
829 ATATTAATAGTCACCTCCACATATTTAAATGATTTTAACTCTAATGGAATCATATACAT 888
1342 -CTATATTAATAATTTCTGCATCTATAATAATATGACTATATGATGGTGTGTATGCA 1400
889 CTGGAGTATGTCATGCTCATATTAATGTTTAAATGTCATATGATATGATATGATATAGA 948
1401 TTTGAATATGCTGCTCATATTAATGTTTAAATGTTTAAATGTTTAAATGTTTAAATGTT 1460
949 ATAAATACCAGCTAGAACTATACGAGAAATCTGAGGTGAGTAAATCAGTAAGCA 1008
1461 ATAAATACCAGCTAGAACTATAGAAACAT--TGATATGAGTTTAAATGTTAA-- 1514
1009 GTTGTATATATACCTGTAAGCATTTATTTTTCATTAATCATTTTATATATCATTTGTA 1068
1515 --TGATATACACTTCCAAACATTTTTCAGTTTACATAATTAAGTTATATCTCTTTATA 1572
1069 ACATCTCTCAGTAATATATAAATCATTTTAC--TTATGGTAAATATATAGCTTAGTATAAG 1127
1573 AAATCTCTCAGTAATATATAAATCATTTTAC--TTATGGTAAATATATAGCTTAGTATAAG 1632
1128 GTGGTTTCCCACCTGGAAAGACACAAAGTAAACCTCTTGGGAGAGGGAACCTGTGTA 1187
1633 GTGGTTTGTGCTAGAAA-----ACAAACAAACAACTCTTGGAGAGGGAACCTCATGTA 1688
1188 AACCCCAACAAACAAAGCTAACTTT----- 1213
1689 AATACCAACAAACAAAGCTAACTTTGTGGACCAAAATGTTTAAATATATTTTAA 1748
1214 ----- 1213
1749 TTGATGAATTAAGATATATATATTTATTTGTGTAACATATGATGTTTGAAGTATGAT 1808
1214 -----TTGGACCAAAATTTTATGCTGCTGTTTGTGATGATATATATTTT 1256
1809 AATTGCAAGATGCAATGAGCAAAATTTTATACCTGTCCTGATTTTGA-TTTT 1867
1257 TAAATCTTCTCTATTTAGCACCAACTGTGCATTAAGAAAGTCTTTCAGGATATAGACAC 1316
1868 AAAAAATTTCTCTATTTAGCACCAACTGTGCATGAAAGAACTTTTCAGGGAATAGGCAC 1927
1317 ATTGAAGAACCAACTGCTCCAGGGAGGCTGTGGATAAATATTCACAAACTGTCTTT 1376
1928 ACTGAGAGTCAAACTGTGCAAGGGGCTGTGTGAAAGACTATTCAAAACTGTGCTTT 1987
1377 AATAAAGAACACATAGAGGCCCAAAAGTAAAGTAAAGACATTTGCGCAAAACCTTAAGT 1436
1988 AATAAAGAAATACATGAGGCCCAAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGT 2042
1437 ATATTTGTCTGCTGCTGCTGTTTTTTTTTTTTTTTTTTTTTCAAGAAATGACAGTTCCCTA 1496
2043 ATATTTGTCTGCTGCTGCTGTTTTCTAT-----GGAATGACAGTTTCTG 2088
1497 CAATATCT-----CCTCTGTTTTTAAACAGAAAGGCTGCGAGGAGAAAGTGGAG 1550
2089 TAAATACCTATTTGTCATTTTCTTTTTCACAGAAAAAGTGTGGAGAAAGAACGGAGAG 2148
1551 TGACAAAGTCTCTAGACTACCTGCAAGTATTTCTTGGTGTAAATAAACACCGAGTGGACAC 1610
2149 TAAACCAATCTCTAGACTACCTGCAAGAGTTTCTTGGTGTAAATAAACACCGAGTGGATA 2208
1611 CGAAAGTGTGAGAACCAACCGCTTATTTAGTGGAGATTTTGGAG 1657

Db 2209 TAGAAGTTGAGACTAAACTGGTTTGTTCGACCAAGATTTGGAG 2255

RESULT 2

ID AAF20978 standard; DNA; 3241 BP.

XX AC AAF20978;

XX DT 14-MAR-2001 (first entry)

XX Human low adenosine antisense oligonucleotide related sequence #2545.

XX Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
 KW human; airway disorder; bronchoconstriction; lung inflammation;
 KW surfactant depletion; respiratory; bronchodilator; antiinflammatory;
 KW immunosuppressive; antiasthmatic; analgesic; hypotensive; cytotatic;
 KW respiratory obstruction; pulmonary obstruction; impeded respiration;
 KW surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
 KW respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
 KW pulmonary hypertension; emphysema; pulmonary transplantation rejection;
 KW chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
 KW cancer; ss.

XX OS Homo sapiens.

XX WO200062736-A2.

XX 26-OCT-2000.

XX 24-MAR-2000; 2000WO-US008020.

XX 06-APR-1999; 99US-0127958P.

XX (UYEC-) UNIV EAST CAROLINA.

XX (NYCE//) NYCE J.W.

XX Nyce JW;

XX WPI; 2000-679539/66.

XX Low adenosine (A) content antisense oligonucleotides which do not trigger
 PT adenosine receptors during metabolism, useful e.g. for treating cancers
 PT and respiratory obstructions.

XX Disclosure; Page 787-788; 1592pp; English.

XX The present invention describes low adenosine (A) content antisense
 CC oligonucleotides and compositions (I) comprising them. In the antisense
 CC oligonucleotides the A is replaced by a 'Universal' or alternative base.
 CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
 CC immunosuppressive, antiasthmatic, hypotensive and cytotatic activities.
 CC The antisense oligonucleotides and (I) can be used to down-regulate the
 CC expression and or activity of target polypeptides associated with
 CC lung/respiratory disorders and malignancies, such as stimulating and
 CC activating peptide factors and transmitters, transcription factors,
 CC immunoglobulins and antibodies, antibody receptors, cytokines and
 CC chemokines, endogenously produced specific and non-specific enzymes,
 CC binding proteins, adhesion molecules and their receptors, cytokine and
 CC chemokine receptors, adenosine receptors, bradykinin receptors, central
 CC nervous system (CNS) and peripheral nervous and non-nervous system
 CC receptors, CNS and peripheral nervous and non-nervous system peptide
 CC transmitters, defensins, growth factors, vasoactive peptides and
 CC receptors, binding proteins and malignancy associated proteins. The
 CC antisense oligonucleotides may be used in this way to treat disorders
 CC including respiratory obstruction (especially pulmonary obstruction
 CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies) and/or
 CC surfactant hypoproduction which are associated with a disease or
 CC condition selected from pulmonary vasoconstriction, inflammation,
 CC allergies, asthma, impeded respiration, respiratory distress syndrome
 CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
 CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
 CC pulmonary transplantation rejection, pulmonary infections, bronchitis,

CC and/or cancer. AAF18434 to AAF21543 represent human polynucleotide
 CC fragments and antisense oligonucleotides used in the exemplification of
 CC the present invention

XX Sequence 3241 BP; 1026 A; 546 C; 632 G; 1037 T; 0 U; 0 Other;

XX Query Match 38.3%; Score 634.6; DB 3; Length 3241;
 XX Best Local Similarity 68.6%; Pred. No. 1e-115;
 XX Matches 1226; Conservative 0; Mismatches 374; Indels 187; Gaps 18;

QY 1 AGGCAACACCTGAACATTCAGAGCTATGAGATGCTTCTGAATTTGATTTGCTAGCTC 60
 Db 536 AGGCAACACGCAAGCTTTCAGAGCCATGAGATGCTTCTCAATTTGATTTGCTAGCTC 585

QY 61 TTGGGCTGCTATGTTTCTGCTTCTGTAGAAATCCCATGAATAGACTGTGGCAG 120

Db 586 TTGGAGCTGCTCATGCTGATGCCATCCCAAGAAATTCACCAAGTGCATTTGGTAAAG 645

QY 121 AGACCTTGACACTGCTCTCCACTCATCGAACTTGCTGATAGGGGATGGGTAATTTCT 180

Db 646 AGACCTTGGCACTGCTTCTACTCATCGAACTTGCTGATAGCCAAATGAGTAATTTCT 705

QY 181 TTTTGATTTCTACAGTCTTTTAAATGCAATGGTAAATTTGGTGGTGGTGGCTAGTT----- 234

Db 706 TTATGATTTCTACAGTCTTAAAGTGCATAGTAAATCATTTGTGATGTTCCITTTACTAT 765

QY 235 -TTTAAAGATCCATTTATCAATAAGTAATGATGTTAATAATATATATATGATGTAACC 293

Db 766 ATATAGAGATCTGTTTATAAATAAATAAGATTTCTGAG-CACATTAGTACATGGTGATAACT 824

QY 294 ATGTTTACTCAGAAGAATTTATATTAAAGTTATGAACCTTACAAATACATTAATAAATGAATG 353

Db 825 ACATCACCAGCAACATTTCTGTTAAAGTTATGAATGCTGGTGTCTGTAAATAATGATTG 884

QY 354 TTGTTTCTCTTTTTCAGAACCTGATGATTCCTCTACTCTCTGAAATAAATAATGTAAGTT 413

Db 885 -TAITTTCTCTCTCTCCAGACTCTGAGGATTCCTGTTCTGTCATATAAATAATGTAAGTT 943

QY 414 AAATATGATTTGATAAAATGATTAATGATGATGTTAGGAATGGTCTACAAATATTAAGTA 469

Db 944 AAATATGATTTGATAAAATGATTAATGATGATGATTAATTTCTGTTTAAAGCTGTA 1003

QY 470 GTATCAGTTAATGGAATGATTAATTTTATCTATTTTCTTTTATGTTGTTGGGATGT 529

Db 1004 TCATTAGTTATCATTTGGAACATTAATTTTCTATATTTTCTATATTTTCTATATGTTGGTGT 1063

QY 530 AAAT-TATGTTGCTATGATTAATGGAATGGTGTAGGAATGGTCTACAAATATTAAGTA 588

Db 1064 GAATGCTGTACTTATAAATAATGATGATGATTTT-----TTATCAAGTA 1108

QY 589 GAATCCATTAAGCAAGTGGATCAGGCCCTTTTGAATGTTGTCTGATTTCTCATCTCTCAAG 648

Db 1109 GAATCCTTTAAACAAGTGGATTAGGCTCTTTGGTGATGTTGTTAGTT-TGCTCTCCCAAG 1167

QY 649 AGCTCTGTTGAGGATTTTTCACCAAGAAATTCATATTCGTCAGAGATCTTCCTAG 708

Db 1168 AGCATGCTGTGAGGATTTTTCAGAAAGAAATTCACACTGAGTGAGGTTGCTGCTAG 1227

QY 709 GCTCCATTCACTCTGCTGTTGGCTTTCTCCCTCACCGTTTCTGAAAGTACTAGCA 768

Db 1228 TCTCCGTCGAGTCTTGAC----TCTTTCTCACTCAACGTTTCTCTGAAAGTATTAGCA 1282

QY 769 ACTTGGGGTTATTTTATGAAATATGCTGATAGACATGAATAATATACAGTGAATGCT 828

Db 1283 ACTCAGAATTTATTTTATAGAACCAATGATCAGTACATTAATAATATATAACAATGCC- 1341

QY 829 ATATTAATAGTCACATTCACATATTTAAATGATTTTAACTCTAATGAATCATATACAT 888

Db 1342 -CTATATTAATAATTTCTGCATCTTAAATATATGATCATATGATGTTGTTGATGCA 1400

QY 889 CTGAGTATGTCATGCTCATATTAATAATGTTTAAATAATGATATCATTTAGTCTTAATAAGA 948

Db 1401 TTTGAATATGCTCTGCTCATATTAATAATGTTAAATATATATAGTTTATTTAGTCTTAATAAGA 1460

Qy	294	ATGTTACTCAGAGAATATATATAAAAGTTATGAACCTTACAATACATTTAAAAATGAATG	353
Db	825	ACATCACCAGCAAAACATTTCTGTATAAGGTTATGAATGCTGTGCTCTGTAAAAATGATTG	884
Qy	354	TGTTTTCCTTTCTTTTCAGAACCTGATGATTTCTTACTCTCGAAAAATAAAAATGATGATT	413
Db	885	-TATTTCTTTCTCTCCAGACTCTGAGGATTCCTGTTCTCTGTACATAAAAATCTAAGTT	943
Qy	414	AAATTAATGATTGTATAAAATGATTTACATGAATCACT-----TTCATATTTTAAAGCTATAAA	469
Db	944	AAATTAATGATTCAGTAAAAATGATGGCATGAATAAGTAAATTTCTGTTTAAAGCTGTAAA	1003
Qy	470	GTATCAGTTTAACATTTGGATGATTTAATTTTATCTATTTTGTCTTTTATGTGTGGGATGT	529
Db	1004	TCATTAGTTATCATTTGGAACTATTAAATTTTCTATATTTTGTGTTTCATATGGGTGGCTGT	1063
Qy	530	AAAT-TATGTCTTATGAATATTAGGAATGTGTAGGAATGGCTCTACAATATTAAAGTA	588
Db	1064	GAATGTCTGACTTATAAATATAGGAATGACTTT-----TTATCAAGTA	1108
Qy	589	GAATCCATTAGCAAGTGGATCAGGCCCTTTTGTATGTTGTCAGTTCTCCATCTCAAAG	648
Db	1109	GAATTCCTTTAAACAAGTGGATTAGGCTCTTTGGTGATGTTGTATAGTT-TGCCTCCCAAG	1167
Qy	649	AGCCTCGTGTGAGGCATTTCTTCCAAAAGAAATCCATATTTGGGTCAGAGATACTTCTCTAG	708
Db	1168	AGCATCGTGTGAGGATTCCTTCAGAAAGATCCACACTGAGTGAAGGTGCGTGTAG	1227
Qy	709	GCTCCATTACCTCTGCTGTGTGGCTTTCTTCACCTCAACGTTTTCGAAAGTACTAGCA	768
Db	1228	TCTCCGTGCACTTCTGAC-----TCCTTCTCACTCTAACGTTTCTCGAAAGTATTAGCA	1282
Qy	769	ACTTGGGGTTATATTTTTAGAAATPATGTCAGTAGACATGAAATATACAGTGAAGTCCT	828
Db	1283	ACTCAGAAATATATTTTTAGAACCAAGATCAGTAGACATTTAAATATATACCAAAATGCC-	1341
Qy	829	ATATTAATAGTCACTTCCACAATATTTAAATGAATTTTAACTCTAAATGGAATCATATACAT	888
Db	1342	-CTATATTAATAATTTCTGCATACCTTAATAAATATGACTATATGATGGTGTGTATGCA	1400
Qy	889	CTGAGTATGTCATGGTCATATAAAATGTTTAAAAATGTGATATCATTTAGCTTAAATAGA	948
Db	1401	TTTGAATATGCTCTGGTCAATTTAAATGTAATAATATATAGTTTATTTAGCTTAAATAGA	1460
Qy	949	ATAAAATCCAGCTAGAACTATACGAGGAAATCTGAGGTGAGGTAATTCAGTAAGGCA	1008
Db	1461	ATAAACTACCAGCTAGAACTGTAGAAACACAT-TGATATGAGTTTAAATGATAA---1514	
Qy	1009	GTGTATTTATACCTCGTARGCATTTATTTTTCATTAATCATTTTCATTTATCATTTGTA	1068
Db	1515	--TGCAATACATTTCCAAAACATTTTTTCCAGTTACATAAATTAAGTTATATCCTTTATA	1572
Qy	1069	ACACTTCTCAGTAATTATATAAAACATCATTTTAC-TTATGGTAATTAATAGCTTAGTATAAG	1127
Db	1573	AAACTCCTCAGTAATCATATAAGCTTCATCTCTTTTGGAAATTTTACTTAATATGTG	1632
Qy	1128	GTGGTTTCCCACTGGAAAAGACACAAAGTAAAAACCTCTTGGAGAGGGAACCTGTGTA	1187
Db	1633	GTGGTTTGTGCTCTAGAAA-----ACAACAAAAAACTCTTTTGAGAGGGAACCTCATGTA	1688
Qy	1188	AAOCCCAAAAAAAGTCTAACTTT-----1213	
Db	1689	AATACCACAAAAAAGCCTTAACTTTCTGGACCACAAATGTTTTTAATAATATTTTTTAA	1748
Qy	1214	-----1213	
Db	1749	TTGATGAATTTAAAAAGTATATATATTATTGTGTACAATATGATGTTTTGAAGTATGTAT	1808
Qy	1214	-----TTGGACCAAAATTTTATGCTTGTGTTTGTATGATATATATTTTTT	1256
Db	1809	ACATTGCAGAAATGGACAAATTTTAACTTGTCTGTGATTTATTGCA-TTTT	1867
Qy	1257	TAAAAATCTTCTCATTTAGCAACCACTGTGCATTTAAAGAAGTTTTTTCAGGTATAGACAC	1316

RESULT 4

RESOLUT 4		
AAA34856		
ID	AAA34858 standard; DNA; 4057 BP.	
XX		
XX		
AC		
AAA34858;		
XX		
XX		
DT		
XX		
XX		
DE	28-JUL-2000 (first entry)	
XX		
XX		
Human adenosine receptor related polynucleotide SEQ ID NO:2547.		
Human; adenosine receptor; low adenosine antisense oligonucleotide;		
phosphorothioate; impaired respiration; inflammation; allergy;		
KW allergic disease; bronchoconstriction; inhibitor; antiinflammatory;		
KW antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway;		
KW lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;		
KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;		
KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;		
KW cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.		

Homo sapiens.

WO200009525-A2

24-FEB-2000.

03-AUG-1999:

03-AUG-1998: 98US-0095212D

(ITVEC-) ITNTV EAST CABOT TNA

Nice, JW.

[illegible]

you can't see it.

vasoconstruction, in

cancers.

Disclosure; Page 717

The present invention

oligonucleotide (ON)
nucleic acids involv

New antisense oligonucleotides useful for treating e.g. pulmonary vasoconstriction, inflammation, allergies, asthma, hypertension, bronchitis, emphysema, respiratory distress syndrome, ischemia or cancers.

Disclosure; Page 717-718; 1343pp; English.

The present invention describes a new composition comprising an antisense oligonucleotide (ON) with low adenosine (up to 15%), which targets nucleic acids involved in bronchoconstriction, allergies, and/or

inflammation. The ON can have antiinflammatory, antiallergic, antiasthmatic, cytostatic and analgesic activities. The compositions are useful for the treatment of diseases associated with inflammation, impaired airways, including lung disease and diseases whose secondary effects afflict the lungs of a subject. They can be used for treating e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma, impeded respiration, respiratory distress syndrome, pain, cystic fibrosis, pulmonary hypertension, emphysema, chronic obstructive pulmonary disease (COPD), and cancers such as leukemias, lymphomas, carcinomas, and cancers which may metastasize to the lungs, including breast and prostate cancer. The reduction of the adenosine content of the ONs reduces side effects. The A-containing ONs break down with the release of deoxyadenosine which activates adenosine receptors causing bronchoconstriction and inflammation. AAA32313 to AAA35312 represent nucleotide sequences given in the sequence listing from the present invention, which correspond to SEQ ID NO:1 to 2815, and then the last 185 sequences are also called SEQ ID NO:1 to 185, but the sequences differ from the previously named sequences. SEQ ID NO:11 to 1680 (AAA32323 to AAA3392) are specifically claimed ONs from the present invention. N.B. Sequences given in the disclosure of the present invention do not match up with their corresponding SEQ ID NO: sequences given in the sequence listing

Sequence 4057 BP; 1303 A; 683 C; 796 G; 1275 T; 0 U; 0 Other;

Query Match 38.3%; Score 634.6; DB 3; Length 4057;
Best Local Similarity 68.6%; Pred. No. 1e-115;
Matches 1226; Conservative 0; Mismatches 374; Indels 187; Gaps 18;

1 AGGCAAACTGAACTTCAGAGCTATGAGATGCTTCGAAATTGAGTTGCTAGCTC 60
226 AGGCAAACTGAACTTCAGAGCTATGAGATGCTTCGAAATTGAGTTGCTAGCTC 120
352 AGGCAAACTGAACTTCAGAGCTATGAGATGCTTCGAAATTGAGTTGCTAGCTC 180
478 AGGCAAACTGAACTTCAGAGCTATGAGATGCTTCGAAATTGAGTTGCTAGCTC 240
604 AGGCAAACTGAACTTCAGAGCTATGAGATGCTTCGAAATTGAGTTGCTAGCTC 300
730 AGGCAAACTGAACTTCAGAGCTATGAGATGCTTCGAAATTGAGTTGCTAGCTC 360
856 AGGCAAACTGAACTTCAGAGCTATGAGATGCTTCGAAATTGAGTTGCTAGCTC 420
982 AGGCAAACTGAACTTCAGAGCTATGAGATGCTTCGAAATTGAGTTGCTAGCTC 480
1108 AGGCAAACTGAACTTCAGAGCTATGAGATGCTTCGAAATTGAGTTGCTAGCTC 540
1234 AGGCAAACTGAACTTCAGAGCTATGAGATGCTTCGAAATTGAGTTGCTAGCTC 600
1360 AGGCAAACTGAACTTCAGAGCTATGAGATGCTTCGAAATTGAGTTGCTAGCTC 660
1486 AGGCAAACTGAACTTCAGAGCTATGAGATGCTTCGAAATTGAGTTGCTAGCTC 720
1612 AGGCAAACTGAACTTCAGAGCTATGAGATGCTTCGAAATTGAGTTGCTAGCTC 780
1738 AGGCAAACTGAACTTCAGAGCTATGAGATGCTTCGAAATTGAGTTGCTAGCTC 840
1864 AGGCAAACTGAACTTCAGAGCTATGAGATGCTTCGAAATTGAGTTGCTAGCTC 900
1990 AGGCAAACTGAACTTCAGAGCTATGAGATGCTTCGAAATTGAGTTGCTAGCTC 960
2116 AGGCAAACTGAACTTCAGAGCTATGAGATGCTTCGAAATTGAGTTGCTAGCTC 1020
2242 AGGCAAACTGAACTTCAGAGCTATGAGATGCTTCGAAATTGAGTTGCTAGCTC 1080
2368 AGGCAAACTGAACTTCAGAGCTATGAGATGCTTCGAAATTGAGTTGCTAGCTC 1140
2494 AGGCAAACTGAACTTCAGAGCTATGAGATGCTTCGAAATTGAGTTGCTAGCTC 1200
2620 AGGCAAACTGAACTTCAGAGCTATGAGATGCTTCGAAATTGAGTTGCTAGCTC 1260
2746 AGGCAAACTGAACTTCAGAGCTATGAGATGCTTCGAAATTGAGTTGCTAGCTC 1320
2872 AGGCAAACTGAACTTCAGAGCTATGAGATGCTTCGAAATTGAGTTGCTAGCTC 1380
3000 AGGCAAACTGAACTTCAGAGCTATGAGATGCTTCGAAATTGAGTTGCTAGCTC 1440
3126 AGGCAAACTGAACTTCAGAGCTATGAGATGCTTCGAAATTGAGTTGCTAGCTC 1500
3252 AGGCAAACTGAACTTCAGAGCTATGAGATGCTTCGAAATTGAGTTGCTAGCTC 1560
3378 AGGCAAACTGAACTTCAGAGCTATGAGATGCTTCGAAATTGAGTTGCTAGCTC 1620
3504 AGGCAAACTGAACTTCAGAGCTATGAGATGCTTCGAAATTGAGTTGCTAGCTC 1680
3630 AGGCAAACTGAACTTCAGAGCTATGAGATGCTTCGAAATTGAGTTGCTAGCTC 1740
3756 AGGCAAACTGAACTTCAGAGCTATGAGATGCTTCGAAATTGAGTTGCTAGCTC 1800
3882 AGGCAAACTGAACTTCAGAGCTATGAGATGCTTCGAAATTGAGTTGCTAGCTC 1860
4008 AGGCAAACTGAACTTCAGAGCTATGAGATGCTTCGAAATTGAGTTGCTAGCTC 1920
4134 AGGCAAACTGAACTTCAGAGCTATGAGATGCTTCGAAATTGAGTTGCTAGCTC 1980
4260 AGGCAAACTGAACTTCAGAGCTATGAGATGCTTCGAAATTGAGTTGCTAGCTC 2040
4386 AGGCAAACTGAACTTCAGAGCTATGAGATGCTTCGAAATTGAGTTGCTAGCTC 2100
4512 AGGCAAACTGAACTTCAGAGCTATGAGATGCTTCGAAATTGAGTTGCTAGCTC 2160
4638 AGGCAAACTGAACTTCAGAGCTATGAGATGCTTCGAAATTGAGTTGCTAGCTC 2220
4764 AGGCAAACTGAACTTCAGAGCTATGAGATGCTTCGAAATTGAGTTGCTAGCTC 2280
4890 AGGCAAACTGAACTTCAGAGCTATGAGATGCTTCGAAATTGAGTTGCTAGCTC 2340
4990 AGGCAAACTGAACTTCAGAGCTATGAGATGCTTCGAAATTGAGTTGCTAGCTC 2400
5090 AGGCAAACTGAACTTCAGAGCTATGAGATGCTTCGAAATTGAGTTGCTAGCTC 2460
5190 AGGCAAACTGAACTTCAGAGCTATGAGATGCTTCGAAATTGAGTTGCTAGCTC 2520
5290 AGGCAAACTGAACTTCAGAGCTATGAGATGCTTCGAAATTGAGTTGCTAGCTC 2580
5390 AGGCAAACTGAACTTCAGAGCTATGAGATGCTTCGAAATTGAGTTGCTAGCTC 2640
5490 AGGCAAACTGAACTTCAGAGCTATGAGATGCTTCGAAATTGAGTTGCTAGCTC 2700
5590 AGGCAAACTGAACTTCAGAGCTATGAGATGCTTCGAAATTGAGTTGCTAGCTC 2760
5690 AGGCAAACTGAACTTCAGAGCTATGAGATGCTTCGAAATTGAGTTGCTAGCTC 2820
5790 AGGCAAACTGAACTTCAGAGCTATGAGATGCTTCGAAATTGAGTTGCTAGCTC 2880
5890 AGGCAAACTGAACTTCAGAGCTATGAGATGCTTCGAAATTGAGTTGCTAGCTC 2940
5990 AGGCAAACTGAACTTCAGAGCTATGAGATGCTTCGAAATTGAGTTGCTAGCTC 3000
6090 AGGCAAACTGAACTTCAGAGCTATGAGATGCTTCGAAATTGAGTTGCTAGCTC 3060
6190 AGGCAAACTGAACTTCAGAGCTATGAGATGCTTCGAAATTGAGTTGCTAGCTC 3120
6290 AGGCAAACTGAACTTCAGAGCTATGAGATGCTTCGAAATTGAGTTGCTAGCTC 3180
6390 AGGCAAACTGAACTTCAGAGCTATGAGATGCTTCGAAATTGAGTTGCTAGCTC 3240
6490 AGGCAAACTGAACTTCAGAGCTATGAGATGCTTCGAAATTGAGTTGCTAGCTC 3300
6590 AGGCAAACTGAACTTCAGAGCTATGAGATGCTTCGAAATTGAGTTGCTAGCTC 3360
6690 AGGCAAACTGAACTTCAGAGCTATGAGATGCTTCGAAATTGAGTTGCTAGCTC 3420
6790 AGGCAAACTGAACTTCAGAGCTATGAGATGCTTCGAAATTGAGTTGCTAGCTC 3480
6890 AGGCAAACTGAACTTCAGAGCTATGAGATGCTTCGAAATTGAGTTGCTAGCTC 3540
6990 AGGCAAACTGAACTTCAGAGCTATGAGATGCTTCGAAATTGAGTTGCTAGCTC 3600
7090 AGGCAAACTGAACTTCAGAGCTATGAGATGCTTCGAAATTGAGTTGCTAGCTC 3660
7190 AGGCAAACTGAACTTCAGAGCTATGAGATGCTTCGAAATTGAGTTGCTAGCTC 3720
7290 AGGCAAACTGAACTTCAGAGCTATGAGATGCTTCGAAATTGAGTTGCTAGCTC 3780
7390 AGGCAAACTGAACTTCAGAGCTATGAGATGCTTCGAAATTGAGTTGCTAGCTC 3840
7490 AGGCAAACTGAACTTCAGAGCTATGAGATGCTTCGAAATTGAGTTGCTAGCTC 3900
7590 AGGCAAACTGAACTTCAGAGCTATGAGATGCTTCGAAATTGAGTTGCTAGCTC 3960
7690 AGGCAAACTGAACTTCAGAGCTATGAGATGCTTCGAAATTGAGTTGCTAGCTC 4020
7790 AGGCAAACTGAACTTCAGAGCTATGAGATGCTTCGAAATTGAGTTGCTAGCTC 4080
7890 AGGCAAACTGAACTTCAGAGCTATGAGATGCTTCGAAATTGAGTTGCTAGCTC 4140
7990 AGGCAAACTGAACTTCAGAGCTATGAGATGCTTCGAAATTGAGTTGCTAGCTC 4200
8090 AGGCAAACTGAACTTCAGAGCTATGAGATGCTTCGAAATTGAGTTGCTAGCTC 4260
8190 AGGCAAACTGAACTTCAGAGCTATGAGATGCTTCGAAATTGAGTTGCTAGCTC 4320
8290 AGGCAAACTGAACTTCAGAGCTATGAGATGCTTCGAAATTGAGTTGCTAGCTC 4380
8390 AGGCAAACTGAACTTCAGAGCTATGAGATGCTTCGAAATTGAGTTGCTAGCTC 4440
8490 AGGCAAACTGAACTTCAGAGCTATGAGATGCTTCGAAATTGAGTTGCTAGCTC 4500
8590 AGGCAAACTGAACTTCAGAGCTATGAGATGCTTCGAAATTGAGTTGCTAGCTC 4560
8690 AGGCAAACTGAACTTCAGAGCTATGAGATGCTTCGAAATTGAGTTGCTAGCTC 4620
8790 AGGCAAACTGAACTTCAGAGCTATGAGATGCTTCGAAATTGAGTTGCTAGCTC 4680
8890 AGGCAAACTGAACTTCAGAGCTATGAGATGCTTCGAAATTGAGTTGCTAGCTC 4740
8990 AGGCAAACTGAACTTCAGAGCTATGAGATGCTTCGAAATTGAGTTGCTAGCTC 4800
9090 AGGCAAACTGAACTTCAGAGCTATGAGATGCTTCGAAATTGAGTTGCTAGCTC 4860
9190 AGGCAAACTGAACTTCAGAGCTATGAGATGCTTCGAAATTGAGTTGCTAGCTC 4920
9290 AGGCAAACTGAACTTCAGAGCTATGAGATGCTTCGAAATTGAGTTGCTAGCTC 4980
9390 AGGCAAACTGAACTTCAGAGCTATGAGATGCTTCGAAATTGAGTTGCTAGCTC 5040
9490 AGGCAAACTGAACTTCAGAGCTATGAGATGCTTCGAAATTGAGTTGCTAGCTC 5100
9590 AGGCAAACTGAACTTCAGAGCTATGAGATGCTTCGAAATTGAGTTGCTAGCTC 5160
9690 AGGCAAACTGAACTTCAGAGCTATGAGATGCTTCGAAATTGAGTTGCTAGCTC 5220
9790 AGGCAAACTGAACTTCAGAGCTATGAGATGCTTCGAAATTGAGTTGCTAGCTC 5280
9890 AGGCAAACTGAACTTCAGAGCTATGAGATGCTTCGAAATTGAGTTGCTAGCTC

Db 2209 TAGAAACTTGAGACTAAACTGGTTGTTGCAGCCAAAGATTTTGGAG 2255

RESULT 5

AAF20980
ID AAF20980 standard; DNA; 4057 BP.

XX
AC AAF20980:

XX
DT 14-MAR-2001 (first entry)

XX
DE Human low adenosine antisense oligonucleotide related sequence #2547.

Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
human; airway disorder; bronchoconstriction; lung inflammation;
surfactant depletion; respiratory; bronchodilator; antiinflammatory;
immunosuppressive; anasthmatic; analgesic; hypotensive; cytostatic;
respiratory obstruction; pulmonary obstruction; impeded respiration;
surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
pulmonary hypertension; emphysema; pulmonary transplantation rejection;
chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
cancer; ss.

XX
OS Homo sapiens.XX
PN WO200062736-A2.

XX
PD 26-OCT-2000.

XX
PF 24-MAR-2000; 2000WO-US008020.

XX
PR 06-APR-1999; 99US-0127958P.

XX
PA (UYEC-) UNIV EAST CAROLINA.

PA (NYCE/) NYCE J W.

XX
PI Nyce JW;

XX
DR WPI; 2000-679539/66.

XX Low adenosine (A) content antisense oligonucleotides which do not trigger
PT adenosine receptors during metabolism, useful e.g. for treating cancers
PT and respiratory obstructions.

PS Disclosure; Page 788-789; 1592pp; English; XX

The present invention describes low adenosine (A) content antisense oligonucleotides and compositions (i) comprising them. In the antisense oligonucleotides the A is replaced by a 'Universal', or alternative base. (i) can have respiratory, bronchodilator, antiinflammatory, analgesic, immunosuppressive, antihistaminic, hypotensive and cytostatic activities. The antisense oligonucleotides and (i) can be used to down-regulate the expression and/or activity of target polypeptides associated with the lung/respiratory disorders and malignancies, such as stimulating and activating peptide factors and transmitters, transcription factors, immunoglobulins and antibodies, antibody receptors, cytokines and chemokines, endogenously produced specific and non-specific enzymes, binding proteins, adhesion molecules and their receptors, cytokine and chemokine receptors, adenosine receptors, bradykinin receptors, central nervous system (CNS) and peripheral nervous and non-nervous system receptors, CNS and peripheral nervous and non-nervous system peptide transmitters, defensins, growth factors, vasoactive peptides and receptors, binding proteins and malignancy associated proteins. The antisense oligonucleotides may be used in this way to treat disorders including respiratory obstruction (especially pulmonary obstruction and/or bronchoconstriction) and/or lung inflammation, allergy(ies) and/or surfactant hypo-production which are associated with a disease or condition selected from pulmonary vasoconstriction, inflammation, allergies, asthma, impeded respiration, respiratory distress syndrome (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary hypertension, emphysema, chronic obstructive pulmonary disease (COPD).

QY 1188 AACCCACAAAACAAAGTCTAAGTTT----- 1213
Db 5208 AATACCACAAAACAAAGCCTAACTTTGTGACCAAAATGTTTAAATAATTTTAA 5267
QY 1214 ----- 1213
Db 5268 TTGATGAATTAAAAAGTATATATATTATGTGTACAATATGATGTTTGAAGTATAT 5327
QY 1214 -----TTGACCAAAATTTTATGCTTGTGTTGATGAATATATATTTT 1256
Db 5328 ACATTCAGAAATGCAAAATGCAAAATTTTATACCTTGTCTGTATTTTGA-TTTT 5386
QY 1257 TAAATCTTCTCATTTAGCAACCACTGTGCATTAAGAAAGTTTTCAGGGTATAGACAC 1316
Db 5387 AAAAAATTTCTCATTTAGCAACCACTGTGCATTAAGAAATTTTTCAGGGTATAGACAC 5446
QY 1317 ATTGAAGAACCAAACTGCCACCGGGAGGCTGTGGATAAACTATTCAAAACCTTTCCTT 1376
Db 5447 ACTGGAGAGTCAAACTGTGCAAGGGGTACTGTGGAAGAGTATTCAAAACCTTTCCTT 5506
QY 1377 AATAAAGACACATAGAGCGCCAAAAGTAAGTTAAAGACATTTGGCAAACTTAAGT 1436
Db 5507 AATAAAGAAATACATTTAGCGCCAAAAGTAAGTTAAAGACATTTTCACACATTT-----CAATGGAAGT 5561
QY 1437 ATATTGCTGACTGCTGCTGTTTCTTTTCTTTTACAAAGAAATTCACAGTTTTCCTA 1496
Db 5562 ATATTGCTGCTGCTGCTATTTCTAT-----CGAATTGACAGTTTCTCT 5607
QY 1497 CAATATCT-----CCTCTGTTCTTTTAAAGAAAAGGTGTGACGAGAAAGTATAGAG 1550
Db 5608 TAATACCTATTTGCTATTTCTTTTTCACAGAAAAGTGTGAGAAAGACGAGAG 5667
QY 1551 TGCAAAAGTTCCTAGACTACCTGCAAGTATTTCTTGTGTAAATAACACCGAGTGACAC 1610
Db 5668 TAAACCAATTCCTAGACTACCTGCAAGTATTTCTTGTGTAAATAACACCGAGTGATTA 5727
QY 1611 CGGAAAGTTGAGAACAAACCGCTTATTTGATGGAAGATTTGGAG 1657
Db 5728 TAGAAAGTTGAGACTAACTGGTTGTTGTCAGCAAAAGATTTGGAG 5774

RESULT 8
ID AN81381
AC AN81381;
XX 25-MAR-2003 (revised)
DT 04-DEC-1990 (first entry)
XX DE Entire nucleotide sequence of the human B-cell differentiation factor
XX DE chromosomal gene (3.2kb BamHI fragment).
XX KW Immunodeficiency disease; cancer therapy; interleukin; lymphocyte; ss.
XX OS Homo sapiens.
XX FH Key
XX FT exon
FT /tag= a
FT /note= "Exon 1"
FT 905..937
FT /tag= b
FT /note= "Exon 2"
FT 1883..2011
FT /tag= c
FT /note= "Exon 3"
FT 2118..2216
FT /tag= d
FT /note= "Exon 4"
XX PN EP261625-A.

XX 30-MAR-1988.
PD
XX 21-SEP-1987; 87EP-00113774.
XX
XX 20-SEP-1986; 86JP-00223284.
PR 21-SEP-1987; 87JP-00236842.
XX (HONJ/) HONJO T.
XX Honjo T, Takatu K, Severinsson B;
PI
XX WPI; 1988-085927/13.
XX P-PSDB; AAP81056.
XX Recombinant human B-cell differentiation factor - used for diagnosis or
PT treatment of immuno-deficiency diseases, various infections and cancers.
FI Example; Fig 5(1)-5(4); 5pp; English.
XX Nucleotide sequence of the exon portions of the human BCF chromosomal
CC gene completely coincided with the nucleotide sequence of human BCF cDNA
CC (AAN81380). The BCF is useful in the diagnosis or treatment of e.g.
CC immunodeficiency diseases occurring due to the deficiency of this factor
CC in a living body and also in the treatment of various infections and
CC cancers. (Updated on 25-MAR-2003 to correct PR field.)
XX
SQ Sequence 3230 BP; 1027 A; 545 C; 622 G; 1036 T; 0 U; 0 Other;
Query Match 36.2%; Score 600.6; DB 1; Length 3230;
Best Local Similarity 67.8%; Pred. No. 5.1e-109; Indels 191; Gaps 19;
Matches 1212; Conservative 0; Mismatches 384;
QY 1 AGGCAAAACACATGAGAGCTATGAGAGCTATGAGAGCTTCTGAATGAGTTGCTAGTCTC 60
Db 527 AGGCAAAACGAGAACGTTTTCAGAGCCATGAGAGCTTCTGCAATGAGTTGCTAGTCTC 586
QY 61 TTGGGGCTGCTATGTTTCTGCTTTGCTAGAAAATCCCATGATAGACTGGTGGCAG 120
Db 587 TTGGAGCTGCTATGCTGATGCTATCCCAAGCAAAATCCCAAGTGCATGTTGGAAG 646
QY 121 AGACCTTGACACTGCTCTCCACTCATCGAACTTGCTGATAGGGATCGGGTAAATTTCT 180
Db 647 AGACCTTGACACTGCTCTCTACTCATCGAACTTGCTGATAGCCAAATGAGTAAATTTCT 706
QY 181 TTTGATTCCTACAGTCTTTAAATGCAATGCGGTAAATGCTGGTGGTGGTCTAGTT----- 234
Db 707 TTTGATTCCTACAGTCTTTAAATGCAATGCGGTAAATGCTGGTGGTGGTCTAGTT 766
QY 235 TTTAAAGTCCATTAATCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAAT 293
Db 767 ATATAGAGTCTGTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 825
QY 294 ATGTTACTCAGAAAGTATATATAAAGTTATGAACCTTACAACTACATACATTAATAATGAATG 353
Db 826 ACATCACCAGCAACATTTCTGTTAAAGTTATGAATGCTGGTGGTGGTGGTGGTGGTGGTGG 885
QY 354 TTGTTTCTTTCTTTTTCAGAACCTGATGATTCCTACTCTCCTGAAATTAATAATGAATGTT 413
Db 886 TATTCTCTCTCTCTCCAGACTCTGAGAGTCTGAGAGTCTGAGAGTCTGAGAGTCTGAGAGT 944
QY 414 AAATTAATGATTTGATAAAATGATTAATCAATCAATCAG-----TTTCATATTTTAACTATAAA 469
Db 945 AAATTAATGATTTGATAAAATGATTAATCAATCAATCAATCAATCAATCAATCAATCAATCA 1004
QY 470 GTATCAGTTAACTGGGATGATTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTT 529
Db 1005 TCATTAGTTATCATTTGGAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTT 1064
QY 530 AAAT-TATGCTGCTATGATTAATTAAGAAAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 588
Db 1065 GAATGCTGCTATTAATTAATTAAGAAAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1109

QY 589 GAATCCATTAAGCAAGTGGATCAGGCCCTTTTGTGATGTTGTCAGTCTCCATCTCAAAG 648
DB 1110 GAATCCCTTAAACAAGTGGATAGGCTCTTTGGTGAATGTTGTTAGTTTGGCTTCCCAAAG 1169
QY 649 AGCTCGTGTGAGGATCTTTTCCAAAAGAAATCCATATTGGGTGAGAGATCTTCTAG 708
DB 1170 AGCATCGTGTGAGG-ATCTTTCCAGAAAGGATCCACATGAGTGAGAGTGGTGTCTAG 1228
QY 709 GCTCCATTCACCTCTGCTGTGGCTTTCTCCACCTCAACGTTTCTGAAAGTACTAGCA 768
DB 1229 TCTCCGTGCGATCTGAC-----TCTTCTCACCTCAACGTTTCTGAAAGTATTAGCA 1283
QY 769 ACTTGGGGTTATATTTTAGAATTTATGTCAGTAGACATGAAATATACAGTGAAGTCT 828
DB 1284 ACTCAGAATTATATTTTAGAACCATGATCAGTAGACATTAATAATATATAACAATGCC- 1342
QY 829 ATATTAATAGTCACCTCCACATTTTAAATGAATTTTAACTCTAATGGAATCATATACAT 888
DB 1343 --CTATATTAATAATCTGCATACCTTAAATAATATGACATATATGATGTTGTGTGAT 1400
QY 889 CTGGAGTATGTCATGTCATATAAATGTTAAATGTGATATCATTTAGTCTAAATAGA 948
DB 1401 TGAATAG--CTGTGTCATATTAATGTAATGTAATATATAGTTT-ATTAGTCTAAATAGA 1456
QY 949 ATAAATTTACAGCTAGACATATACAGGAAATTTCTGAGTGAGGTAATCAGTAAGGCA 1008
DB 1457 ATAAATCTACAGCTAGACATATACAGGAAATTTCTGAGTGAGGTAATCAGTAAGGCA 1008
QY 1009 GTTGTATTTATACCTCGTAAGCATTTTTCATTAATCATTTTCAATTTATCATCATTTGA 1068
DB 1514 ----ATTACACTTCCAAACATTTTTCAGTTTCAATTAATGTTATATCTTTTATA 1568
QY 1069 ACATTTCTAGTAAATATAAATCATATTTAC--TTATGGTAATTTATAGCTTAGTATAAG 1127
DB 1569 AAATCTCTAGTAAATATAAATCATATGCTTCTATCTTTTGAATTTTATCTTAATATG 1628
QY 1128 GTGGTTTCCACCTGGAAGACACAGTAAGAACTTTTGGAGAGGAACTTGTGTA 1187
DB 1629 GTGGTTTGTGCTTGAAGAA-----ACAAACAAACAACTTTTGGAGAGGAACTGTGTA 1684
QY 1188 AACCCCAACAAACAACTTAACTTTT----- 1214
DB 1685 AATACCAACAAACAACTTAACTTTTGTGGACCAAAATTTTAAATATTTTAA 1744
QY 1215 ----- 1214
DB 1745 TTGATGAATTAAGATPATATATATTTATGTTGACAAATGATGTTTGAAGTATGAT 1804
QY 1215 -----TGGACCAATTTTATGCTTGTGTTGATGATTAATTTT 1256
DB 1805 ACATTCAGAAATGACAAATGACAAATTTTATACCTTGTCTTGAATTTTGA-TTTT 1863
QY 1257 TAAATCTTCTATTTAGCAACCACTGTGATTAAGAAAGTTTTCAGGGTATAGACAC 1316
DB 1864 AAAAAATTTCTCATTTAGCAACCACTGTGATTAAGAAAGTTTTCAGGGTATAGACAC 1923
QY 1317 ATTGAAGAACCAAACTGCCACGGGAGGCTGTGGATAAATTTTCCAAACTTGTCTTT 1376
DB 1924 ACTGGAGAGTCAAACTGTGCAAGGGGTACTGTGGAAAGACTTATCAAAACTTGTCTTT 1983
QY 1377 AATAAAGAACACATAGAGCGCAAAAGTAAGTTAAAGACATTTGGCAAAACTTAAGT 1436
DB 1984 AATAAAGAACATATTGACGGCCAAAGTAAGTTTACACACATTCATCAAGTATATTT 2043
QY 1437 ATATTGTCTGACTCTGCTGTTTTTTTTTTTTTTTTTTTACAGAAATTCAGAGTTCTCTA 1496
DB 2044 TGTCTGGCTG-----TGCCTATTTCTATGGAATTCAGAGTTTCTCTG 2085
QY 1497 CAATATCT-----CCTCTGTTCTTTTAAACAGAAAGGTGTGAGAGAAAGATGGAGAG 1550
DB 2086 TAATACCTATTGTTCATTTTCTTTTTCACAGAAAGGTGTGAGAGAAAGATGGAGAG 2145
QY 1551 TGACAAAGTCTAGACTACCTGCAAGTATTTCTTGGTGTATTAACACCCGAGTGGACAC 1610

DB 2146 TAAACCAATTCCTAGACTACCTGCAAGAGTTTCTTGGTGTAAATGAACACCGAGTGGATAA 2205
QY 1611 CGAAAGTTGAGAACAAACCGGCTTTATTGTAGTGAAGATTTTGGAG 1657
DB 2206 TAGAAAGTTGAGACTAAACTGTTTGTTCAGCCAAAGATTTTGGAG 2252
RESULT 9
AAQ74056
ID AAQ74056 standard; DNA; 3230 BP.
XX AAQ74056;
XX AC AAQ74056;
XX DT 29-JAN-1996 (first entry)
XX Human interleukin-5.
XX Interleukin-5; primer; mRNA; specificity; pharmaceutical; ss.
XX OS Homo sapiens.
XX PN JP07123984-A.
XX PD 16-MAY-1995.
XX PF 05-NOV-1993; 93JP-00275852.
XX PR 05-NOV-1993; 93JP-00275852.
XX PA (HITB) HITACHI CHEM CO LTD.
XX WPI; 1995-211627/28.
XX A primer for the detection and the determin. of a specific messenger RNA -
XX can detect and determine specific mRNA(s) with high reliability.
XX Example 22; Page 22-24; 35pp; Japanese.
XX AAQ74056 is the human interleukin-5 gene. This gene is amplified by the
XX primers AAQ74031-Q74032. The primers are used specifically for the
XX detection and isolation of this sequence. They have the advantage of high
XX sensitivity and reliability and are useful in the pharmaceutical industry
XX
SQ Sequence 3230 BP; 1027 A; 545 C; 622 G; 1036 T; 0 U; 0 Other;
Query Match 36.2%; Score 600.6; DB 2; Length 3230;
Best Local Similarity 67.8%; Pred. No. 5.1e-109;
Matches 1212; Conservative 0; Mismatches 384; Indels 191; Gaps 19;
QY 1 AGGCAACACCTGACATTTGAGAGCTATGAGATGCTTCTGAATTTGAGTTTCTAGCTC 60
DB 527 AGGCAACACCTGACATTTGAGAGCTATGAGATGCTTCTGAATTTGAGTTTCTAGCTC 586
QY 61 TTGGGCTGCTATGTTTCTGCTTGTAGAAATCCCATGAAATAGACTGTTGGCAG 120
DB 587 TTGAGCTGCTAGCTGATGCTATCCCAAGAAATCCCAAGTGCATTTGTTGAAG 646
QY 121 AGACTTGAACATGCTCTCCACTCATGAACTTGGCTGATAGCGGATGGGGTAAATTTCT 180
DB 647 AGACTTGGCACTGCTTCTACTCATCGAACTCTGCTGATAGCCAAATGAGGTAAATTTCT 706
QY 181 TTTTGTCTCTACAGTCTTTTAAATGATGAGTAAATTTGGTGGTGGCTGAGTT----- 234
DB 707 TTATGATCTTACAGTCTGTAAGTGCATAGGTAATCAITTTGATGTTTCTTTACTAT 766
QY 235 -TTTAAAGATCCATTAATCAATGAATGAATGAGTGTAAATATAATATAATGGTAAAC 293
DB 767 ATATAGAGATCTGTTATAAATAAATGAATTTCTGAG-CACATTAATGATGGGTGATAACT 825
QY 294 ATGTTACTCAGAGAAATTAATTAAGATTAATGAATTAATTAATTAATTAATTAATG 353
DB 826 ACATCACCAGCAACATCTCTGTTAAAGTTATGAATGCTGTTGTTGTTAAATTAATG 885

QY 354 TTGTTTCCTTCTTTTTCAGAACCTGATGATTCCTPACTCCTGAAATAAATAAATGTAAGTT 413
Db -TAITTCCTTCTCTCCTCAGACTCTGAGGATTCCTGTTCTCTGTACATAAATAATGTAAGTT 944
QY 414 AAATTAATGATTGATAAATAATGATTAATCATGATCAG- - - - -TTTCATATTTTAAGCTATAAA 469
Db AAATTAATGATTGATAAATAATGATTAATCATGATTAATCATGATTAATCATGATTAATCATGATTA 1004
QY 470 GTATCAGTTAATCATGAGGATGATTAATTTATCTATTTTCTATTTTCTATTTTCTATTTTCTATTTT 529
Db TCATTAAGTTATCATTTGGAATCATTTAAATTTCTATTTTCTATTTTCTATTTTCTATTTTCTATTTT 1064
QY 530 AAAT-TATGTCCTTATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATG 588
Db GAATGCTCTGATTAATTAATTAATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATG 1109
QY 589 GAATCCATTAAGCAAGTGGATCAGGCCCTTTTTCATGTTTGTCTGATTTTCTCATCTCAAAAG 648
Db GAATCCCTTTAAACAAGTGGATTAAGTCTTTTGGTGAATTTTCTGATTTTCTGATTTTCTGATTTT 1110
QY 649 AGCTCTGTCAGGCAATCTTTCCAAAGAAATTCATATTTGGGTGAGATTAATTTCTCTAG 708
Db AGCATCGTGTGAGG-ATTCTTTCCAGAGAGGATTCACACTGAGTGAGAGGTGCGTGTAG 1170
QY 709 GCTCATTCACCTCTGCTGTTGGCTTTCTCCTCACTCAACGTTTCTTCTGAAAGTACTAGCA 768
Db TCTCGGTGAGTTCTGAC- - - - -TCTTCTCCTCTACGTTTCTTCTGAAAGTACTAGCA 1229
QY 769 ACTTGGGGTTATTTTATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATG 828
Db ACTCAGAAATTAATTTTATGAAACCATGATCAGTAGACATTAATTAATTAATTAATTAATTAATTAAT 1284
QY 829 ATATTATAGTCACTTCCACATATTTAAATGATTTTAACTCTAATGGAATCATATACAT 888
Db --CTATTAATTAATTTCTGCAATCTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1343
QY 889 CTGAGTATGTCATGTCATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 948
Db TGAATATG- - - - -CCTGGTCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1401
QY 949 ATAAATTAACAGTACATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1008
Db ATAAATTAACAGTACATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1457
QY 1009 GTTGTATTAATACCTCTGAAGCAATTTTATTTTCAATTAATTAATTAATTAATTAATTAATTAAT 1068
Db -1514 - - - - -ATTACACTTCCAAACATTTTTCAGTTACATTAATTAATTAATTAATTAATTAAT 1513
QY 1069 ACATCTCTCAGTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1127
Db AAATCTCTCAGTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1569
QY 1128 GTGGTTTCCACCTGGAAAGACACAAGTAAACCTCTTGGGAGAGGGAACCTTGTA 1187
Db GTGGTTTGGTCCCTAGAAA- - - - -ACAAACAAATAAATCTTTGGAGAGGGAACCTTGTA 1628
QY 1188 AACCCCAAAACAAAGTCTAACTTTT- - - - -1214
Db AATACCAAAACAAAGCTAACTTTTGTGGACCAAAATTTGTTTAAATTAATTTTAA 1744
QY 1215 - - - - -1214
Db TTGATGAATTAATAAGTATATATTAATTTATGTTGATCAATTAATTAATTAATTAATTAATTAAT 1745
QY 1215 - - - - -TGGACCAAAATTTTATGCTCTGTTTATGATGAATTAATTTT 1256
Db ACATTGAGAAATGACAAATGACCAATTTTATACCTCTCTGATTAATTTTGA- - - - -1256
QY 1257 TAAATCTTCTCTATTTAGCACCAACTGTGCAATTAAGAAATTTTTCAGGATTAATGACAC 1316
Db AAAAAATTTCTCTATTTAGCACCAACTGTGCAATTAAGAAATTTTTCAGGAAATAGGCAC 1864

QY 1317 ATTGAAGAACCAAACTGCCACCGGGAGGCTGTGGATAAACTATTCCAAAACCTTGTCTTTT 1376
Db ACTGGAGAGTCAAACTGTGCAAGGGGTACTGTGGAAAGACTATTTCAAAACCTTGTCTTT 1983
QY 1377 ATAAAAGACACATAGAGCGGCCCAAAAGTAAGTTAAAGACATTTGGCAAAAACCTTAAGT 1436
Db ATAAAAGAAATACATTTGACCGGCCAAAAGTAAGTTTACACACATTTCAATGGAAGCTATATT 2043
QY 1437 ATATTTGTCTGACTCTGCTGTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTT 1496
Db TGCTCTGGCTG- - - - -TGCTTATTTCTATGGAATTCACAGTTTCTCTG 2085
QY 1497 CAATATCT- - - - -CCTCTGTTCTTTTAAACAGAAAGGTGTGAGAGAAAGATGGAGAG 1550
Db TAATACCTATTGTCAATTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTT 2086
QY 1551 TGCAAAAGTTCCTAGACTACCTGCAAGTATTTCTTGGTCTAATAAACACCGAGTGGACAC 1610
Db TAAACCAATTCCTAGACTACCTGCAAGTATTTCTTGGTCTAATAAACACCGAGTGGATAA 2205
QY 1611 CGAAAGTTGAGAAACAAACCGGCTTATTGTAGTGGAAAGATTTTGGAG 1657
Db TAGAAAGTTGAGACTAAACTGTTTGTTCAGCCAAAGATTTTGGAG 2252

RESULT 10

AAC73725
ID AAC73725 standard; DNA; 3230 BP.
XX AAC73725;
XX AC AC
XX XX
DT 02-FEB-2001 (first entry)
XX Human IL-5 nucleotide sequence.
DE Human; interleukin-5; IL-5; signal transduction.
XX Human; interleukin-5; IL-5; signal transduction.
KW antisense oligonucleotide; antiasthmatic; immunosuppressive; cytostatic;
KW IL-5 receptor-alpha; asthma; eosinophilic syndrome; infection;
KW inflammation; cancer; ds.
XX Homo sapiens.
XX WO200058512-A1.
XX 05-OCT-2000.
XX 17-MAR-2000; 2000WO-US007318.
XX 26-MAR-1999; 99US-00280799.
XX (ISIS-) ISIS PHARM INC.
XX Dean NM, Karras JG, McKay R;
XX WPI; 2000-594648/56.
XX Antisense oligonucleotide compound used to treat asthma and eosinophilic
XX syndrome in humans modulates interleukin-5 signal transduction.
XX Example 22; Page 127-128; 156pp; English.
XX The present sequence was used to design oligonucleotides for antisense
XX modulation of interleukin-5 (IL-5) signal transduction. Oligonucleotides
XX were designed to target nucleic acids encoding IL-5 and IL-5 receptor-
XX alpha. The antisense oligonucleotides may be used for the treatment of
XX diseases associated with IL-5 signal transduction, IL-5 expression or IL-
XX 5 receptor-alpha expression. Such diseases include asthma and
XX eosinophilic syndrome. The oligonucleotides are also useful for research
XX uses and to prevent or delay infection, inflammation or tumour formation
SQ Sequence 3230 BP; 1027 A; 545 C; 622 G; 1036 T; 0 U; 0 Other;

Query Match 36.2%; Score 600.6; DB 3; Length 3230;

Best Local Similarity 67.8%; Pred. No. 5.1e-109;		
Matches 1212; Conservative 0; Mismatches 384; Indels 191; Gaps 19;		
QY 1 AGGCAACACATGAACTTTTCAGAGCTATGAGATGCTTCGAAATTTGAGTTGCTAGCTC 60	Db 1514 -----ATTACACTTCCAAAAATTTTTTCCAGTTTACATAATTAAGTTATATCCTTTATA 1568	
Db 527 AGGCAACACGCAAGCTTTTCAGAGCTATGAGATGCTTCGCAATTTGAGTTTGTAGCTC 586	QY 1069 ACACCTTCAGTAATATATAAATCAATTTTAC-TTATGGTAATATATAGCTTAGTATAAG 1127	
QY 61 TTGGGGTGGCTATGTTTCTGCTTTGCTGTAGAAAATCCCATGAATAGACTGGTGGCAG 120	Db 1569 AAATCTCTCAGTAATCATATAAGCTTCATCTACTTTTGAANAATTTTATCTTAATATGTG 1628	
Db 587 TTGAGCTGCTCATGCTGTATGCCATCCCAAGAAATCCCAAGTGCATTGGTGAAG 646	QY 1128 GTGGTTTCCCACTGGAAAAAGACACAACTCTTTGGGAGAGGGAACCTTTGTGTA 1187	
QY 121 AGACTTGACACTGCTCTCCACTCATCGAATCTGGCTGATAGGGATGGGTAAATTTTCT 180	Db 1629 GTGGTTTCTGCTAGAAA-----ACAAACAAAAAATCTTTTGGAGAGGGAACCTCATGTA 1684	
Db 647 AGACTTGGCACTGCTTTCTACTCATCGAATCTGCTGATAGCAATGAGGTAATTTTCT 706	QY 1188 AACCCCAACAAACAAAGTCTAACTTTT----- 1214	
QY 181 TTTTGATTCCTACAGTCTTTTAAATGATGGTAATTTGGTGGTGGCTAGTT----- 234	Db 1685 AATACCAAAACAAAGGCTTAACITTTTGGGACCAAAATTTGTTTAATAATTTATTTTAA 1744	
Db 707 TTATGATTCCTACAGTCTGTAAGTGCATAGGTATCATTTTGATGGTTCCTTTACTAT 766	QY 1215 ----- 1214	
QY 235 -TTTAAAGATCCATTAATCAATGAAGTAAGTGTATTAATATATATGATGGTAAC 293	Db 1745 TTGATGAATTAAGAAAGTATATATTTATTTGTGTACAATATGATGTTTGAAGTATGTAT 1804	
Db 767 ATATAGAGATCTGTTATAAATAAAGATTCTGAG-CACATTTAGTACATGGGTGATAACT 825	QY 1215 -----TGGACCAAAATTTTATGCCCTTTTGTGATGAATTAATTTT 1256	
QY 294 ATGTTACTCAGAGAAATATATATAAAGATTATGAACCTTACAATACATTAATAAATGAATG 353	Db 1805 ACATTCGCAAGTGCACAAATGACCAAAATTTTATACCTTGTCTTGATTTTGA-TTTT 1863	
Db 826 ACATCAGCAGAAACATTTCTGTTAAAGTTATGAATGCTGGTGTGTTAAATAATGATTG 885	QY 1257 TAAAAATCTTCTCATTTAGCACCAACTGTGCAATTAAGAAAGTTTTCAGGGTATAGACAC 1316	
QY 354 TTGTTTCTCTTTTTCAGAACCTGATGATTCCTACTCTCGAAATTAATAATGTAAGTT 413	Db 1864 AAAAAATTTTCTCATTTAGCACCAACTGTGCACTGAAGAAATCTTTTCAGGGAATAGGCAC 1923	
Db 886 -TATTTCTTCTCTCCAGACTCTGAGGATTCCTGTTCTGTACATAAATAATGTAAGTT 944	QY 1317 ATTGAAGAACCAACTGCCACGGGAGGCTGTGGATAAACTATTCCAAAACTTGTCTTTT 1376	
QY 414 AAATATGATTTGATTAATAATGATTAAGTATGAGT-----TTTCAATTTTAACTATAAA 469	Db 1924 ACTGGAGAGTCAAACTGTGCAAGGGGTACTGTGGAAGACTATTCAAAACTTGTCTT 1983	
Db 945 AAATATGATTTGATTAATAATGATTAAGTATGAGT-----TTTCAATTTTAACTATAA 1004	QY 1377 AATAAAGAACACATAGAGCGCCAAAAAGTAAAGTAAAGACATTTTGGCAAAAACTTAAGT 1436	
QY 470 GTATCAGTTAACTTTGGGATGATTAATTTTATTTTATTTTATTTTATTTGTTGCGGATGT 529	Db 1984 AATAAAGAAATACATTTGACGGCCAAAAAGTAAAGTTACACATTTCAATGGAAGCTATATT 2043	
Db 1005 TCAATGATTTATCAITGGAACTATTTTATTTTCTATATTTTGTGTTTCAATGGTGGCTGT 1064	QY 1437 ATATTTGCTGACTGCTGCTGTTTTTTTTTTTTTTTTTTTCAAGAAATTCACAGTTTCTTA 1496	
QY 530 AAAT-TATGTCTTATGAATATTAAGAAATGATGTTAGGAATGGCTCTACAATTAAGTA 588	Db 2044 TGCTCTGGCTG-----TGCTATTTCTATGGAATTTGACAGTTTCTG 2085	
Db 1065 GAATGCTGTACTTATAAATATAGGAATGACTTT-----TTATCAAGTA 1109	QY 1497 CAATATCT-----CCTCTGTTCTTTTAAAGAAAGGTGTCAGAGAAAGATGGAGAG 1550	
QY 589 GAATCCATTAAGCAAGTGCATCAGCCCTTTTGTGATTTGATGTTCTCATCTCAAG 648	Db 2086 TAATACCTATTTGCTATTTTCTTTTTCACAGAAAGTGTGGAGAAAGACGGAGAG 2145	
Db 1110 GAATCCTTTAAACAGTGGATGAGCTCTTTGGTGTGTTGTTAGTTTGGCTTCCCAAG 1169	QY 1551 TGACAAAGTCTCAGACTACCTGCAAGTATTTCTTGGTGTATAATAACACCGAGTGGACAC 1610	
QY 649 AGCTCTGTTGTCAGGCAATTTTCCAAAGAAATCCATATTGGGTGAGAGATCTTCTAG 708	Db 2146 TAAACCAATTTCTAGACTACCTGCAAGATTTCTTGGTGTATGAACACCGAGTGGATA 2205	
Db 1170 AGCATGTTGTAGG-ATTTCTTCCAGAAAGATTCACACTGAGTGAAGTGGTGTAG 1228	QY 1611 CGGAAAGTTGAGAAACAAACCGGCTTATTTGTTAGTGGAGATTTTGGAG 1657	
QY 709 GCTCAATTCACCTCTGCTGTTGGCTTCTCCTCACCTCAACGTTTTTCTGAAAGTACTAGCA 768	Db 2206 TAGAAAGTTGAGACTAAACTGGTTTGTTCGAGCCAAAGATTTTGGAG 2252	
Db 1229 TCTCGTGGAGTTCTGAC-----TCTTTCTCACCTCAACGTTTCTGAAAGTATTAGCA 1283	RESULT 11	
QY 769 ACTTGGGGTTATTTTTAGAAATTTATGCTCAGTAGACATGAAAAATATACAGTGAAGTCT 828	ABX04379	
Db 1284 ACTCAGATTTATTTTTAGAACCATGATCAGTAGACATTAATAATATATAACAAATGCC- 1342	ID ABX04379 standard; cdna; 3230 BP.	
QY 829 ATATTAATAGTCACTTCCACATTTTAAATGATTTTAACTCTAATGGAATCATATACAT 888	XX ABX04379;	
Db 1343 --CTATATTAATTTCTGCTACTTAAATAATTTATGACTATATGATGGTGTGATGCAT 1400	AC AC	
QY 889 CTGGAGTATGTCATGGTCATATTAATAATTTTAAATTTGTAATCATTTAGTCTTAATAGA 948	DT DT	
Db 1401 TGAATATG---CCTGGTCAATTAATAATGTAATAATATAGTTT-ATTAGTCTAAATAGA 1456	XX 13-JAN-2003 (first entry)	
QY 949 ATAAAAATCCAGCTAGAACTATAGGAGAAATTTCTGAGGTGAGGTAAATCAGTAAAGCA 1008	XX Human Interleukin 5 cDNA.	
Db 1457 ATAAAAATCCAGCTAGAACTATAGGAGAACTATAGGAGAAATTTCTGAGGTGAGGTAAATGTC- 1513	DE DE	
QY 1009 GTTGTATTATACCTCGTAAGCATTTTATTTTCTCAATTAATCAATTTATATCAATTTGTA 1068	XX Human; ss; antisense; gene; interleukin 5; IL-5; IL-5 receptor; antiasthmatic; immunosuppressant; eosinophilic syndrome; asthma.	
	OS OS	
	XX Homo sapiens.	
	XX US2002128216-A1.	
	PN 12-SEP-2002.	
	XX 07-MAR-2001; 2001US-00800629.	
	PF 26-MAR-1999; 99US-00280799.	
	XX	
	PR	

PR 17-MAR-2000; 2000WO-US007318.

XX (DEAN/) DEAN N M.
PA (XARR/) KARRAS J G.
PA (MCKAY/) MCKAY R.
PA (MANO/) MANOHARAN M.
XX
XX
PI Dean NM, Karras JG, McKay R, Manoharan M;
XX
XX WPI; 2003-039602/03.

XX Novel antisense compound for treating disease/condition e.g. eosinophilic
PT syndrome or asthma associated with interleukin-5 or IL-5 receptor
PT expression or IL-5 signal transduction, modulates IL-5 signal
PT transduction.
XX
XX

PS Example 20; Page 48-49; 77pp; English.

XX The invention relates to an antisense compound of 8-30 nucleobases in
CC length, which modulates interleukin (IL)-5 signal transduction. Also
CC include are a pharmaceutical composition comprising the antisense
CC oligonucleotide and a pharmaceutically acceptable carrier or diluent, and
CC a diagnostic kit for detecting the expression level of the membrane form
CC versus soluble form of IL-5 receptor α . The antisense compound is useful
CC for modulating IL-5 signal transduction, modulating expression of
CC mammalian IL-5 or modulating the expression of mammalian IL-5 receptor α ,
CC in cells or tissues, for altering the ratio of the isoforms of mammalian
CC IL-5 receptor α in mammalian cells or tissues, treating a mammalian
CC having a disease or condition associated with IL-5 signal transduction,
CC IL-5 expression or IL-5 receptor α expression, where the disease or
CC condition include eosinophilic syndrome or asthma. An antisense compound
CC which alters splicing of an RNA encoding IL-5 receptor α is also useful
CC for treating a mammal having a disease or condition. The present sequence
CC is a cDNA encoding Human IL5, a target of the antisense compounds of the
CC invention
XX

SQ Sequence 3230 BP; 1027 A; 545 C; 622 G; 1036 T; 0 U; 0 Other;

Query Match 36.2%; Score 600.6; DB 7; Length 3230;
Best Local Similarity 67.8%; Pred. No. 5.1e-109;
Matches 1212; Conservative 0; Mismatches 384; Indels 191; Gaps 19;

QY 1 AGGCAACACTGACATTTTCAGAGCTATGAGATGCTCTTGAAATTTGAGTTTCTCTAGCTC 60
DB 527 AGGCAACGAGAACGTTTCAGAGCCATGAGGATGCTCTGCAATTTGAGTTTCTAGCTC 586
QY 61 TTGGGGTGCCTATGTTTCTGCTTCTGTAGAAAATCCCATGATAGACTGGTGGGAG 120
DB 587 TTGGAGCTGCTAGCTGTATGCCATCCACAGAAATCCCAAGTGCAATGGTGAAG 646
QY 121 AGACCTTGACACTGCTCTCCACTCATGCACTTGGCTGTATAGGGATGGGTAATTTCT 180
DB 647 AGACCTTGGCACTGCTTTCTACTCATCGAACTCTGCTGATAGCAATGAGTAATTTCT 706
QY 181 TTTTGATCTCTACAGTCTTTAAAATGATGGGTAATTTGGTGGTGGCTAGTT----- 234
DB 707 TTATGATCTCTACAGTCTGTAAAGTCATAGGTAATCATTTTGATGGTTCTTTACTAT 766
QY 235 -TTTAAAGATCCATATCAATATGAAGTAATGAGTGTAAATATATATATATGCGTAACC 293
DB 767 ATATAGAGATCTGTATATAATAATAAGATTTCTGAG-CACATTAGTACATGGGTGATACT 825
QY 294 ATGTTACTCAGAAGAAATATATATAAAGTTATGAACCTTACAATACATTAATAAATGAATG 353
DB 826 ACATCAGCAAGAACATCTGTAAAGTTATGATGCTGGTGTGCTGTGTAATAATGATTTG 885
QY 354 TTGTTTCTTTCTTTTTCAGAACTGATGATTTCTACTCTCTGAAAATAAATAATGTAAGTT 413
DB 886 -TATTTCTTCTCTCTCCAGACTCTGAGGATTTCTGTTCTCTGTATACATAAATAATGTAAGTT 944
QY 414 AATATTGATTTGTAATAAATGATTTACATGATCAG-----TTTCATATTTTAACTATAA 469
DB 945 AATATTGATTTGTAATAAATGATGGCAATGAATGAATTAATTTCTGTTTAACTGTAAAT 1004

QY 470 GTATCAGTTAAACATTTGGGATGATTAATTTTATCTATTTTCTATTTTATAGTGGGATGT 529
DB 1005 TCATTAGTTATCATTTGGAACCTATTTATTTTCTATATTTTCTATTTTCTATTTGCTGCT 1064
QY 530 AAAT-TATGTCTTATGAATATAGGAATGCTGTAGGAATGGCTCTACAATATTAAGTA 588
DB 1065 GAATGCTGTACTTATAAATATGAGGAATGACTTT-----TTATCAAGTA 1109
QY 589 GAATCCATTAAGCAAGTGGATCAGCCCTTTTGTAGTGTCTCAGTTCTCCATCTCAAG 648
DB 1110 GAATCCCTTTAAACAAGTGATAGGCTCTTTGGTGAATGTTTCTTTAGTTTGGCTTCCCAAG 1169
QY 649 AGCCTCGTGTGAGGCAATCTTTTCCAAAAGAAATTCATATTCGGTGCAGAGATCTCTAG 708
DB 1170 AGCATCGTGTGAGG-ATTTCTTTCCAGAAGGATCCACACTGAGTGAGAGGTGGTGTAG 1228
QY 709 GGTCCATTCACCTCTGTGCTGGCTTCTCCTCACTCAACGTTTTTCTGAAAAGTACTAGCA 768
DB 1229 TCTCGTGCAGTTCTGAC-----TCTTTCTCACTCTAACGTTTCTGAAAAGTATTAGCA 1283
QY 769 ACTTGGGCTTATATTTTATAGAAATATGCTCAGTAGACATGAAATATACAGTGAAGTCT 828
DB 1284 ACTCAGAATTTATTTTATAGAACCATGATCAGTAGACATTAATAATATATAACAATGCC- 1342
QY 829 ATATTAAATAGTCACTCCACATATTTAAATGAATTTTAACTCTAATGGAATCATATACAT 888
DB 1343 --CTATATTAATAATTTCTGCATCTTAAATAATTAATGACTATATCATGCTGTGTATGCA 1400
QY 889 CTGGAGTATGTCATGGCTCATATTAATAATGTTAAAGTGTGATATCATTTAGTCTAAATAGA 948
DB 1401 TGAATATG---CCTGCTCATATTAATAATGTTAAATATATATAGTTT-ATTAGTCTAAATAGA 1456
QY 949 ATAAATTTACCAGCTAGAACTATACGAGGAAATTTCTGAGGTGAGGTAATCAGTAAAGCA 1008
DB 1457 ATAAAACTACCAGCTAGAACTGTAGAAACACAT--TGATATGAGTTTAAATGTATAATGC- 1513
QY 1009 GTTGTATTTATACCTCGTAAGCATTTATTTTTCATTAATCATTTCTATTTATTTCTGTA 1068
DB 1514 -----ATTACACTTCCAAAACATTTTTTCCAGTTTACATAATTAAGTTATATCTTTATA 1568
QY 1069 ACACCTCTCAGTAATATATAAACATCATTTTAC-TTATGGTAAATATATAGCTTAGTATAAG 1127
DB 1569 AAACCTCTCAGTAATCATATAAGCTTCTATCTACTTTGTGAAATTTTATCTTAATATGTG 1628
QY 1128 GTGGTTTCCACCTGGGAAAAGACAGTAAAAACCTCTTCGGAGAGAGGGAACCTGTGTGTA 1187
DB 1629 GTGGTTTGTGCTAGAAA-----ACAAACAAAAAACTCTTTGGAGAGGGAACCTCATGTA 1684
QY 1188 AACCCCAACAAACAAAGCTTAACTTTT-----1214
DB 1685 AATACCAACAAACAAAGCTTAACCTTTGGGACCAAAATGTTTAAATATTTTAA 1744
QY 1215 -----1214
DB 1745 TTGATGAATTAATAAGTATATATATTTATTTGTGTAATATGATGTTTGAAGTATGTAT 1804
QY 1215 -----TGGACCAAAATTTTATGCTTGTGTTTGTGATGAATATATATTTT 1256
DB 1805 ACATTGCAAGATGGCAATGGACCAATTTTATACCTTGTCTTGTATTTTGTGA-TTTT 1863
QY 1257 TAAATCTTCTCTCATTTAGCACCACCTGTGCTGATTAAGAAGTTTTTTCAGGGGTATAGACAC 1316
DB 1864 AAAAATTTTCTCATTTAGCACCACCTGTGCTGCTGCAAGAAATCTTTTCAGGGAATAGGCAC 1923
QY 1317 ATTGAAGAACCAAACTGCCGCGGGAGGCTGTGGATAAACTATTTCCAAAACCTGTCTTT 1376
DB 1924 ACTGGAGAGTCAAACTGTGCAAGGGGGTACTGTGGAAGAGCTATTTCAAAAAATTTGCTCT 1983
QY 1377 AATAAAGAACACATAGAGCGCCAAAAGTAAGTTTAAAGACATTTTGGCAAAACCTTAAGT 1436
DB 1984 AATAAAGAAATACATTTGACGCCCAAAAAGTAAGTTACACATTCATTCATGGAGCTATATT 2043


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XX PI Daly M, Hudson TJ, Lander ES, Rioux J, Siminovitch K;
XX XX
XX DR WPI; 2001-367874/38.
XX XX
XX PT Testing for the presence of polymorphisms associated with inflammatory
XX PT bowel disease, using a hybridization assay.
XX XX
XX PS Disclosure; Page 262; 463pp; English.
XX XX
XX CC The present invention describes a method for detecting the presence of
XX CC polymorphisms associated with inflammatory bowel diseases such as
XX CC ulcerative colitis and Crohn's disease. The methods can be used to detect
XX CC the presence of genetic polymorphisms associated with inflammatory bowel
XX CC disease and correlating their occurrence with disease states. They may be
XX CC used in this way for phenotypic correlations, forensics, paternity
XX CC testing, medicine and genetic analysis. The present sequence is a gene
XX CC containing a polymorphic site described in the exemplification of the
XX CC invention
XX SQ Sequence 700 BP; 242 A; 101 C; 137 G; 218 T; 0 U; 2 Other;

Query Match      13.4%; Score 221.6; DB 4; Length 700;
Best Local Similarity 75.3%; Pred. No. 2.4e-34;
Matches 338; Conservative 0; Mismatches 85; Indels 26; Gaps 4;

QY 1215 TGGACCAAAATTTTATGCTTGTGTTGATGAATATATTTTAAATCTTCTCTATTTA 1274
DB 83 TGGACCAAAATTTTATGCTTGTGTTGATGAATATATTTTAAATCTTCTCTATTTA 141
QY 1275 GCACCAACTGCAATTAAGAAGTTTTCAGGTATAGACACATTCAGAACCAACTGC 1334
DB 142 GCACCAACTGCACTGAAGAAATCTTTCAGGGAATAGGCACACTGGAGAGTCMAACTGT 201
QY 1335 CCACGGGGAGCTGTGATATAAATCTTCCAAATCTCTTTAATAAAGAACACATAGA 1394
DB 202 GCAAGGGGTACTGTGGAAGACTATTNAAAACCTTGTCTCTAATAAGAAATACATTGA 261
QY 1395 GCGCCAAAAGTAAGTTAAAGACATTTGGCAAAAACCTTAAGTATATTTGCTGACTCTGC 1454
DB 262 CGGCCAAAAGTAAGTTACACACATTT-----CAATGGAAGCTATTTTGTCTGGCTGTGC 316
QY 1455 CTGTTTTTTTTTTTTTTTTTACAGAAATGACAGTTTCTCTACAATATCT-----CCTC 1508
DB 317 CTATTTCTAT-----GGAAATGACAGTTTCTCTGTAATACCTATTGTGCTATT 362
QY 1509 TGTTCCTTTTACAGAAAAGGTGTGCGAGGAAAGATGGAGAGTGACAAAAGTTCTTAGACT 1568
DB 363 TCTTTTTTTCACAGAAAAGGTGTGGAAGAAAGACGAGAGTAACCAATTCCTTAGACT 422
QY 1569 ACCTGCAAGTATTTCTTGGTGTATATACACCCAGTGGACACCGGAAAGTTGAGAACAAA 1628
DB 423 ACCTGCAAGAGTTTCTTGGTGTATATGACACCCAGTGGATATAGAAAGTTGAGACTAA 482
QY 1629 CCGGCTTATTGTAGTGAAGATTTTGGAG 1657
DB 483 CTGGTTTGTGACGCAAGATTTTGGAG 511

RESULT 14
AAH92591
ID AAH92591 standard; DNA; 700 BP.
XX AC AAH92591;
XX XX
XX DT 09-OCT-2001 (first entry)
XX XX
XX DE Human inflammatory bowel disease related gene fragment IGR1291a.
XX KW Human; inflammatory bowel disease; Crohn's disease; ulcerative colitis;
XX KW single nucleotide polymorphism; SNP; chromosome 19p13; paternity test;
XX KW chromosome 5q31-33; forensic test; gene therapy; ds.
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OS Homo sapiens.
XX XX
XX PN WO200142511-A2.
XX XX
XX PD 14-JUN-2001.
XX XX
XX PF 11-DEC-2000; 2000WO-US033632.
XX XX
XX PR 10-DEC-1999; 98US-0170257P.
XX PR 10-APR-2000; 2000US-0196046P.
XX XX
XX PA (WHED ) WHITEHEAD INST BIOMEDICAL RES.
XX PA (ELLI-) ELLIPSIS BIOTHERAPEUTICS CORP.
XX XX
XX PI Daly M, Hudson TJ, Lander ES, Rioux J, Siminovitch K;
XX XX
XX DR WPI; 2001-367874/38.
XX XX
XX PT Testing for the presence of polymorphisms associated with inflammatory
XX PT bowel disease, using a hybridization assay.
XX XX
XX PS Disclosure; Page 261; 463pp; English.
XX XX
XX CC The present invention describes a method for detecting the presence of
XX CC polymorphisms associated with inflammatory bowel diseases such as
XX CC ulcerative colitis and Crohn's disease. The methods can be used to detect
XX CC the presence of genetic polymorphisms associated with inflammatory bowel
XX CC disease and correlating their occurrence with disease states. They may be
XX CC used in this way for phenotypic correlations, forensics, paternity
XX CC testing, medicine and genetic analysis. The present sequence is a gene
XX CC containing a polymorphic site described in the exemplification of the
XX CC invention
XX SQ Sequence 700 BP; 216 A; 117 C; 133 G; 234 T; 0 U; 0 Other;

Query Match      13.0%; Score 216; DB 4; Length 700;
Best Local Similarity 74.3%; Pred. No. 3e-33;
Matches 315; Conservative 0; Mismatches 100; Indels 9; Gaps 3;

QY 1 AGGCAAAACATGAAACATTCAGAGCTATGAGAATGCTTCTGAAATTTGATTTGCTAGCTC 60
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QY 61 TTGGGGCTGCTATGTTTCTGCTTGTGTAGAAATCCCATGAATAGACTGGTGGCAG 120
DB 339 TTGGAGCTGCTTACGTGTATGCCATCCCAACAGAAATCCCAAGTGCAATGGTGAAG 398
QY 121 AGACCTTGACACTGTCTCTCCACTCATCGAACTTGGCTGATAGCGGATGGGTAATTTTCT 180
DB 399 AGACCTTGGCACTGCTTCTACTCATCGAACTTGTCTGATAGCCAAATGAGTAAATTTCT 458
QY 181 TTTTCATTTCTACAGTCTTTTAAATGCAATGGTAAATTTGGTGGTGGCTAGTT----- 234
DB 459 TTATCATTTCTACAGTCTGTAAAGTGCAATAGTAAATCATTTGTATGTTGCTTCTTACTAT 518
QY 235 -TTTAAAGATCCATTATCAATAATGAAGTATAGTGTTAATAATATATATATGGTAACT 293
DB 519 ATATAGAGATCTGTTATTAATAATAAGTTCAGAG-CACATTAGTACATGGGTGAACT 577
QY 294 ATGTTTACTCAGAAGAATTATATTTAAAGCTTATGAACCTTATACAATACATTAATAATGATG 353
DB 578 ACATCACCAGCAAAACATTTCTGTAAAAGTTATGAATGCTGGTGTGCTGTAAAAATGATTG 637
QY 354 TTGTTTCTCTTTCTTTTTCAGAACCTGATGANTCTTACTCTCTGAAATAAATAATGTAAGTT 413
DB 638 -TATTTCCTTTCTCTCCAGACTCTGAGGATTTCTGTTTCTTCTGTACATAAAAAATGTAAGTT 696
QY 414 AAAT 417
DB 697 AAAT 700

RESULT 15
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

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(without alignments)
10561.839 Million cell updates/sec

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Searched: 3470272 seqs, 21671516995 residues

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5	170	10.3	610	6	AR254492	Sequence
C 6	170	10.3	610	6	AR254493	Sequence
7	170	10.3	610	6	BD211558	Canine an
C 8	170	10.3	610	6	BD211559	Canine an
9	144	8.7	402	6	AR241538	Sequence
C 10	144	8.7	402	6	AR241539	Sequence
11	144	8.7	402	6	AR254494	Sequence
C 12	144	8.7	402	6	AR254495	Sequence
13	144	8.7	402	6	BD211560	Canine an
C 14	144	8.7	402	6	BD211561	Canine an
15	144	8.7	405	6	AR300436	Sequence
16	144	8.7	405	6	AX083339	Sequence
17	129	7.8	343	6	AX083948	Sequence
C 18	129	7.8	345	6	AR241540	Sequence
19	129	7.8	345	6	AR241541	Sequence
C 20	129	7.8	345	6	AR254496	Sequence
21	129	7.8	345	6	AR254497	Sequence
C 22	129	7.8	345	6	BD211562	Canine an
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C 24	129	7.8	356	4	AF091133	Canis fam
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26	43	2.6	1140	4	OALV1	U17052 Ovis aries
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28	42	2.5	529	4	SSC133452	AJ133452 Sus scrofa
29	41	2.5	405	4	AF068770	Felis cat
30	41	2.5	405	4	BTNTLEUS	Z67872 B.taurus mR
31	41	2.5	838	4	AF025436	Felis cat
32	39	2.4	405	4	ECU91947	U91947 Equus caball
33	39	1.8	354	4	AF051372	Felis cat
34	30	1.8	144571	9	BX664726	Human DNA
C 35	29	1.7	143520	9	BX005214	Human DNA
C 36	29	1.7	159990	9	AL954139	Human DNA
C 37	29	1.7	163795	9	BX005192	Human DNA
C 38	29	1.7	174366	9	AL590491	Human DNA
C 39	29	1.7	209112	2	AC084146	Human DNA
40	28	1.7	405	9	AF294756	Homo sapi
41	28	1.7	564	10	CPU34588	U34588 Cavia porce
C 42	28	1.7	162083	9	AC005962	Homo sapi
43	28	1.7	232707	2	BX323828	Danio rer
44	27	1.6	186373	9	AC006229	Homo sapi
45	27	1.6	188500	2	AC109790	Bos taurus

ALIGNMENTS

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LOCUS	Canis familiaris interleukin-5 gene, complete cds.				
DEFINITION	Canis familiaris interleukin-5 gene, complete cds.				
ACCESSION	AF331920				
VERSION	AF331920.1	GI:15919182			
KEYWORDS	Canis familiaris (dog)				
SOURCE	Canis familiaris				
ORGANISM	Canis familiaris				
REFERENCE	1 (bases 1 to 1658)				
AUTHORS	Yang, S., Sellins, K.S., Weber, E. and McCall, C.				
TITLE	Canine interleukin-5: molecular characterization of the gene and expression of biologically active recombinant protein				

J. Interferon Cytokine Res. 21 (6), 361-367 (2001)
 21334408
 MEDLINE
 11440633
 PUBLISHED
 2 (bases 1 to 1658)
 REFERENCE
 Yang, S.
 AUTHORS
 Direct Submission
 TITLE
 Submitted (22-DEC-2000) Immunology, Heeka Corporation, 1613
 JOURNAL Prospect Parkway, Ft Collins, CO 80525, USA
 Location/Qualifiers
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 /db_xref="taxon:9615"
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 Best Local Similarity 100.0%; Pred. No. 0;
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Qy 61 TTGGGGTGCGTATGTTTCTGCTTTGCTGTAGAAAATCCCATGAATAGACTGGTGGCAG 120
 Db 61 TTGGGGTGCGTATGTTTCTGCTTTGCTGTAGAAAATCCCATGAATAGACTGGTGGCAG 120

Qy 121 AGACCTTGACACTGCTCTCCACTCATCGAATCTGGCTGATAGCGATGGGTAAATTTCT 180
 Db 121 AGACCTTGACACTGCTCTCCACTCATCGAATCTGGCTGATAGCGATGGGTAAATTTCT 180

Qy 181 TTTTGTCTTACAGTCTTTTAAATGTCATGGTAATTTGGTGGTGGCTAGTTTAA 240
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Qy 241 GATCCATATCAATATGAAGTAATGAGTGTATTAATATATATATATATATATATATAT 300
 Db 241 GATCCATATCAATATGAAGTAATGAGTGTATTAATATATATATATATATATATATAT 300

Qy 301 TCAGAAGAAAT 360
 Db 301 TCAGAAGAAAT 360

Qy 361 CTCTCTTTTTCAGAACCTGATGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 420
 Db 361 CTCTCTTTTTCAGAACCTGATGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 420

Qy 421 GATTGTATAAATCATATACATGATGATGATGATGATGATGATGATGATGATGATGATGAT 480
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Qy 481 CATTGGGATGATTTTATCTATTTTATCTATTTTATCTATTTTATCTATTTTATCTATTT 540
 Db 481 CATTGGGATGATTTTATCTATTTTATCTATTTTATCTATTTTATCTATTTTATCTATTT 540

Qy 541 TTATGAATATAGGAATGGTGTAGGAATGGCTCTCAATATTAATTAAGTACCAATTAAG 600
 Db 541 TTATGAATATAGGAATGGTGTAGGAATGGCTCTCAATATTAATTAAGTACCAATTAAG 600

Qy 601 CAAGTGGATCAGGCCCTTTTGTGATGTTGTGATGTTGTGATGTTGTGATGTTGTGATGTT 660

Db 601 CAAGTGGATCAGGCCCTTTTGTGATGTTGTGATGTTGTGATGTTGTGATGTTGTGATGTT 660
 Qy 661 GGCATTTCTTCCAAAGAAATTCATATTTGGTTCAGAGATATCTTCTAGGCTCAATTCACC 720
 Db 661 GGCATTTCTTCCAAAGAAATTCATATTTGGTTCAGAGATATCTTCTAGGCTCAATTCACC 720
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 Qy 781 ATTTTGAATATATGGTTCAGTAGACATGAAATATACAGTGAAGTCTCTATTAATAGTC 840
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 Qy 841 ACTTCCACATATTTAAATGATTTTAACTCTAATGGAATCATATACATCTGGAGTATGTC 900
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 Db 1081 AATTATATAAATCATTTTACTTATGTTAAATATAGCTTATAGTGAAGTGGTTCCTCACC 1140
 Qy 1141 TGGAAAGACACAGTAATTAATCACTTGGGAGAGGAACTTGTGTAATCAATCAATCAATCA 1200
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 Qy 1201 AAAGTCTAACTTTTGGACCAAAATTTTATGCTTGTGTTTGTGATGAATTTATTTTAA 1260
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 Qy 1261 ATCTTCTCATTTAGACCAAACTGTGCATTTAAAGAGTTTTCAGGATAGACACATTTG 1320
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 Qy 1321 AAGAACCAAACTGCCCGGAGGCTGTGATAACTATTTCCTCAAACTTGTCTTTAATA 1380
 Db 1321 AAGAACCAAACTGCCCGGAGGCTGTGATAACTATTTCCTCAAACTTGTCTTTAATA 1380
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 Db 1501 ATCTCTCTGTTTCTTTTAAACAGAAAGGTTGTCAGGAGAAAGATGGAGAGTGACAAAGTT 1560
 Qy 1561 CCTAGACTACCTGCAAGTATTTCTTGGTGAATTAATCAACCCGAGTGGACCCGGAAGTTG 1620
 Db 1561 CCTAGACTACCTGCAAGTATTTCTTGGTGAATTAATCAACCCGAGTGGACCCGGAAGTTG 1620
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Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 TTGGGGCTGCTATGTTTCTGCTTTCCTGCTAGAAAATCCCATGAATAGACTGGTGGCAG 120
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RESULT 6
AR254493/c
LOCUS AR254493 610 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 82 from patent US 6482403.
ACCESSION AR254493
VERSION AR254493.1 GI:27303381
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 610)
AUTHORS Sim,G.-K., Yang,S., Dreitz,M.J. and Wonderling,R.S.
TITLE Canine IL-13 immunoregulatory proteins and uses thereof
JOURNAL Patent: US 6482403-A 82 19-NOV-2002;
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DB 548 TTGGGGCTGCTATGTTTCTGCTTTCCTGCTAGAAAATCCCATGAATAGACTGGTGGCAG 489
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RESULT 7
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LOCUS BD211558 610 bp DNA linear PAT 17-JUL-2003
DEFINITION Canine and feline immunoregulatory proteins, nucleic acid molecules
and method of using the same.
ACCESSION BD211558
VERSION BD211558.1 GI:33021328
KEYWORDS JP 2002516104-A/64.
SOURCE Canis familiaris (dog)
ORGANISM Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE 1 (bases 1 to 610)
AUTHORS Sim,G., Yang,S., Dreitz,M.J. and Wonderling,R.S.

RESULT 8
BD211559/c
LOCUS BD211559 610 bp DNA linear PAT 17-JUL-2003
DEFINITION Canine and feline immunoregulatory proteins, nucleic acid molecules
and method of using the same.
ACCESSION BD211559
VERSION BD211559.1 GI:33021329
KEYWORDS JP 2002516104-A/65.
SOURCE Canis familiaris (dog)
ORGANISM Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE 1 (bases 1 to 610)
AUTHORS Sim,G., Yang,S., Dreitz,M.J. and Wonderling,R.S.

TITLE Canine and feline immunoregulatory proteins, nucleic acid molecules
and method of using the same
Patent: JP 2002516104-A 64 04-JUN-2002;
JOURNAL HESKA CORP
COMMENT OS Canis familiaris (dog)
PN JP 2002516104-A/64
PD 04-JUN-2002
PF 28-MAY-1999 JP 2000551002
PR 29-MAY-1998 US 60/087306
PI GEKKEE SIM,SHUMIN YANG,MATTHEW J DREITZ,RAWANI S WONDERLING PC
C12N15/09,A61K31/7088,A61K38/21,A61K39/00,A61K39/395,
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molecules and
CC method of using the same
FH Key Location/Qualifiers
FT CDS (29)..(430).

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Query Match      10.3%; Score 170; DB 6; Length 610;
Best Local Similarity 100.0%; Pred. No. 3e-74;
Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 8
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DEFINITION Canine and feline immunoregulatory proteins, nucleic acid molecules
and method of using the same.
ACCESSION BD211559
VERSION BD211559.1 GI:33021329
KEYWORDS JP 2002516104-A/65.
SOURCE Canis familiaris (dog)
ORGANISM Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE 1 (bases 1 to 610)
AUTHORS Sim,G., Yang,S., Dreitz,M.J. and Wonderling,R.S.

TITLE Canine and feline immunoregulatory proteins, nucleic acid molecules
and method of using the same
Patent: JP 2002516104-A 65 04-JUN-2002;
JOURNAL HESKA CORP
COMMENT OS Canis familiaris (dog)
PN JP 2002516104-A/65
PD 04-JUN-2002
PF 28-MAY-1999 JP 2000551002
PR 29-MAY-1998 US 60/087306
PI GEKKEE SIM,SHUMIN YANG,MATTHEW J DREITZ,RAWANI S WONDERLING PC
C12N15/09,A61K31/7088,A61K38/21,A61K39/00,A61K39/395,
PC A61K39/395,
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PC C07K14/54,
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PC G01N33/50,C12N15/00,A61K37/02,A61K37/66,C12N5/00 CC Canine
and feline immunoregulatory proteins, nucleic acid CC
molecules and
CC method of using the same
FH Key Location/Qualifiers
FT CDS (29)..(430).

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and feline immunoregulatory proteins, nucleic acid CC
molecules and
CC method of using the same
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Best Local Similarity 100.0%; Pred. No. 38-74; Indels 0; Gaps 0;
Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 61 TTGGGCTGCTATGTTCTGCTTTGCTGTAGAAAATCCCATGAAATAGACTGTGGCAG 120
DB 548 TTGGGCTGCTATGTTCTGCTTTGCTGTAGAAAATCCCATGAAATAGACTGTGGCAG 489
QY 121 AGACCTTGACATGCTCTCCACTCATCGAACTTGGCTGATAGCGATGGG 170
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RESULT 9

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DEFINITION Sequence 83 from patent US 6471957.
ACCESSION AR241538
VERSION AR241538.1 GI:27287247
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 402)
AUTHORS Sim,G.-K., Yang,S., Dreitz,M.J. and Wonderling,R.S.
TITLE Canine IL-4 immunoregulatory proteins and uses thereof
JOURNAL Patent: US 6471957-A 83 29-OCT-2002;
FEATURES Location/Qualifiers
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/organism="unknown"
/mol_type="genomic DNA"

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Query Match 8.7%; Score 144; DB 6; Length 402;
Best Local Similarity 100.0%; Pred. No. 4.2e-61;
Matches 144; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 27 ATGGAATGCTTCTGAATTTGAGTTTGTAGCTCTTGGGCTGCCCTATGTTTCTGCCCTTT 86
DB 1 ATGGAATGCTTCTGAATTTGAGTTTGTAGCTCTTGGGCTGCCCTATGTTTCTGCCCTTT 60
QY 87 GCTGTAGAAAATCCCATGAAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACTCAT 146
DB 61 GCTGTAGAAAATCCCATGAAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACTCAT 120
QY 147 CGAACTTGGCTGATAGCGATGGG 170
DB 121 CGAACTTGGCTGATAGCGATGGG 144

RESULT 10

AR241539/c

LOCUS AR241539 402 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 84 from patent US 6471957.
ACCESSION AR241539
VERSION AR241539.1 GI:27287248
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 402)
AUTHORS Sim,G.-K., Yang,S., Dreitz,M.J. and Wonderling,R.S.
TITLE Canine IL-4 immunoregulatory proteins and uses thereof
JOURNAL Patent: US 6471957-A 84 29-OCT-2002;
FEATURES Location/Qualifiers
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DB 282 CGAACTTGGCTGATAGCGATGGG 259

RESULT 11

AR254494
LOCUS AR254494 402 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 83 from patent US 6482403.
ACCESSION AR254494
VERSION AR254494.1 GI:27303382
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 402)
AUTHORS Sim,G.-K., Yang,S., Dreitz,M.J. and Wonderling,R.S.
TITLE Canine IL-13 immunoregulatory proteins and uses thereof
JOURNAL Patent: US 6482403-A 83 19-NOV-2002;
FEATURES Location/Qualifiers
source 1..402
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Best Local Similarity 100.0%; Pred. No. 4.2e-61;
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QY 87 GCTGTAGAAAATCCCATGAAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACTCAT 146
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QY 147 CGAACTTGGCTGATAGCGATGGG 170
DB 121 CGAACTTGGCTGATAGCGATGGG 144

RESULT 12

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AR254495/c
LOCUS AR254495 402 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 84 from patent US 6482403.
ACCESSION AR254495
VERSION AR254495.1 GI:27303383
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 402)
AUTHORS Sim,G., Yang,S., Dreitz,M.J. and Wonderling,R.S.
TITLE Caniney IL-13 immunoregulatory proteins and uses thereof
JOURNAL Patent: US 6482403-A 84 19-NOV-2002;
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Db 282 CGAACTTGGCTGATAGCGGATGG 259

RESULT 13
BD211560 402 bp DNA linear PAT 17-JUL-2003
LOCUS Canine and feline immunoregulatory proteins, nucleic acid molecules
DEFINITION Canine and method of using the same.
ACCESSION BD211560.1 GI:33021330
VERSION BD211560.1
KEYWORDS JP 2002516104-A/66.
SOURCE Canis familiaris (dog)
ORGANISM Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE 1 (bases 1 to 402)
AUTHORS Sim,G., Yang,S., Dreitz,M.J. and Wonderling,R.S.
TITLE Canine and feline immunoregulatory proteins, nucleic acid molecules
JOURNAL Patent: JP 2002516104-A 66 04-JUN-2002;
HESKA CORP
OS Canis familiaris (dog)
PN JP 2002516104-A/66
PD 04-JUN-2002
PF 28-MAY-1999 JP 2000551002
PR 29-MAY-1998 US 60/087306
PI GEKKEE SIM, SHUMIN YANG, MATTHEW J DREITZ, RAMANI S WONDERLING PC
C12N15/09,A61K31/7088,A61K38/00,A61K39/00,A61K39/395,
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PC C07K14/54,
PC C07K14/56,C07K16/24,C07K16/28,C12N1/21,C12N5/10, PC
G01N33/15,
HESKA CORP
OS Canis familiaris (dog)
PN JP 2002516104-A/66
PD 04-JUN-2002
PF 28-MAY-1999 JP 2000551002
PR 29-MAY-1998 US 60/087306
PI GEKKEE SIM, SHUMIN YANG, MATTHEW J DREITZ, RAMANI S WONDERLING PC
C12N15/09,A61K31/7088,A61K38/00,A61K39/00,A61K39/395,
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PC C07K14/54,
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PC G01N33/50,C12N15/00,A61K37/02,A61K37/66,C12N5/00 CC Canine
and feline immunoregulatory proteins, nucleic acid CC
molecules and
CC method of using the same
FH Key Location/Qualifiers
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Qy 27 ATGAGAATGCTTCTGAATTTGAGTTTCTAGCTCTTGGGGCTGCCCTATGTTTCTGCTTT 86

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Matches 144; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 27 ATGAGAATGCTTCTGAATTTGAGTTTCTAGCTCTTGGGGCTGCCCTATGTTTCTGCTTT 86
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Qy 87 GCTGTAGAAAATCCCATGAATAGACTGGTGGGAGACCTTGACACTGCTCTCCACTCAT 146
Db 61 GCTGTAGAAAATCCCATGAATAGACTGGTGGGAGACCTTGACACTGCTCTCCACTCAT 120
Qy 147 CGAACTTGGCTGATAGCGGATGG 170
Db 121 CGAACTTGGCTGATAGCGGATGG 144

RESULT 14
BD211561/c 402 bp DNA linear PAT 17-JUL-2003
LOCUS Canine and feline immunoregulatory proteins, nucleic acid molecules
DEFINITION Canine and method of using the same.
ACCESSION BD211561.1 GI:33021331
VERSION BD211561.1
KEYWORDS JP 2002516104-A/67.
SOURCE Canis familiaris (dog)
ORGANISM Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE 1 (bases 1 to 402)
AUTHORS Sim,G., Yang,S., Dreitz,M.J. and Wonderling,R.S.
TITLE Canine and feline immunoregulatory proteins, nucleic acid molecules
JOURNAL Patent: JP 2002516104-A 67 04-JUN-2002;
HESKA CORP
OS Canis familiaris (dog)
PN JP 2002516104-A/67
PD 04-JUN-2002
PF 28-MAY-1999 JP 2000551002
PR 29-MAY-1998 US 60/087306
PI GEKKEE SIM, SHUMIN YANG, MATTHEW J DREITZ, RAMANI S WONDERLING PC
C12N15/09,A61K31/7088,A61K38/00,A61K39/00,A61K39/395,
PC A61K39/395,
PC A61K45/00,A61K48/00,A61P37/02,A61P37/04,C07K14/475,C07K14/535,
PC C07K14/54,
PC C07K14/56,C07K16/24,C07K16/28,C12N1/21,C12N5/10, PC
G01N33/15,
PC G01N33/50,C12N15/00,A61K37/02,A61K37/66,C12N5/00 CC Canine
and feline immunoregulatory proteins, nucleic acid CC
molecules and
CC method of using the same
FH Key Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 4.2e-61;
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Qy 27 ATGAGAATGCTTCTGAATTTGAGTTTCTAGCTCTTGGGGCTGCCCTATGTTTCTGCTTT 86

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Db 402 ATGAGATGCTTCTGAATTTGAGTTTCTAGCTCTTGGGGCTGCCTATGTTTCTGCCTTT 343
Qy 87 GCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACTCAT 146
Db 342 GCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACTCAT 283
Qy 147 CGAACTTGGCTGATAGCGGATGGG 170
Db 282 CGAACTTGGCTGATAGCGGATGGG 259
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RESULT 15

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AR300436
LOCUS AR300436 405 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 1 from patent US 6537781.
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ACCESSION AR300436
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VERSION AR300436.1 GI:31687875
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KEYWORDS

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SOURCE Unknown.
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ORGANISM Unknown.
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Unclassified.
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REFERENCE 1 (bases 1 to 405)
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AUTHORS Guo,H., Lawton,R., Mermer,B. and Aiyappa,A.P.
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TITLE Methods and compositions concerning canine interleukin 5
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JOURNAL Patent: US 6537781-A 1 25-MAR-2003;
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Db 1 ATGAGATGCTTCTGAATTTGAGTTTCTAGCTCTTGGGGCTGCCTATGTTTCTGCCTTT 60

Qy 87 GCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACTCAT 146
Db 61 GCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACTCAT 120

Qy 147 CGAACTTGGCTGATAGCGGATGGG 170
Db 121 CGAACTTGGCTGATAGCGGATGGG 144
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